ATP1A2. ATPase, Class I, Type 8B, Member 2 (ATP8B2, Accession XM_036933) is another VGAM2505 host target gene. ATP8B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP8B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8B2 BINDING SITE, designated SEQ ID:32513, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84751] Another function of VGAM2505 is therefore inhibition of ATPase, Class I, Type 8B, Member 2 (ATP8B2, Accession XM_036933). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8B2. Basigin (OK blood group) (BSG, Accession XM_042018) is another VGAM2505 host target gene. BSG BINDING SITE1 and BSG BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BSG, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BSG BINDING

SITE1 and BSG BINDING SITE2, designated SEQ ID:33668 and SEQ ID:7457 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84752] Another function of VGAM2505 is therefore inhibition of Basigin (OK blood group) (BSG, Accession XM_042018), a gene which is a LEUKOCYTE ACTIVATION ANTIGEN and a member of the immunoglobulin superfamily. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BSG. The function of BSG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM958.Calcium Channel, Voltage-dependent, Alpha 2/delta Subunit 2 (CACNA2D2, Accession NM_006030) is another VGAM2505 host target gene. CACNA2D2 BINDING SITE1 through CACNA2D2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CACNA2D2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CACNA2D2 BINDING SITE1 through CACNA2D2 BINDING

SITE3, designated SEQ ID:12652, SEQ ID:12649 and SEQ ID:12650 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84753] Another function of VGAM2505 is therefore inhibition of Calcium Channel, Voltage-dependent, Alpha 2/delta Subunit 2 (CACNA2D2, Accession NM_006030), a gene which is a calcium channel protein which plays an important role in excitation-contraction coupling. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNA2D2. The function of CACNA2D2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM203.Cadherin 5, Type 2, VE-cadherin (vascular epithelium) (CDH5, Accession NM_001795) is another VGAM2505 host target gene. CDH5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDH5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH5 BINDING SITE, designated SEQ ID:7546,

to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84754] Another function of VGAM2505 is therefore inhibition of Cadherin 5, Type 2, VE-cadherin (vascular epithelium) (CDH5, Accession NM_001795), a gene which associates with alpha-catenin forming a link to the cytoskeleton. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH5. The function of CDH5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1342.CCAAT/enhancer Binding Protein (C/EBP), Alpha (CEBPA, Accession NM_004364) is another VGAM2505 host target gene. CEBPA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CEBPA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CEBPA BINDING SITE, designated SEQ ID:10572, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84755] Another function of VGAM2505 is therefore inhibition of CCAAT/enhancer Binding Protein (C/EBP), Alpha (CEBPA, Accession NM_004364). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEBPA. C-type (calcium dependent, carbohydrate-recognition domain) Lectin, Superfamily Member 12 (CLECSF12, Accession XM_084768) is another VGAM2505 host target gene. CLECSF12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLECSF12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLECSF12 BINDING SITE, designated SEQ ID:37684, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84756] Another function of VGAM2505 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition domain) Lectin, Superfamily Member 12 (CLECSF12, Accession XM_084768), a gene which is a pattern-recognition receptor . Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with CLECSF12. The function of CLECSF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM121.Collagen, Type V, Alpha 3 (COL5A3, Accession NM_015719) is another VGAM2505 host target gene. COL5A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL5A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL5A3 BINDING SITE, designated SEQ ID:17933, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84757] Another function of VGAM2505 is therefore inhibition of Collagen, Type V, Alpha 3 (COL5A3, Accession NM_015719). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL5A3. Casein Kinase 2, Alpha Prime Polypeptide (CSNK2A2, Accession NM_001896) is another VGAM2505 host target gene. CSNK2A2 BINDING SITE is HOST TARGET binding site

found in the 5` untranslated region of mRNA encoded by CSNK2A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSNK2A2 BINDING SITE, designated SEQ ID:7623, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84758] Another function of VGAM2505 is therefore inhibition of Casein Kinase 2, Alpha Prime Polypeptide (CSNK2A2, Accession NM_001896), a gene which catalyzes the phosphorylation of serine or threonine residues in proteins. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK2A2. The function of CSNK2A2 has been established by previous studies. Phosphorylation of the human p53 protein (OMIM Ref. No. 191170) at ser392 is responsive to ultraviolet (UV) but not gamma irradiation. Keller et al. (2001) identified and purified a mammalian UV-activated protein kinase complex that phosphorylates ser392 in vitro. This kinase complex contains CK2 and the chromatin transcriptional elongation factor FACT, a heterodimer of SPT16 (OMIM Ref. No.

605012) and SSRP1 (OMIM Ref. No. 604328). In vitro studies showed that FACT alters the specificity of CK2 in the complex such that it selectively phosphorylates p53 over other substrates, including casein. In addition, phosphorylation by the kinase complex was found to enhance p53 activity. These results provided a potential mechanism for p53 activation by UV irradiation Doray et al. (2002) demonstrated that the Golgi-localized, gamma-ear-containing adenosine diphosphate ribosylation factor-binding proteins (GGA1, 606004 and GGA3, 606006) and the coat protein adaptor protein-1 (AP-1) complex (see OMIM Ref. No. AP1G2, 603534) colocalize in clathrin-coated buds of the trans-Golgi networks of mouse L cells and human HeLa cells. Binding studies revealed a direct interaction between the hinge domains of the GGAs and the gamma-ear domain of AP-1. Further, AP-1 contained bound casein kinase-2 that phosphorylated GGA1 and GGA3, thereby causing autoinhibition. Doray et al. (2002) demonstrated that this autoinhibition could induce the directed transfer of mannose 6-phosphate receptors (see OMIM Ref. No. 154540) from the GGAs to AP-1. Mannose 6-phosphate receptors that were defective in binding to GGAs were poorly incorporated into adaptor protein com-

plex containing clathrin coated vesicles. Thus, Doray et al. (2002) concluded that GGAs and the AP-1 complex interact to package mannose 6-phosphate receptors into AP-1-containing coated vesicles Animal model experiments lend further support to the function of CSNK2A2. To determine the functional and developmental role of protein kinase casein kinase II, Xu et al. (1999) used homologous recombination to disrupt the gene encoding Csnk2a2 in transgenic mice. They found that Csnk2a2 is preferentially expressed in late stages of spermatogenesis, and male mice in which Csnk2a2 has been disrupted are infertile, with oligospermia and globozoospermia ('round-headed spermatozoa'). This was the first demonstration of the unique role for a Ck2 isoform in development. The primary spermatogenic defect in the Csnk2a2 -/- testis is a specific abnormality of anterior head shaping of elongating spermatids; this is the first defined gene that regulates sperm head morphogenesis. As the germ cells differentiate, they are capable of undergoing chromatin condensation, although many abnormal cells are deleted through apoptosis or Sertoli cell phagocytosis. The few that survived to populate the epididymis exhibited head abnormalities similar to those described in human globo-

zoospermia; thus, Csnk2a2 may be a candidate gene for inherited abnormalities of sperm morphogenesis

[84759] It is appreciated that the abovementioned animal model for CSNK2A2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[84760] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84761] Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S. : Cooperation of GGAs and AP-1 in packaging MPRs at the trans-Golgi network. Science 297: 1700-1703, 2002. ; and

[84762] Xu, X.; Toselli, P. A.; Russell, L. D.; Seldin, D. C. : Globozoospermia in mice lacking the casein kinase II alpha-prime catalytic subunit. Nature Genet. 23: 118-121, 1999.

[84763] Further studies establishing the function and utilities of CSNK2A2 are found in John Hopkins OMIM database record ID 115442, and in sited publications numbered 12596, 12601-12602, 87 and 12600 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Cytochrome P450, Subfamily IIB (phenobarbital-inducible), Polypeptide 6 (CYP2B6, Acces-

sion NM_000767) is another VGAM2505 host target gene. CYP2B6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP2B6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP2B6 BINDING SITE, designated SEQ ID:6416, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84764] Another function of VGAM2505 is therefore inhibition of Cytochrome P450, Subfamily IIB (phenobarbital-inducible), Polypeptide 6 (CYP2B6, Accession NM_000767), a gene which oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2B6. The function of CYP2B6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Deleted In Lung and Esophageal Cancer 1 (DLEC1, Accession NM_007336) is another VGAM2505 host target gene.

DLEC1 BINDING SITE1 and DLEC1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DLEC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLEC1 BINDING SITE1 and DLEC1 BINDING SITE2, designated SEQ ID:14265 and SEQ ID:14272 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84765] Another function of VGAM2505 is therefore inhibition of Deleted In Lung and Esophageal Cancer 1 (DLEC1, Accession NM_007336). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLEC1. Dystonia 1, Torsion (autosomal dominant; torsin A) (DYT1, Accession NM_000113) is another VGAM2505 host target gene. DYT1 BINDING SITE1 and DYT1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DYT1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DYT1 BINDING SITE1 and

DYT1 BINDING SITE2, designated SEQ ID:5578 and SEQ ID:5579 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84766] Another function of VGAM2505 is therefore inhibition of Dystonia 1, Torsion (autosomal dominant; torsin A) (DYT1, Accession NM_000113). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DYT1. ELK1, Member of ETS Oncogene Family (ELK1, Accession NM_005229) is another VGAM2505 host target gene. ELK1 BINDING SITE1 and ELK1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ELK1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELK1 BINDING SITE1 and ELK1 BINDING SITE2, designated SEQ ID:11730 and SEQ ID:11731 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84767] Another function of VGAM2505 is therefore inhibition of ELK1, Member of ETS Oncogene Family (ELK1, Accession

NM_005229), a gene which stimulates transcription. can form a ternary complex with the serum response factor and the ets and srf motifs of the fos serum response element. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELK1. The function of ELK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.Fasciculation and Elongation Protein Zeta 1 (zygin I) (FEZ1, Accession NM_022549) is another VGAM2505 host target gene. FEZ1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FEZ1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FEZ1 BINDING SITE, designated SEQ ID:22876, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84768] Another function of VGAM2505 is therefore inhibition of Fasciculation and Elongation Protein Zeta 1 (zygin I) (FEZ1, Accession NM_022549), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans

UNC-76. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEZ1. The function of FEZ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM37.Fibroblast Growth Factor Receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1, Accession NM_023109) is another VGAM2505 host target gene. FGFR1 BINDING SITE1 through FGFR1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FGFR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE1 through FGFR1 BINDING SITE3, designated SEQ ID:23369, SEQ ID:17975 and SEQ ID:6204 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84769] Another function of VGAM2505 is therefore inhibition of Fibroblast Growth Factor Receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1, Accession NM_023109). Accordingly, utilities of VGAM2505 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1. Hypoxia-inducible Factor 1, Alpha Subunit (basic helix-loop-helix transcription factor) (HIF1A, Accession NM_001530) is another VGAM2505 host target gene. HIF1A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HIF1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIF1A BINDING SITE, designated SEQ ID:7265, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84770] Another function of VGAM2505 is therefore inhibition of Hypoxia-inducible Factor 1, Alpha Subunit (basic helix-loop-helix transcription factor) (HIF1A, Accession NM_001530), a gene which is a basic helix-loop-helix transcription factor and mediates transcriptional responses to hypoxia and dioxin-signaling. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIF1A. The function of HIF1A and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM229.High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483) is another VGAM2505 host target gene. HMGA2 BINDING SITE1 through HMGA2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HMGA2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGA2 BINDING SITE1 through HMGA2 BINDING SITE3, designated SEQ ID:9562, SEQ ID:9564 and SEQ ID:9565 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84771] Another function of VGAM2505 is therefore inhibition of High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483), a gene which may affect transcription and cell differentiation; shares common DNA-binding motif with other HMG HMG I/Y family members. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGA2. The function of HMGA2 and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM552.Heparan Sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4, Accession XM_056254) is another VGAM2505 host target gene. HS3ST4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HS3ST4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HS3ST4 BINDING SITE, designated SEQ ID:36370, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84772] Another function of VGAM2505 is therefore inhibition of Heparan Sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4, Accession XM_056254). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HS3ST4. Hormonally Upregulated Neu-associated Kinase (HUNK, Accession NM_014586) is another VGAM2505 host target gene. HUNK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HUNK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of HUNK BINDING SITE, designated SEQ ID:15953, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84773] Another function of VGAM2505 is therefore inhibition of Hormonally Upregulated Neu-associated Kinase (HUNK, Accession NM_014586). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUNK. Hypoxia Up-regulated 1 (HYOU1, Accession XM_006464) is another VGAM2505 host target gene. HYOU1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HYOU1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HYOU1 BINDING SITE, designated SEQ ID:30001, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84774] Another function of VGAM2505 is therefore inhibition of Hypoxia Up-regulated 1 (HYOU1, Accession XM_006464). Accordingly, utilities of VGAM2505 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with HYOU1. Potassium Voltage-gated Channel, Isk-related Family, Member 1-like (KCNE1L, Accession NM_012282) is another VGAM2505 host target gene. KCNE1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNE1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNE1L BINDING SITE, designated SEQ ID:14613, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84775] Another function of VGAM2505 is therefore inhibition of Potassium Voltage-gated Channel, Isk-related Family, Member 1-like (KCNE1L, Accession NM_012282), a gene which is a potassium voltage-gated channel. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNE1L. The function of KCNE1L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1864.Lymphocyte-activation Gene

3 (LAG3, Accession NM_002286) is another VGAM2505 host target gene. LAG3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LAG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAG3 BINDING SITE, designated SEQ ID:8066, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84776] Another function of VGAM2505 is therefore inhibition of Lymphocyte-activation Gene 3 (LAG3, Accession NM_002286), a gene which is involved in lymphocyte activation. binds to hla class-ii antigens. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAG3. The function of LAG3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2353.LFG (Accession XM_084780) is another VGAM2505 host target gene. LFG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LFG, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LFG BINDING SITE, designated SEQ ID:37692, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84777] Another function of VGAM2505 is therefore inhibition of LFG (Accession XM_084780). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LFG. Low Density Lipoprotein-related Protein 1 (alpha-2-macroglobulin receptor) (LRP1, Accession NM_002332) is another VGAM2505 host target gene. LRP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRP1 BINDING SITE, designated SEQ ID:8136, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84778] Another function of VGAM2505 is therefore inhibition of Low Density Lipoprotein-related Protein 1

(alpha-2-macroglobulin receptor) (LRP1, Accession NM_002332), a gene which is a recycling lipoprotein receptor with possible growth-modulating effects. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP1. The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM885.Lysozyme (renal amyloidosis) (LYZ, Accession NM_000239) is another VGAM2505 host target gene. LYZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LYZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LYZ BINDING SITE, designated SEQ ID:5757, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84779] Another function of VGAM2505 is therefore inhibition of Lysozyme (renal amyloidosis) (LYZ, Accession NM_000239), a gene which a bacteriolytic enzyme. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with LYZ. The function of LYZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM929.Mediterranean Fever (MEFV, Accession NM_000243) is another VGAM2505 host target gene. MEFV BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEFV, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEFV BINDING SITE, designated SEQ ID:5768, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84780] Another function of VGAM2505 is therefore inhibition of Mediterranean Fever (MEFV, Accession NM_000243). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEFV. Matrix Metalloproteinase 15 (membrane-inserted) (MMP15, Accession NM_002428) is another VGAM2505 host target gene. MMP15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MMP15, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMP15 BINDING SITE, designated SEQ ID:8264, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84781] Another function of VGAM2505 is therefore inhibition of Matrix Metalloproteinase 15 (membrane-inserted) (MMP15, Accession NM_002428). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMP15. Myeloproliferative Leukemia Virus Oncogene (MPL, Accession NM_005373) is another VGAM2505 host target gene. MPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPL BINDING SITE, designated SEQ ID:11849, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84782] Another function of VGAM2505 is therefore inhibition of

Myeloproliferative Leukemia Virus Oncogene (MPL, Accession NM_005373). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPL. Membrane Protein, Palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3, Accession NM_001932) is another VGAM2505 host target gene. MPP3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MPP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPP3 BINDING SITE, designated SEQ ID:7642, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84783] Another function of VGAM2505 is therefore inhibition of Membrane Protein, Palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3, Accession NM_001932). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPP3. Nipsnap Homolog 1 (C. elegans) (NIPSNAP1, Accession NM_003634) is another VGAM2505 host target gene. NIPSNAP1 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by NIPSNAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NIPSNAP1 BINDING SITE, designated SEQ ID:9702, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84784] Another function of VGAM2505 is therefore inhibition of Nipsnap Homolog 1 (C. elegans) (NIPSNAP1, Accession NM_003634). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NIPSNAP1. Notch Homolog 3 (Drosophila) (NOTCH3, Accession NM_000435) is another VGAM2505 host target gene. NOTCH3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NOTCH3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NOTCH3 BINDING SITE, designated SEQ ID:6017, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84785] Another function of VGAM2505 is therefore inhibition of Notch Homolog 3 (Drosophila) (NOTCH3, Accession NM_000435), a gene which may function in cell fate specification during development. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOTCH3. The function of NOTCH3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM128.Protocadherin Beta 11 (PCDHB11, Accession NM_018931) is another VGAM2505 host target gene. PCDHB11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHB11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHB11 BINDING SITE, designated SEQ ID:21001, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84786] Another function of VGAM2505 is therefore inhibition of Protocadherin Beta 11 (PCDHB11, Accession NM_018931). Accordingly, utilities of VGAM2505 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with PCDHB11. Phosducin-like (PDCL, Accession NM_005388) is another VGAM2505 host target gene. PDCL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDCL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDCL BINDING SITE, designated SEQ ID:11865, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84787] Another function of VGAM2505 is therefore inhibition of Phosducin-like (PDCL, Accession NM_005388), a gene which may regulate G-protein signaling and similar to phosducins. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDCL. The function of PDCL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1708.Phosphodiesterase 6B, CGMP-specific, Rod, Beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NM_000283) is another

VGAM2505 host target gene. PDE6B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE6B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE6B BINDING SITE, designated SEQ ID:5827, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84788] Another function of VGAM2505 is therefore inhibition of Phosphodiesterase 6B, CGMP-specific, Rod, Beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NM_000283). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE6B. Plexin A1 (PLXNA1, Accession XM_051261) is another VGAM2505 host target gene. PLXNA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLXNA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLXNA1 BINDING SITE, designated SEQ ID:35791, to the

nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84789] Another function of VGAM2505 is therefore inhibition of Plexin A1 (PLXNA1, Accession XM_051261). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLXNA1. Prostaglandin I2 (prostacyclin) Synthase (PTGIS, Accession NM_000961) is another VGAM2505 host target gene. PTGIS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTGIS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGIS BINDING SITE, designated SEQ ID:6670, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84790] Another function of VGAM2505 is therefore inhibition of Prostaglandin I2 (prostacyclin) Synthase (PTGIS, Accession NM_000961), a gene which catalyzes the isomerization of prostaglandin h2 to prostacyclin (= prostaglandin i2). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with PTGIS. The function of PTGIS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Protein Tyrosine Phosphatase, Non-receptor Type 7 (PTPN7, Accession NM_002832) is another VGAM2505 host target gene. PTPN7 BINDING SITE1 through PTPN7 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPN7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPN7 BINDING SITE1 through PTPN7 BINDING SITE3, designated SEQ ID:8710, SEQ ID:27888 and SEQ ID:27891 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84791] Another function of VGAM2505 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type 7 (PTPN7, Accession NM_002832). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN7. Retinoic Acid Receptor, Beta (RARB, Accession NM_016152) is another VGAM2505 host target gene.

RARB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RARB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RARB BINDING SITE, designated SEQ ID:18237, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84792] Another function of VGAM2505 is therefore inhibition of Retinoic Acid Receptor, Beta (RARB, Accession NM_016152), a gene which is one member of the steroid/thyroid hormone receptor family of ligand-activated transcription factors. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RARB. The function of RARB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM179.Rabphilin 3A-like (without C2 domains) (RPH3AL, Accession NM_006987) is another VGAM2505 host target gene. RPH3AL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPH3AL, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPH3AL BINDING SITE, designated SEQ ID:13848, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84793] Another function of VGAM2505 is therefore inhibition of Rabphilin 3A-like (without C2 domains) (RPH3AL, Accession NM_006987), a gene which is a protein transporter. could play a role in neurotransmitter release by regulating membrane flow in the nerve terminal. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPH3AL. The function of RPH3AL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM923.Spondyloepiphyseal Dysplasia, Late (SEDL, Accession NM_014563) is another VGAM2505 host target gene. SEDL BINDING SITE1 and SEDL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SEDL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the comple-

mentarity of the nucleotide sequences of SEDL BINDING SITE1 and SEDL BINDING SITE2, designated SEQ ID:15907 and SEQ ID:15908 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84794] Another function of VGAM2505 is therefore inhibition of Spondyloepiphyseal Dysplasia, Late (SEDL, Accession NM_014563), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEDL. The function of SEDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Solute Carrier Family 14 (urea transporter), Member 2 (SLC14A2, Accession NM_007163) is another VGAM2505 host target gene. SLC14A2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC14A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC14A2 BINDING SITE, designated SEQ ID:14008, to the

nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84795] Another function of VGAM2505 is therefore inhibition of Solute Carrier Family 14 (urea transporter), Member 2 (SLC14A2, Accession NM_007163), a gene which is a renal urea transporter 2. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC14A2. The function of SLC14A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Sorting Nexin 15 (SNX15, Accession XM_057307) is another VGAM2505 host target gene. SNX15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNX15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:36504, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84796] Another function of VGAM2505 is therefore inhibition of Sorting Nexin 15 (SNX15, Accession XM_057307). Accord-

ingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15. Sp4 Transcription Factor (SP4, Accession NM_003112) is another VGAM2505 host target gene. SP4 BINDING SITE1 and SP4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SP4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SP4 BINDING SITE1 and SP4 BINDING SITE2, designated SEQ ID:9082 and SEQ ID:9083 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84797] Another function of VGAM2505 is therefore inhibition of Sp4 Transcription Factor (SP4, Accession NM_003112), a gene which binds to gt and gc boxes promoters elements. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP4. The function of SP4 has been established by previous studies. Hagen et al. (1992) performed recognition site screening for factors which bind to the uteroglobin promoter sequence GT box and cloned

cDNAs encoding the DNA-binding proteins SP3 (OMIM Ref. No. 601804) and SP4, thus revealing the existence of a multigene family of SP proteins. They found that SP1, SP3, and SP4 exhibit similar structural features: all contain DNA-binding domains composed of 3 zinc fingers of the Cys2/His2 type near the C terminus, and all recognize GC- and GT-box sequences. Additionally, the N termini of all 3 proteins are composed of long serine/threonine- and glutamine-rich regions that have been identified in SP1 as transactivation domains. Hagen et al. (1992) showed by Northern blot analysis that SP4 is abundantly expressed as a 7.5-kb message in brain, but barely detectable in other human cell lines. Hagen et al. (1995) used cotransfection experiments to show that SP4 is an activator protein like SP1. However, in contrast to SP1, they found that SP4 is not able to act synergistically through adjacent binding sites. Animal model experiments lend further support to the function of SP4. Gollner et al. (2001) found that Sp4 knockout mice, with a complete absence of Sp4 expression due to targeted deletion of the exons encoding the N-terminal activation domains, showed a complex phenotype. They developed until birth without obvious abnormalities. After birth, two-thirds died within 4 weeks. Sur-

viving mice were growth retarded. Males homozygous for the null mutation did not breed; the reason for this remained obscure since they showed complete spermatogenesis, and pheromone receptor genes in the vomeronasal organ appeared unaffected. Female null mice had a smaller thymus, spleen, and uterus and exhibited a pronounced delay in sexual maturation. Thus, the phenotype of the Sp4-null mice differed significantly from those described for the Sp1- and Sp3-null mice. The authors concluded that the structural similarities, the common recognition motif, and the overlapping expression pattern of these 3 transcription factors do not reflect similar physiologic functions.

[84798] It is appreciated that the abovementioned animal model for SP4 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[84799] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84800] Gollner, H.; Bouwman, P.; Mangold, M.; Karis, A.; Braun, H.; Rohner, I.; Del Rey, A.; Besedovsky, H.-O.; Meinhardt, A.; van den Broek, M.; Cutforth, T.; Grosveld, F.; Philipsen,

S.; Suske, G. : Complex phenotype of mice homozygous for a null mutation in the Sp4 transcription factor gene. Genes Cells 6: 689-697, 2001. ; and

[84801] Hagen, G.; Dennig, J.; Preiss, M.; Beato, M.; Suske, G. : Functional analyses of the transcription factor Sp4 reveal properties distinct from Sp1 and Sp3. J. Biol. Chem. 270: 24989-24994.

[84802] Further studies establishing the function and utilities of SP4 are found in John Hopkins OMIM database record ID 600540, and in sited publications numbered 7687-7691 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Tyrosine Aminotransferase (TAT, Accession NM_000353) is another VGAM2505 host target gene. TAT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAT BINDING SITE, designated SEQ ID:5913, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84803] Another function of VGAM2505 is therefore inhibition of

Tyrosine Aminotransferase (TAT, Accession NM_000353), a gene which is tyrosine aminotransferase and strongly similar to rat Rn.9947, which plays a role in gluconeogenesis. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAT. The function of TAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2434.Thromboxane A2 Receptor (TBXA2R, Accession NM_001060) is another VGAM2505 host target gene. TBXA2R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBXA2R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBXA2R BINDING SITE, designated SEQ ID:6725, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84804] Another function of VGAM2505 is therefore inhibition of Thromboxane A2 Receptor (TBXA2R, Accession NM_001060), a gene which activates Ca2+-activated chloride channels; stimulates platelet aggregation and

smooth muscle constriction. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBXA2R. The function of TBXA2R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Tumor Necrosis Factor (ligand) Superfamily, Member 9 (TNFSF9, Accession NM_003811) is another VGAM2505 host target gene. TNFSF9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFSF9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF9 BINDING SITE, designated SEQ ID:9903, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84805] Another function of VGAM2505 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 9 (TNFSF9, Accession NM_003811). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF9. Tensin (TNS, Accession NM_022648) is another

VGAM2505 host target gene. TNS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TNS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNS BINDING SITE, designated SEQ ID:22900, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84806] Another function of VGAM2505 is therefore inhibition of Tensin (TNS, Accession NM_022648). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNS. TZFP (Accession NM_014383) is another VGAM2505 host target gene. TZFP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TZFP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TZFP BINDING SITE, designated SEQ ID:15719, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84807] Another function of VGAM2505 is therefore inhibition of TZFP (Accession NM_014383), a gene which is probably a transcription factor. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TZFP. The function of TZFP has been established by previous studies. Fanconi anemia (FA) is a genetically heterogeneous disorder composed of at least 8 different complementation groups identified by somatic cell hybrid analysis. However, because FA patients have similar clinical phenotypes (e.g., predisposition to cancer) and cellular phenotypes (hypersensitivity to DNA crosslinking agents), a common molecular pathway has been hypothesized. FANCC (OMIM Ref. No. 227645) has been detected in both the cytoplasm and nucleus and has been shown to interact with other cellular proteins, including FANCA (OMIM Ref. No. 227650). Using a yeast 2-hybrid screen of a B-cell cDNA library with N-terminal sequences of FANCC as bait, and by confirming the interactions using GST pull-down assays, followed by RT-PCR, Hoatlin et al. (1999) isolated a cDNA encoding FAZF. Sequence analysis predicted that the 487-amino acid protein, which is similar to PLZF (OMIM Ref. No. 176797), contains an N-terminal POZ/BTB

domain and 3 zinc fingers. Northern blot analysis detected weak expression of a 1.4-kb transcript in most tissues tested except peripheral blood leukocytes, where strong expression was detected, and testis, where strong expression of 2.0-, 2.7-, and 4.4-kb transcripts was detected. Coimmunoprecipitation analysis showed that FAZF associates with FANCC independent of the BTB/POZ domain. Indirect immunofluorescence and confocal microscopy demonstrated almost entirely nuclear expression for FAZF and colocalization with FANCC, which Hoatlin et al. (1999) confirmed is also expressed in cytoplasm in some cells; FANCC and PLZF did not colocalize. EMSA analysis suggested that PLZF and FAZF bind to CpG islands, interact with each other through the POZ domain of PLZF, and repress transcription by a similar mechanism. By database searching, genomic analysis, RT-PCR, and yeast 2-hybrid screening, Lin et al. (1999) cloned FAZF, which they termed TZFP. Genomic sequence analysis determined that the TZFP gene contains 5 exons. Northern blot analysis detected expression of 3 transcripts only in testis.

[84808] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[84809] Hoatlin, M. E.; Zhi, Y.; Ball, H.; Silvery, K.; Melnick, A.; Stone, S.; Arai, S.; Hawe, N.; Owen, G.; Zelent, A.; Licht, J. D. : A novel BTB/POZ transcriptional repressor protein interacts with the Fanconi anemia group C protein and PLZF. Blood 94: 3737-3747, 1999. ; and

[84810] Lin, W.; Lai, C.-H.; Tang, C.-J. C.; Huang, C.-J.; Tang, T. K. : Identification and gene structure of a novel human PLZF-related transcription factor gene, TZFP. Biochem. Biophys. Res. Com.

[84811] Further studies establishing the function and utilities of TZFP are found in John Hopkins OMIM database record ID 605859, and in sited publications numbered 6782-6783 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Zinc Finger Protein 133 (clone pHZ-13) (ZNF133, Accession NM_003434) is another VGAM2505 host target gene. ZNF133 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF133, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF133 BINDING SITE, designated SEQ ID:9486, to the nu-

cleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84812] Another function of VGAM2505 is therefore inhibition of Zinc Finger Protein 133 (clone pHZ-13) (ZNF133, Accession NM_003434). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF133. Zinc Finger Protein 42 (myeloid-specific retinoic acid- responsive) (ZNF42, Accession NM_003422) is another VGAM2505 host target gene. ZNF42 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF42, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF42 BINDING SITE, designated SEQ ID:9469, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84813] Another function of VGAM2505 is therefore inhibition of Zinc Finger Protein 42 (myeloid-specific retinoic acid- responsive) (ZNF42, Accession NM_003422), a gene which may be one regulator of transcriptional events during hemopoietic development. Accordingly, utilities of

VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF42. The function of ZNF42 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM173.1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) (AGPAT1, Accession NM_006411) is another VGAM2505 host target gene. AGPAT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AGPAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AGPAT1 BINDING SITE, designated SEQ ID:13115, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84814] Another function of VGAM2505 is therefore inhibition of 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) (AGPAT1, Accession NM_006411). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AG-

PAT1. Adenylate Kinase 5 (AK5, Accession NM_012093) is another VGAM2505 host target gene. AK5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AK5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AK5 BINDING SITE, designated SEQ ID:14393, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84815] Another function of VGAM2505 is therefore inhibition of Adenylate Kinase 5 (AK5, Accession NM_012093). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AK5. APCL (Accession NM_005883) is another VGAM2505 host target gene. APCL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APCL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APCL BINDING SITE, designated SEQ ID:12498, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5216.

[84816] Another function of VGAM2505 is therefore inhibition of APCL (Accession NM_005883). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APCL. Rho GTPase Activating Protein 5 (ARHGAP5, Accession XM_085082) is another VGAM2505 host target gene. ARHGAP5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARHGAP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP5 BINDING SITE, designated SEQ ID:37816, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84817] Another function of VGAM2505 is therefore inhibition of Rho GTPase Activating Protein 5 (ARHGAP5, Accession XM_085082). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP5. ATPase, (Na+)/K+ Transporting, Beta 4 Polypeptide (ATP1B4, Accession NM_012069) is another VGAM2505 host target

gene. ATP1B4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP1B4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1B4 BINDING SITE, designated SEQ ID:14323, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84818] Another function of VGAM2505 is therefore inhibition of ATPase, (Na+)/K+ Transporting, Beta 4 Polypeptide (ATP1B4, Accession NM_012069). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B4. BA108L7.2 (Accession NM_030971) is another VGAM2505 host target gene. BA108L7.2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BA108L7.2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BA108L7.2 BINDING SITE, designated SEQ ID:25239, to the nucleotide sequence of VGAM2505 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5216.

[84819] Another function of VGAM2505 is therefore inhibition of BA108L7.2 (Accession NM_030971). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BA108L7.2. BCL2-associated Athanogene 5 (BAG5, Accession NM_004873) is another VGAM2505 host target gene. BAG5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAG5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAG5 BINDING SITE, designated SEQ ID:11302, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84820] Another function of VGAM2505 is therefore inhibition of BCL2-associated Athanogene 5 (BAG5, Accession NM_004873). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG5. BMF (Accession NM_033503) is another VGAM2505 host target gene. BMF BINDING SITE1 and BMF BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA en-

coded by BMF, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BMF BINDING SITE1 and BMF BINDING SITE2, designated SEQ ID:27276 and SEQ ID:27280 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84821] Another function of VGAM2505 is therefore inhibition of BMF (Accession NM_033503). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMF. Chromosome 9 Open Reading Frame 9 (C9orf9, Accession NM_018956) is another VGAM2505 host target gene. C9orf9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf9 BINDING SITE, designated SEQ ID:21026, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84822] Another function of VGAM2505 is therefore inhibition of Chromosome 9 Open Reading Frame 9 (C9orf9, Accession NM_018956). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf9. Centaurin, Alpha 1 (CENTA1, Accession NM_006869) is another VGAM2505 host target gene. CENTA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CENTA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENTA1 BINDING SITE, designated SEQ ID:13739, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84823] Another function of VGAM2505 is therefore inhibition of Centaurin, Alpha 1 (CENTA1, Accession NM_006869). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENTA1. Claudin 6 (CLDN6, Accession NM_021195) is another VGAM2505 host target gene. CLDN6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

CLDN6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLDN6 BINDING SITE, designated SEQ ID:22171, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84824] Another function of VGAM2505 is therefore inhibition of Claudin 6 (CLDN6, Accession NM_021195). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN6. Calsenilin, Presenilin Binding Protein, EF Hand Transcription Factor (CSEN, Accession NM_013434) is another VGAM2505 host target gene. CSEN BINDING SITE is HOST TARGET binding site found in the 3` un-translated region of mRNA encoded by CSEN, correspond-ing to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSEN BINDING SITE, designated SEQ ID:15087, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84825] Another function of VGAM2505 is therefore inhibition of

Calsenilin, Presenilin Binding Protein, EF Hand Transcription Factor (CSEN, Accession NM_013434). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSEN. Diacylglycerol Kinase, Zeta 104kDa (DGKZ, Accession NM_003646) is another VGAM2505 host target gene. DGKZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGKZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKZ BINDING SITE, designated SEQ ID:9721, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84826] Another function of VGAM2505 is therefore inhibition of Diacylglycerol Kinase, Zeta 104kDa (DGKZ, Accession NM_003646). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKZ. DKFZp434A2417 (Accession XM_038526) is another VGAM2505 host target gene. DKFZp434A2417 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434A2417, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434A2417 BINDING SITE, designated SEQ ID:32860, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84827] Another function of VGAM2505 is therefore inhibition of DKFZp434A2417 (Accession XM_038526). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434A2417. DKFZP434C212 (Accession XM_044196) is another VGAM2505 host target gene. DKFZP434C212 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C212, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434C212 BINDING SITE, designated SEQ ID:34168, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84828] Another function of VGAM2505 is therefore inhibition of DKFZP434C212 (Accession XM_044196). Accordingly,

utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C212. DKFZp434J0226 (Accession XM_051327) is another VGAM2505 host target gene. DKFZp434J0226 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp434J0226, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434J0226 BINDING SITE, designated SEQ ID:35805, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84829] Another function of VGAM2505 is therefore inhibition of DKFZp434J0226 (Accession XM_051327). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434J0226. DKFZP434L187 (Accession XM_044070) is another VGAM2505 host target gene. DKFZP434L187 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434L187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L187 BINDING SITE, designated SEQ ID:34123, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84830] Another function of VGAM2505 is therefore inhibition of DKFZP434L187 (Accession XM_044070). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434L187. DKFZp547H025 (Accession NM_020161) is another VGAM2505 host target gene. DKFZp547H025 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547H025, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547H025 BINDING SITE, designated SEQ ID:21369, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84831] Another function of VGAM2505 is therefore inhibition of DKFZp547H025 (Accession NM_020161). Accordingly, utilities of VGAM2505 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp547H025. DKFZP564O0523 (Accession NM_032120) is another VGAM2505 host target gene. DKFZP564O0523 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0523, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564O0523 BINDING SITE, designated SEQ ID:25804, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84832] Another function of VGAM2505 is therefore inhibition of DKFZP564O0523 (Accession NM_032120). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O0523. Dystrophia Myotonica-containing WD Repeat Motif (DMWD, Accession XM_027569) is another VGAM2505 host target gene. DMWD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DMWD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of DMWD BINDING SITE, designated SEQ ID:30531, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84833] Another function of VGAM2505 is therefore inhibition of Dystrophia Myotonica-containing WD Repeat Motif (DMWD, Accession XM_027569). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMWD. FBP17 (Accession XM_052666) is another VGAM2505 host target gene. FBP17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBP17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBP17 BINDING SITE, designated SEQ ID:36048, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84834] Another function of VGAM2505 is therefore inhibition of FBP17 (Accession XM_052666). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBP17.

FLJ00007 (Accession XM_048928) is another VGAM2505 host target gene. FLJ00007 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00007, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00007 BINDING SITE, designated SEQ ID:35313, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84835] Another function of VGAM2505 is therefore inhibition of FLJ00007 (Accession XM_048928). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00007. FLJ10748 (Accession NM_018203) is another VGAM2505 host target gene. FLJ10748 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10748, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10748 BINDING SITE, designated SEQ ID:20085, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM

RNA, also designated SEQ ID:5216.

[84836] Another function of VGAM2505 is therefore inhibition of FLJ10748 (Accession NM_018203). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10748. FLJ12363 (Accession NM_032167) is another VGAM2505 host target gene. FLJ12363 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12363, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12363 BINDING SITE, designated SEQ ID:25866, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84837] Another function of VGAM2505 is therefore inhibition of FLJ12363 (Accession NM_032167). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12363. FLJ12529 (Accession NM_024811) is another VGAM2505 host target gene. FLJ12529 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12529, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12529 BINDING SITE, designated SEQ ID:24191, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84838] Another function of VGAM2505 is therefore inhibition of FLJ12529 (Accession NM_024811). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12529. FLJ12903 (Accession NM_022753) is another VGAM2505 host target gene. FLJ12903 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12903, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12903 BINDING SITE, designated SEQ ID:22978, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84839] Another function of VGAM2505 is therefore inhibition of FLJ12903 (Accession NM_022753). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12903. FLJ12973 (Accession NM_024908) is another VGAM2505 host target gene. FLJ12973 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12973, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12973 BINDING SITE, designated SEQ ID:24406, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84840] Another function of VGAM2505 is therefore inhibition of FLJ12973 (Accession NM_024908). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12973. FLJ14950 (Accession NM_032865) is another VGAM2505 host target gene. FLJ14950 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14950, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14950 BINDING SITE, designated SEQ ID:26672, to the nucleotide

sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84841] Another function of VGAM2505 is therefore inhibition of FLJ14950 (Accession NM_032865). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14950. FLJ20079 (Accession NM_017656) is another VGAM2505 host target gene. FLJ20079 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20079, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20079 BINDING SITE, designated SEQ ID:19176, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84842] Another function of VGAM2505 is therefore inhibition of FLJ20079 (Accession NM_017656). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20079. FLJ20113 (Accession NM_017670) is another VGAM2505 host target gene. FLJ20113 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ20113, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20113 BINDING SITE, designated SEQ ID:19211, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84843] Another function of VGAM2505 is therefore inhibition of FLJ20113 (Accession NM_017670). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20113. FLJ21709 (Accession XM_085480) is another VGAM2505 host target gene. FLJ21709 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21709, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21709 BINDING SITE, designated SEQ ID:38167, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84844] Another function of VGAM2505 is therefore inhibition of FLJ21709 (Accession XM_085480). Accordingly, utilities of

VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21709. FLJ22002 (Accession NM_024838) is another VGAM2505 host target gene. FLJ22002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22002 BINDING SITE, designated SEQ ID:24245, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84845] Another function of VGAM2505 is therefore inhibition of FLJ22002 (Accession NM_024838). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22002. FLJ22531 (Accession NM_024650) is another VGAM2505 host target gene. FLJ22531 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22531, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22531

BINDING SITE, designated SEQ ID:23944, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84846] Another function of VGAM2505 is therefore inhibition of FLJ22531 (Accession NM_024650). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22531. FLJ22794 (Accession XM_166220) is another VGAM2505 host target gene. FLJ22794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:44023, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84847] Another function of VGAM2505 is therefore inhibition of FLJ22794 (Accession XM_166220). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22794. GMPPB (Accession XM_171044) is another VGAM2505 host target gene. GMPPB BINDING SITE is HOST

TARGET binding site found in the 5` untranslated region of mRNA encoded by GMPPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GMPPB BINDING SITE, designated SEQ ID:45812, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84848] Another function of VGAM2505 is therefore inhibition of GMPPB (Accession XM_171044). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GMPPB. H-plk (Accession NM_015852) is another VGAM2505 host target gene. H-plk BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by H-plk, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H-plk BINDING SITE, designated SEQ ID:17984, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84849] Another function of VGAM2505 is therefore inhibition of

H-plk (Accession NM_015852). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H-plk. ICK (Accession NM_014920) is another VGAM2505 host target gene. ICK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:17195, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84850] Another function of VGAM2505 is therefore inhibition of ICK (Accession NM_014920). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK. KIAA0063 (Accession NM_014876) is another VGAM2505 host target gene. KIAA0063 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0063, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0063 BINDING SITE,

designated SEQ ID:17016, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84851] Another function of VGAM2505 is therefore inhibition of KIAA0063 (Accession NM_014876). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0063. KIAA0429 (Accession NM_014751) is another VGAM2505 host target gene. KIAA0429 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0429, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0429 BINDING SITE, designated SEQ ID:16471, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84852] Another function of VGAM2505 is therefore inhibition of KIAA0429 (Accession NM_014751). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0429. KIAA0450 (Accession NM_014638) is another VGAM2505 host target gene. KIAA0450 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0450, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0450 BINDING SITE, designated SEQ ID:16028, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84853] Another function of VGAM2505 is therefore inhibition of KIAA0450 (Accession NM_014638). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0450. KIAA0459 (Accession XM_027862) is another VGAM2505 host target gene. KIAA0459 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:30574, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84854] Another function of VGAM2505 is therefore inhibition of

KIAA0459 (Accession XM_027862). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459. KIAA0513 (Accession NM_014732) is another VGAM2505 host target gene. KIAA0513 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0513, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:16354, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84855] Another function of VGAM2505 is therefore inhibition of KIAA0513 (Accession NM_014732). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513. KIAA0532 (Accession XM_047659) is another VGAM2505 host target gene. KIAA0532 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0532, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0532 BINDING SITE, designated SEQ ID:35024, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84856] Another function of VGAM2505 is therefore inhibition of KIAA0532 (Accession XM_047659). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0532. KIAA0557 (Accession XM_085507) is another VGAM2505 host target gene. KIAA0557 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0557, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0557 BINDING SITE, designated SEQ ID:38211, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84857] Another function of VGAM2505 is therefore inhibition of KIAA0557 (Accession XM_085507). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0557. KIAA0562 (Accession NM_014704) is another

VGAM2505 host target gene. KIAA0562 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0562, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:16242, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84858] Another function of VGAM2505 is therefore inhibition of KIAA0562 (Accession NM_014704). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0562. KIAA0841 (Accession XM_049237) is another VGAM2505 host target gene. KIAA0841 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE, designated SEQ ID:35362, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84859] Another function of VGAM2505 is therefore inhibition of KIAA0841 (Accession XM_049237). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841. KIAA1196 (Accession XM_028968) is another VGAM2505 host target gene. KIAA1196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1196 BINDING SITE, designated SEQ ID:30816, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84860] Another function of VGAM2505 is therefore inhibition of KIAA1196 (Accession XM_028968). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1196. KIAA1198 (Accession XM_032674) is another VGAM2505 host target gene. KIAA1198 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1198, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE, designated SEQ ID:31706, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84861] Another function of VGAM2505 is therefore inhibition of KIAA1198 (Accession XM_032674). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198. KIAA1257 (Accession XM_031577) is another VGAM2505 host target gene. KIAA1257 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1257, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE, designated SEQ ID:31431, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84862] Another function of VGAM2505 is therefore inhibition of KIAA1257 (Accession XM_031577). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1257. KIAA1373 (Accession XM_048195) is another VGAM2505 host target gene. KIAA1373 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1373, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1373 BINDING SITE, designated SEQ ID:35126, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84863] Another function of VGAM2505 is therefore inhibition of KIAA1373 (Accession XM_048195). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1373. KIAA1416 (Accession XM_098762) is another VGAM2505 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41802, to the nucleotide sequence of VGAM2505 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5216.

[84864] Another function of VGAM2505 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. KIAA1554 (Accession XM_170834) is another VGAM2505 host target gene. KIAA1554 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1554, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1554 BINDING SITE, designated SEQ ID:45614, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84865] Another function of VGAM2505 is therefore inhibition of KIAA1554 (Accession XM_170834). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1554. KIAA1571 (Accession XM_027744) is another VGAM2505 host target gene. KIAA1571 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1571, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1571 BINDING SITE, designated SEQ ID:30565, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84866] Another function of VGAM2505 is therefore inhibition of KIAA1571 (Accession XM_027744). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1571. KIAA1610 (Accession XM_040622) is another VGAM2505 host target gene. KIAA1610 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1610, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1610 BINDING SITE, designated SEQ ID:33338, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84867] Another function of VGAM2505 is therefore inhibition of KIAA1610 (Accession XM_040622). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1610. KIAA1615 (Accession XM_044021) is another VGAM2505 host target gene. KIAA1615 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1615, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1615 BINDING SITE, designated SEQ ID:34083, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84868] Another function of VGAM2505 is therefore inhibition of KIAA1615 (Accession XM_044021). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1615. KIAA1719 (Accession XM_042936) is another VGAM2505 host target gene. KIAA1719 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1719 BINDING SITE, designated SEQ ID:33821, to the

nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84869] Another function of VGAM2505 is therefore inhibition of KIAA1719 (Accession XM_042936). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1719. KIAA1904 (Accession XM_056282) is another VGAM2505 host target gene. KIAA1904 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:36375, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84870] Another function of VGAM2505 is therefore inhibition of KIAA1904 (Accession XM_056282). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904. KIAA1910 (Accession XM_055514) is another VGAM2505 host target gene. KIAA1910 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1910 BINDING SITE, designated SEQ ID:36286, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84871] Another function of VGAM2505 is therefore inhibition of KIAA1910 (Accession XM_055514). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1910. KIAA1938 (Accession XM_166407) is another VGAM2505 host target gene. KIAA1938 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1938, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1938 BINDING SITE, designated SEQ ID:44277, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84872] Another function of VGAM2505 is therefore inhibition of KIAA1938 (Accession XM_166407). Accordingly, utilities

of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1938. Karyopherin Alpha 6 (importin alpha 7) (KPNA6, Accession NM_012316) is another VGAM2505 host target gene. KPNA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KPNA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KPNA6 BINDING SITE, designated SEQ ID:14687, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84873] Another function of VGAM2505 is therefore inhibition of Karyopherin Alpha 6 (importin alpha 7) (KPNA6, Accession NM_012316). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KPNA6. MCLC (Accession NM_015127) is another VGAM2505 host target gene. MCLC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCLC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of MCLC BINDING SITE, designated SEQ ID:17490, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84874] Another function of VGAM2505 is therefore inhibition of MCLC (Accession NM_015127). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCLC. Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 3 (mouse) (MEIS3, Accession XM_085721) is another VGAM2505 host target gene. MEIS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEIS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEIS3 BINDING SITE, designated SEQ ID:38311, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84875] Another function of VGAM2505 is therefore inhibition of Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 3 (mouse) (MEIS3, Accession XM_085721). Accordingly, utilities of VGAM2505 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with MEIS3. MGC10924 (Accession NM_030571) is another VGAM2505 host target gene. MGC10924 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10924, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10924 BINDING SITE, designated SEQ ID:24945, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84876] Another function of VGAM2505 is therefore inhibition of MGC10924 (Accession NM_030571). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10924. MGC14376 (Accession NM_032895) is another VGAM2505 host target gene. MGC14376 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC14376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14376 BINDING SITE, designated SEQ ID:26722, to

the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84877] Another function of VGAM2505 is therefore inhibition of MGC14376 (Accession NM_032895). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14376. MGC15730 (Accession NM_032880) is another VGAM2505 host target gene. MGC15730 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC15730, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15730 BINDING SITE, designated SEQ ID:26700, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84878] Another function of VGAM2505 is therefore inhibition of MGC15730 (Accession NM_032880). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15730. MGC16703 (Accession XM_054591) is another VGAM2505 host target gene. MGC16703 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by MGC16703, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16703 BINDING SITE, designated SEQ ID:36179, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84879] Another function of VGAM2505 is therefore inhibition of MGC16703 (Accession XM_054591). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16703. MGC2474 (Accession NM_023931) is another VGAM2505 host target gene. MGC2474 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE, designated SEQ ID:23414, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84880] Another function of VGAM2505 is therefore inhibition of MGC2474 (Accession NM_023931). Accordingly, utilities

of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2474. MGC9912 (Accession NM_080664) is another VGAM2505 host target gene. MGC9912 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC9912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC9912 BINDING SITE, designated SEQ ID:27951, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84881] Another function of VGAM2505 is therefore inhibition of MGC9912 (Accession NM_080664). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9912. NADH Dehydrogenase (ubiquinone) 1, Subcomplex Unknown, 2, 14.5kDa (NDUFC2, Accession NM_004549) is another VGAM2505 host target gene. NDUFC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDUFC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of NDUFC2 BINDING SITE, designated SEQ ID:10894, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84882] Another function of VGAM2505 is therefore inhibition of NADH Dehydrogenase (ubiquinone) 1, Subcomplex Unknown, 2, 14.5kDa (NDUFC2, Accession NM_004549). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFC2. Nup43 (Accession NM_024647) is another VGAM2505 host target gene. Nup43 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Nup43, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Nup43 BINDING SITE, designated SEQ ID:23934, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84883] Another function of VGAM2505 is therefore inhibition of Nup43 (Accession NM_024647). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with Nup43. OBTP (Accession NM_017601) is another VGAM2505 host target gene. OBTP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OBTP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OBTP BINDING SITE, designated SEQ ID:19079, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84884] Another function of VGAM2505 is therefore inhibition of OBTP (Accession NM_017601). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OBTP. Oxysterol Binding Protein-like 2 (OSBPL2, Accession NM_144498) is another VGAM2505 host target gene. OSBPL2 BINDING SITE1 and OSBPL2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OSBPL2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL2 BINDING SITE1

and OSBPL2 BINDING SITE2, designated SEQ ID:29318 and SEQ ID:16850 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84885] Another function of VGAM2505 is therefore inhibition of Oxysterol Binding Protein-like 2 (OSBPL2, Accession NM_144498). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL2. Platelet Derived Growth Factor C (PDGFC, Accession NM_016205) is another VGAM2505 host target gene. PDGFC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PDGFC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFC BINDING SITE, designated SEQ ID:18302, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84886] Another function of VGAM2505 is therefore inhibition of Platelet Derived Growth Factor C (PDGFC, Accession NM_016205). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PDGFC. Phosphatidylinositol-4-phosphate 5-kinase, Type I, Gamma (PIP5K1C, Accession XM_047620) is another VGAM2505 host target gene. PIP5K1C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIP5K1C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIP5K1C BINDING SITE, designated SEQ ID:35016, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84887] Another function of VGAM2505 is therefore inhibition of Phosphatidylinositol-4-phosphate 5-kinase, Type I, Gamma (PIP5K1C, Accession XM_047620). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP5K1C. Pleiomorphic Adenoma Gene-like 2 (PLAGL2, Accession XM_047007) is another VGAM2505 host target gene. PLAGL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLAGL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAGL2 BINDING SITE, designated SEQ ID:34877, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84888] Another function of VGAM2505 is therefore inhibition of Pleiomorphic Adenoma Gene-like 2 (PLAGL2, Accession XM_047007). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAGL2. PP3501 (Accession NM_021731) is another VGAM2505 host target gene. PP3501 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PP3501, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP3501 BINDING SITE, designated SEQ ID:22331, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84889] Another function of VGAM2505 is therefore inhibition of PP3501 (Accession NM_021731). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PP3501. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840) is another VGAM2505 host target gene. PPP1R16B BINDING SITE1 and PPP1R16B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PPP1R16B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R16B BINDING SITE1 and PPP1R16B BINDING SITE2, designated SEQ ID:30773 and SEQ ID:30769 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84890] Another function of VGAM2505 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R16B. RASD Family, Member 2 (RASD2, Accession NM_014310) is another VGAM2505 host target gene. RASD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

RASD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASD2 BINDING SITE, designated SEQ ID:15600, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84891] Another function of VGAM2505 is therefore inhibition of RASD Family, Member 2 (RASD2, Accession NM_014310). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASD2. Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958) is another VGAM2505 host target gene. RNF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE, designated SEQ ID:10095, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84892] Another function of VGAM2505 is therefore inhibition of

Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF8. SCAMP5 (Accession NM_138967) is another VGAM2505 host target gene. SCAMP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAMP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAMP5 BINDING SITE, designated SEQ ID:29074, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84893] Another function of VGAM2505 is therefore inhibition of SCAMP5 (Accession NM_138967). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP5. Sema Domain, Immunoglobulin Domain (Ig), Transmembrane Domain (TM) and Short Cytoplasmic Domain, (semaphorin) 4G (SEMA4G, Accession NM_017893) is another VGAM2505 host target gene. SEMA4G BINDING SITE1 and SEMA4G BINDING SITE2 are HOST TARGET bind-

ing sites found in untranslated regions of mRNA encoded by SEMA4G, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA4G BINDING SITE1 and SEMA4G BINDING SITE2, designated SEQ ID:19564 and SEQ ID:45413 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84894] Another function of VGAM2505 is therefore inhibition of Sema Domain, Immunoglobulin Domain (Ig), Transmembrane Domain (TM) and Short Cytoplasmic Domain, (semaphorin) 4G (SEMA4G, Accession NM_017893). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA4G. Trinucleotide Repeat Containing 4 (TNRC4, Accession NM_007185) is another VGAM2505 host target gene. TNRC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNRC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNRC4 BINDING SITE, des-

ignated SEQ ID:14040, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84895] Another function of VGAM2505 is therefore inhibition of Trinucleotide Repeat Containing 4 (TNRC4, Accession NM_007185). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNRC4. Tubby Homolog (mouse) (TUB, Accession NM_003320) is another VGAM2505 host target gene. TUB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUB BINDING SITE, designated SEQ ID:9323, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84896] Another function of VGAM2505 is therefore inhibition of Tubby Homolog (mouse) (TUB, Accession NM_003320). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUB. Ubiquitin Specific Protease 22

(USP22, Accession XM_042698) is another VGAM2505 host target gene. USP22 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP22 BINDING SITE, designated SEQ ID:33751, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84897] Another function of VGAM2505 is therefore inhibition of Ubiquitin Specific Protease 22 (USP22, Accession XM_042698). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP22. Vacuolar Protein Sorting 33A (yeast) (VPS33A, Accession NM_022916) is another VGAM2505 host target gene. VPS33A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS33A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS33A BINDING SITE, designated SEQ ID:23231, to the

nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84898] Another function of VGAM2505 is therefore inhibition of Vacuolar Protein Sorting 33A (yeast) (VPS33A, Accession NM_022916). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS33A. Williams-Beuren Syndrome Chromosome Region 23 (WBSCR23, Accession NM_025042) is another VGAM2505 host target gene. WBSCR23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WBSCR23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WBSCR23 BINDING SITE, designated SEQ ID:24637, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84899] Another function of VGAM2505 is therefore inhibition of Williams-Beuren Syndrome Chromosome Region 23 (WBSCR23, Accession NM_025042). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

WBSCR23. LOC112724 (Accession NM_138412) is another VGAM2505 host target gene. LOC112724 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC112724, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112724 BINDING SITE, designated SEQ ID:28777, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84900] Another function of VGAM2505 is therefore inhibition of LOC112724 (Accession NM_138412). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112724. LOC115399 (Accession XM_055874) is another VGAM2505 host target gene. LOC115399 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115399, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115399 BINDING SITE, designated SEQ ID:36346, to the nucleotide sequence of VGAM2505 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5216.

[84901] Another function of VGAM2505 is therefore inhibition of LOC115399 (Accession XM_055874). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115399. LOC116113 (Accession XM_166413) is another VGAM2505 host target gene. LOC116113 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC116113, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC116113 BINDING SITE, designated SEQ ID:44284, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84902] Another function of VGAM2505 is therefore inhibition of LOC116113 (Accession XM_166413). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116113. LOC116411 (Accession XM_058095) is another VGAM2505 host target gene. LOC116411 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC116411, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC116411 BINDING SITE, designated SEQ ID:36568, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84903] Another function of VGAM2505 is therefore inhibition of LOC116411 (Accession XM_058095). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116411. LOC124976 (Accession XM_058879) is another VGAM2505 host target gene. LOC124976 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124976, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124976 BINDING SITE, designated SEQ ID:36783, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84904] Another function of VGAM2505 is therefore inhibition of LOC124976 (Accession XM_058879). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC124976. LOC130813 (Accession XM_065904) is another VGAM2505 host target gene. LOC130813 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:37310, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84905] Another function of VGAM2505 is therefore inhibition of LOC130813 (Accession XM_065904). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813. LOC132625 (Accession XM_067946) is another VGAM2505 host target gene. LOC132625 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC132625, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132625 BINDING SITE, designated SEQ ID:37373, to

the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84906] Another function of VGAM2505 is therefore inhibition of LOC132625 (Accession XM_067946). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132625. LOC135818 (Accession XM_059804) is another VGAM2505 host target gene. LOC135818 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135818, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135818 BINDING SITE, designated SEQ ID:37093, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84907] Another function of VGAM2505 is therefore inhibition of LOC135818 (Accession XM_059804). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135818. LOC143187 (Accession NM_145206) is another VGAM2505 host target gene. LOC143187 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC143187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143187 BINDING SITE, designated SEQ ID:29744, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84908] Another function of VGAM2505 is therefore inhibition of LOC143187 (Accession NM_145206). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143187. LOC144248 (Accession XM_084786) is another VGAM2505 host target gene. LOC144248 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144248, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144248 BINDING SITE, designated SEQ ID:37700, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84909] Another function of VGAM2505 is therefore inhibition of LOC144248 (Accession XM_084786). Accordingly, utilities

of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144248. LOC144524 (Accession XM_096624) is another VGAM2505 host target gene. LOC144524 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144524, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144524 BINDING SITE, designated SEQ ID:40433, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84910] Another function of VGAM2505 is therefore inhibition of LOC144524 (Accession XM_096624). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144524. LOC145468 (Accession XM_057874) is another VGAM2505 host target gene. LOC145468 BINDING SITE1 and LOC145468 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC145468, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of LOC145468 BINDING SITE1 and LOC145468 BINDING SITE2, designated SEQ ID:36545 and SEQ ID:36546 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84911] Another function of VGAM2505 is therefore inhibition of LOC145468 (Accession XM_057874). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145468. LOC145693 (Accession XM_085205) is another VGAM2505 host target gene. LOC145693 BINDING SITE1 and LOC145693 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC145693, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145693 BINDING SITE1 and LOC145693 BINDING SITE2, designated SEQ ID:37924 and SEQ ID:38031 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84912] Another function of VGAM2505 is therefore inhibition of LOC145693 (Accession XM_085205). Accordingly, utilities

of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145693. LOC146733 (Accession XM_097076) is another VGAM2505 host target gene. LOC146733 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146733, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146733 BINDING SITE, designated SEQ ID:40729, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84913] Another function of VGAM2505 is therefore inhibition of LOC146733 (Accession XM_097076). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146733. LOC146784 (Accession XM_085588) is another VGAM2505 host target gene. LOC146784 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146784, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC146784 BINDING SITE, designated SEQ ID:38237, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84914] Another function of VGAM2505 is therefore inhibition of LOC146784 (Accession XM_085588). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146784. LOC146839 (Accession XM_097107) is another VGAM2505 host target gene. LOC146839 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146839, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146839 BINDING SITE, designated SEQ ID:40753, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84915] Another function of VGAM2505 is therefore inhibition of LOC146839 (Accession XM_097107). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146839. LOC146957 (Accession XM_085652) is another VGAM2505 host target gene. LOC146957 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146957, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146957 BINDING SITE, designated SEQ ID:38284, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84916] Another function of VGAM2505 is therefore inhibition of LOC146957 (Accession XM_085652). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146957. LOC147817 (Accession XM_085903) is another VGAM2505 host target gene. LOC147817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE, designated SEQ ID:38384, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84917] Another function of VGAM2505 is therefore inhibition of

LOC147817 (Accession XM_085903). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817. LOC147958 (Accession XM_103258) is another VGAM2505 host target gene. LOC147958 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147958, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147958 BINDING SITE, designated SEQ ID:42152, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84918] Another function of VGAM2505 is therefore inhibition of LOC147958 (Accession XM_103258). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147958. LOC148137 (Accession NM_144692) is another VGAM2505 host target gene. LOC148137 BINDING SITE1 and LOC148137 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC148137, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE1 and LOC148137 BINDING SITE2, designated SEQ ID:29514 and SEQ ID:29515 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84919] Another function of VGAM2505 is therefore inhibition of LOC148137 (Accession NM_144692). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148137. LOC149506 (Accession XM_097661) is another VGAM2505 host target gene. LOC149506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149506, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE, designated SEQ ID:41000, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84920] Another function of VGAM2505 is therefore inhibition of LOC149506 (Accession XM_097661). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC149506. LOC149577 (Accession XM_097675) is another VGAM2505 host target gene. LOC149577 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149577 BINDING SITE, designated SEQ ID:41024, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84921] Another function of VGAM2505 is therefore inhibition of LOC149577 (Accession XM_097675). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149577. LOC150155 (Accession XM_047977) is another VGAM2505 host target gene. LOC150155 BINDING SITE1 and LOC150155 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC150155, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150155 BINDING SITE1

and LOC150155 BINDING SITE2, designated SEQ ID:35086 and SEQ ID:35087 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84922] Another function of VGAM2505 is therefore inhibition of LOC150155 (Accession XM_047977). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150155. LOC151201 (Accession XM_098021) is another VGAM2505 host target gene. LOC151201 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151201, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE, designated SEQ ID:41321, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84923] Another function of VGAM2505 is therefore inhibition of LOC151201 (Accession XM_098021). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201. LOC151475 (Accession XM_098063) is an-

other VGAM2505 host target gene. LOC151475 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151475 BINDING SITE, designated SEQ ID:41355, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84924] Another function of VGAM2505 is therefore inhibition of LOC151475 (Accession XM_098063). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151475. LOC153525 (Accession XM_098383) is another VGAM2505 host target gene. LOC153525 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153525, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153525 BINDING SITE, designated SEQ ID:41638, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84925] Another function of VGAM2505 is therefore inhibition of LOC153525 (Accession XM_098383). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153525. LOC153688 (Accession XM_098416) is another VGAM2505 host target gene. LOC153688 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153688, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153688 BINDING SITE, designated SEQ ID:41658, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84926] Another function of VGAM2505 is therefore inhibition of LOC153688 (Accession XM_098416). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153688. LOC154282 (Accession XM_098505) is another VGAM2505 host target gene. LOC154282 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154282, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154282 BINDING SITE, designated SEQ ID:41698, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84927] Another function of VGAM2505 is therefore inhibition of LOC154282 (Accession XM_098505). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154282. LOC154726 (Accession XM_088024) is another VGAM2505 host target gene. LOC154726 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154726, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154726 BINDING SITE, designated SEQ ID:39477, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84928] Another function of VGAM2505 is therefore inhibition of LOC154726 (Accession XM_088024). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC154726. LOC155006 (Accession XM_088117) is another VGAM2505 host target gene. LOC155006 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155006, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155006 BINDING SITE, designated SEQ ID:39523, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84929] Another function of VGAM2505 is therefore inhibition of LOC155006 (Accession XM_088117). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155006. LOC157247 (Accession XM_088275) is another VGAM2505 host target gene. LOC157247 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157247 BINDING SITE, designated SEQ ID:39576, to the nucleotide sequence of VGAM2505 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5216.

[84930] Another function of VGAM2505 is therefore inhibition of LOC157247 (Accession XM_088275). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157247. LOC195977 (Accession XM_113625) is another VGAM2505 host target gene. LOC195977 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC195977, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC195977 BINDING SITE, designated SEQ ID:42300, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84931] Another function of VGAM2505 is therefore inhibition of LOC195977 (Accession XM_113625). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC195977. LOC200014 (Accession XM_114087) is another VGAM2505 host target gene. LOC200014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200014, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200014 BINDING SITE, designated SEQ ID:42689, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84932] Another function of VGAM2505 is therefore inhibition of LOC200014 (Accession XM_114087). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200014. LOC200314 (Accession XM_117225) is another VGAM2505 host target gene. LOC200314 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200314, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200314 BINDING SITE, designated SEQ ID:43293, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84933] Another function of VGAM2505 is therefore inhibition of LOC200314 (Accession XM_117225). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC200314. LOC200860 (Accession XM_117289) is another VGAM2505 host target gene. LOC200860 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200860, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200860 BINDING SITE, designated SEQ ID:43353, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84934] Another function of VGAM2505 is therefore inhibition of LOC200860 (Accession XM_117289). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200860. LOC204804 (Accession XM_115599) is another VGAM2505 host target gene. LOC204804 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC204804, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC204804 BINDING SITE, designated SEQ ID:43097, to

the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84935] Another function of VGAM2505 is therefore inhibition of LOC204804 (Accession XM_115599). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC204804. LOC219653 (Accession XM_166093) is another VGAM2505 host target gene. LOC219653 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219653, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219653 BINDING SITE, designated SEQ ID:43869, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84936] Another function of VGAM2505 is therefore inhibition of LOC219653 (Accession XM_166093). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219653. LOC219920 (Accession XM_167787) is another VGAM2505 host target gene. LOC219920 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC219920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219920 BINDING SITE, designated SEQ ID:44804, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84937] Another function of VGAM2505 is therefore inhibition of LOC219920 (Accession XM_167787). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219920. LOC220662 (Accession XM_165978) is another VGAM2505 host target gene. LOC220662 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220662, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220662 BINDING SITE, designated SEQ ID:43822, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84938] Another function of VGAM2505 is therefore inhibition of LOC220662 (Accession XM_165978). Accordingly, utilities

of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220662. LOC221250 (Accession XM_166301) is another VGAM2505 host target gene. LOC221250 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221250, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221250 BINDING SITE, designated SEQ ID:44117, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84939] Another function of VGAM2505 is therefore inhibition of LOC221250 (Accession XM_166301). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221250. LOC221296 (Accession XM_166325) is another VGAM2505 host target gene. LOC221296 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221296, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC221296 BINDING SITE, designated SEQ ID:44167, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84940] Another function of VGAM2505 is therefore inhibition of LOC221296 (Accession XM_166325). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221296. LOC221336 (Accession XM_166427) is another VGAM2505 host target gene. LOC221336 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221336, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221336 BINDING SITE, designated SEQ ID:44319, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84941] Another function of VGAM2505 is therefore inhibition of LOC221336 (Accession XM_166427). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221336. LOC221424 (Accession XM_168060) is another VGAM2505 host target gene. LOC221424 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221424, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221424 BINDING SITE, designated SEQ ID:44978, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84942] Another function of VGAM2505 is therefore inhibition of LOC221424 (Accession XM_168060). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221424. LOC221663 (Accession XM_168131) is another VGAM2505 host target gene. LOC221663 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221663, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221663 BINDING SITE, designated SEQ ID:45039, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84943] Another function of VGAM2505 is therefore inhibition of

LOC221663 (Accession XM_168131). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221663. LOC253092 (Accession XM_173583) is another VGAM2505 host target gene. LOC253092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253092 BINDING SITE, designated SEQ ID:46549, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84944] Another function of VGAM2505 is therefore inhibition of LOC253092 (Accession XM_173583). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253092. LOC254428 (Accession XM_170932) is another VGAM2505 host target gene. LOC254428 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254428, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC254428 BINDING SITE, designated SEQ ID:45716, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84945] Another function of VGAM2505 is therefore inhibition of LOC254428 (Accession XM_170932). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254428. LOC255177 (Accession XM_172941) is another VGAM2505 host target gene. LOC255177 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255177, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255177 BINDING SITE, designated SEQ ID:46201, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84946] Another function of VGAM2505 is therefore inhibition of LOC255177 (Accession XM_172941). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255177. LOC256306 (Accession XM_172976) is an-

other VGAM2505 host target gene. LOC256306 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256306, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256306 BINDING SITE, designated SEQ ID:46236, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84947] Another function of VGAM2505 is therefore inhibition of LOC256306 (Accession XM_172976). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256306. LOC257468 (Accession XM_170838) is another VGAM2505 host target gene. LOC257468 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257468 BINDING SITE, designated SEQ ID:45626, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84948] Another function of VGAM2505 is therefore inhibition of LOC257468 (Accession XM_170838). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257468. LOC51193 (Accession NM_016331) is another VGAM2505 host target gene. LOC51193 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51193 BINDING SITE, designated SEQ ID:18455, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84949] Another function of VGAM2505 is therefore inhibition of LOC51193 (Accession NM_016331). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51193. LOC51219 (Accession NM_016418) is another VGAM2505 host target gene. LOC51219 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51219, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51219 BINDING SITE, designated SEQ ID:18544, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84950] Another function of VGAM2505 is therefore inhibition of LOC51219 (Accession NM_016418). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51219. LOC81034 (Accession NM_030780) is another VGAM2505 host target gene. LOC81034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC81034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC81034 BINDING SITE, designated SEQ ID:25069, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84951] Another function of VGAM2505 is therefore inhibition of LOC81034 (Accession NM_030780). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC81034. LOC89932 (Accession XM_027341) is another VGAM2505 host target gene. LOC89932 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC89932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89932 BINDING SITE, designated SEQ ID:30488, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84952] Another function of VGAM2505 is therefore inhibition of LOC89932 (Accession XM_027341). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC89932. LOC90288 (Accession XM_030669) is another VGAM2505 host target gene. LOC90288 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90288 BINDING SITE, designated SEQ ID:31106, to the nucleotide sequence of VGAM2505 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5216.

[84953] Another function of VGAM2505 is therefore inhibition of LOC90288 (Accession XM_030669). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90288. LOC90371 (Accession XM_031261) is another VGAM2505 host target gene. LOC90371 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90371, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90371 BINDING SITE, designated SEQ ID:31320, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84954] Another function of VGAM2505 is therefore inhibition of LOC90371 (Accession XM_031261). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90371. LOC90591 (Accession XM_032811) is another VGAM2505 host target gene. LOC90591 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90591, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90591 BINDING SITE, designated SEQ ID:31756, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84955] Another function of VGAM2505 is therefore inhibition of LOC90591 (Accession XM_032811). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90591. LOC91115 (Accession XM_036218) is another VGAM2505 host target gene. LOC91115 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91115, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE, designated SEQ ID:32394, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84956] Another function of VGAM2505 is therefore inhibition of LOC91115 (Accession XM_036218). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC91115. LOC91252 (Accession XM_037173) is another VGAM2505 host target gene. LOC91252 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91252, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91252 BINDING SITE, designated SEQ ID:32552, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84957] Another function of VGAM2505 is therefore inhibition of LOC91252 (Accession XM_037173). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91252. LOC92267 (Accession XM_043979) is another VGAM2505 host target gene. LOC92267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92267 BINDING SITE, designated SEQ ID:34054, to the

nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84958] Another function of VGAM2505 is therefore inhibition of LOC92267 (Accession XM_043979). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92267. LOC92697 (Accession XM_046715) is another VGAM2505 host target gene. LOC92697 BINDING SITE1 and LOC92697 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC92697, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92697 BINDING SITE1 and LOC92697 BINDING SITE2, designated SEQ ID:34800 and SEQ ID:34801 respectively, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84959] Another function of VGAM2505 is therefore inhibition of LOC92697 (Accession XM_046715). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92697. Protocadherin 11 X-linked (PCDH11X, Acces-

sion NM_032968) is another VGAM2506 host target gene. PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDH11X, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2, designated SEQ ID:26785 and SEQ ID:26800 respectively, to the nucleotide sequence of VGAM2506 RNA, herein designated VGAM RNA, also designated SEQ ID:5217.

[84960] Another function of VGAM2506 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032968), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM2506 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.LOC124602 (Accession XM_058829) is another

VGAM2506 host target gene. LOC124602 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124602, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124602 BINDING SITE, designated SEQ ID:36759, to the nucleotide sequence of VGAM2506 RNA, herein designated VGAM RNA, also designated SEQ ID:5217.

[84961] Another function of VGAM2506 is therefore inhibition of LOC124602 (Accession XM_058829). Accordingly, utilities of VGAM2506 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124602. LOC201229 (Accession XM_113925) is another VGAM2506 host target gene. LOC201229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201229 BINDING SITE, designated SEQ ID:42540, to the nucleotide sequence of VGAM2506 RNA, herein designated VGAM RNA, also designated SEQ ID:5217.

[84962] Another function of VGAM2506 is therefore inhibition of LOC201229 (Accession XM_113925). Accordingly, utilities of VGAM2506 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201229. LOC203397 (Accession XM_114695) is another VGAM2506 host target gene. LOC203397 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203397 BINDING SITE, designated SEQ ID:43039, to the nucleotide sequence of VGAM2506 RNA, herein designated VGAM RNA, also designated SEQ ID:5217.

[84963] Another function of VGAM2506 is therefore inhibition of LOC203397 (Accession XM_114695). Accordingly, utilities of VGAM2506 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203397. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2507 (VGAM2507) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[84964] VGAM2507 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2507 was detected is described hereinabove with reference to Figs. 1-8.

[84965] VGAM2507 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2507 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84966] VGAM2507 gene encodes a VGAM2507 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2507 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2507 precursor RNA is designated SEQ ID:2493, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2493 is located at position 38544 relative to the genome of Mouse Cytomegalovirus 1.

[84967] VGAM2507 precursor RNA folds onto itself, forming VGAM2507 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84968] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2507 folded precursor RNA into VGAM2507 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2507 RNA is designated SEQ ID:5218, and is provided hereinbelow with reference to the sequence listing part.

[84969] VGAM2507 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2507 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84970] VGAM2507 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2507 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2507 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84971] The complementary binding of VGAM2507 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2507 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2507 host target RNA into VGAM2507 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84972] It is appreciated that VGAM2507 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2507 host target genes. The mRNA of each one of this plurality of VGAM2507 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2507 RNA, herein designated VGAM RNA, and which when bound by VGAM2507 RNA causes inhibition of translation of respective one or more VGAM2507 host target proteins.

[84973] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2507 gene, herein designated VGAM GENE, on one or more VGAM2507 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84974] It is yet further appreciated that a function of VGAM2507 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2507 correlate with, and may be deduced from, the identity of the host target genes which VGAM2507 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[84975] Nucleotide sequences of the VGAM2507 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2507 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2507 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2507 are further described hereinbelow with reference to Table 1.

[84976] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2507 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2507 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84977] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2507 gene, herein designated VGAM is inhibition of expression of VGAM2507 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2507 correlate with, and may be deduced from, the identity of the target genes which VGAM2507 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84978] BCL2-like 2 (BCL2L2, Accession NM_004050) is a VGAM2507 host target gene. BCL2L2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL2L2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL2L2 BINDING SITE, designated SEQ ID:10258, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84979] A function of VGAM2507 is therefore inhibition of BCL2-like 2 (BCL2L2, Accession NM_004050), a gene which promotes cell survival. Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL2L2. The function of BCL2L2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM431.Solute Carrier Family 16 (monocarboxylic acid transporters), Member 2 (putative transporter) (SLC16A2, Accession NM_006517) is another VGAM2507 host target gene. SLC16A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by SLC16A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC16A2 BINDING SITE, designated SEQ ID:13268, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84980] Another function of VGAM2507 is therefore inhibition of Solute Carrier Family 16 (monocarboxylic acid transporters), Member 2 (putative transporter) (SLC16A2, Accession NM_006517). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A2. FLJ14525 (Accession NM_032800) is another VGAM2507 host target gene. FLJ14525 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14525, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14525 BINDING SITE, designated SEQ ID:26548, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84981] Another function of VGAM2507 is therefore inhibition of FLJ14525 (Accession NM_032800). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14525. FLJ20378 (Accession NM_017795) is another VGAM2507 host target gene. FLJ20378 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20378, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20378 BINDING SITE, designated SEQ ID:19435, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84982] Another function of VGAM2507 is therefore inhibition of FLJ20378 (Accession NM_017795). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20378. Thyroid Hormone Receptor Interactor 13 (TRIP13, Accession NM_004237) is another VGAM2507 host target gene. TRIP13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP13, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIP13 BINDING SITE, designated SEQ ID:10434, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84983] Another function of VGAM2507 is therefore inhibition of Thyroid Hormone Receptor Interactor 13 (TRIP13, Accession NM_004237). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP13. LOC120939 (Accession XM_073688) is another VGAM2507 host target gene. LOC120939 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC120939, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120939 BINDING SITE, designated SEQ ID:37513, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84984] Another function of VGAM2507 is therefore inhibition of LOC120939 (Accession XM_073688). Accordingly, utilities

of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120939. LOC152200 (Accession XM_098174) is another VGAM2507 host target gene. LOC152200 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152200, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152200 BINDING SITE, designated SEQ ID:41438, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84985] Another function of VGAM2507 is therefore inhibition of LOC152200 (Accession XM_098174). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152200. LOC203276 (Accession XM_117523) is another VGAM2507 host target gene. LOC203276 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC203276 BINDING SITE, designated SEQ ID:43488, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84986] Another function of VGAM2507 is therefore inhibition of LOC203276 (Accession XM_117523). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203276. LOC203305 (Accession XM_117529) is another VGAM2507 host target gene. LOC203305 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203305, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203305 BINDING SITE, designated SEQ ID:43512, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84987] Another function of VGAM2507 is therefore inhibition of LOC203305 (Accession XM_117529). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203305. LOC255696 (Accession XM_173933) is another VGAM2507 host target gene. LOC255696 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255696, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255696 BINDING SITE, designated SEQ ID:46567, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84988] Another function of VGAM2507 is therefore inhibition of LOC255696 (Accession XM_173933). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255696. LOC90019 (Accession NM_138567) is another VGAM2507 host target gene. LOC90019 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90019, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90019 BINDING SITE, designated SEQ ID:28870, to the nucleotide sequence of VGAM2507 RNA, herein designated VGAM RNA, also designated SEQ ID:5218.

[84989] Another function of VGAM2507 is therefore inhibition of

LOC90019 (Accession NM_138567). Accordingly, utilities of VGAM2507 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90019. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2508 (VGAM2508) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84990] VGAM2508 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2508 was detected is described hereinabove with reference to Figs. 1-8.

[84991] VGAM2508 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2508 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84992] VGAM2508 gene encodes a VGAM2508 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2508 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2508 precursor RNA is designated SEQ ID:2494, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2494 is located at position 168766 relative to the genome of Mouse Cytomegalovirus 1.

[84993] VGAM2508 precursor RNA folds onto itself, forming VGAM2508 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84994] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2508 folded precursor RNA into VGAM2508 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide se-

quence of VGAM2508 RNA is designated SEQ ID:5219, and is provided hereinbelow with reference to the sequence listing part.

[84995] VGAM2508 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2508 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84996] VGAM2508 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2508 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2508 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84997] The complementary binding of VGAM2508 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2508 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2508 host target RNA into VGAM2508 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84998] It is appreciated that VGAM2508 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2508 host target genes. The mRNA of each one of this plurality of VGAM2508 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2508 RNA, herein designated VGAM RNA, and which when bound by VGAM2508 RNA causes inhibition of translation of respective one or more VGAM2508 host target proteins.

[84999] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2508 gene, herein designated VGAM GENE, on one or more VGAM2508 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85000] It is yet further appreciated that a function of VGAM2508

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2508 correlate with, and may be deduced from, the identity of the host target genes which VGAM2508 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85001] Nucleotide sequences of the VGAM2508 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2508 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2508 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2508 are further described hereinbelow with reference to Table 1.

[85002] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2508 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2508 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85003] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2508 gene, herein designated VGAM is inhibition of expression of VGAM2508 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2508 correlate with, and may be deduced from, the identity of the target genes which VGAM2508 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85004] Aristaless-like Homeobox 3 (ALX3, Accession NM_006492) is a VGAM2508 host target gene. ALX3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALX3 BINDING SITE, designated SEQ ID:13222, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85005] A function of VGAM2508 is therefore inhibition of Aristaless-like Homeobox 3 (ALX3, Accession NM_006492), a gene which is involved in cell-type differentiation and development. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with ALX3. The function of ALX3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Amyloid Beta (A4) Precursor Protein-binding, Family A, Member 2 (X11-like) (APBA2, Accession NM_005503) is another VGAM2508 host target gene. APBA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APBA2 BINDING SITE, designated SEQ ID:12018, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85006] Another function of VGAM2508 is therefore inhibition of Amyloid Beta (A4) Precursor Protein-binding, Family A, Member 2 (X11-like) (APBA2, Accession NM_005503), a gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

APBA2. The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM925.Bone Morphogenetic Protein 1 (BMP1, Accession NM_006131) is another VGAM2508 host target gene. BMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BMP1 BINDING SITE, designated SEQ ID:12768, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85007] Another function of VGAM2508 is therefore inhibition of Bone Morphogenetic Protein 1 (BMP1, Accession NM_006131), a gene which cleaves procollagens leading to formation of extracellular matrix. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMP1. The function of BMP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with refer-

ence to VGAM247.Core-binding Factor, Runt Domain, Alpha Subunit 2; Translocated To, 1; Cyclin D-related (CBFA2T1, Accession NM_004349) is another VGAM2508 host target gene. CBFA2T1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CBFA2T1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBFA2T1 BINDING SITE, designated SEQ ID:10543, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85008] Another function of VGAM2508 is therefore inhibition of Core-binding Factor, Runt Domain, Alpha Subunit 2; Translocated To, 1; Cyclin D-related (CBFA2T1, Accession NM_004349), a gene which produces a chimeric gene made up of the 5-prime region of the AML1 gene fused to the 3-prime region of the ETO gene through translocation. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T1. The function of CBFA2T1 and its association with various diseases and clinical conditions, has been established by previous stud-

ies, as described hereinabove with reference to VGAM113.Cell Division Cycle 25B (CDC25B, Accession NM_021874) is another VGAM2508 host target gene. CDC25B BINDING SITE1 and CDC25B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CDC25B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDC25B BINDING SITE1 and CDC25B BINDING SITE2, designated SEQ ID:22417 and SEQ ID:22413 respectively, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85009] Another function of VGAM2508 is therefore inhibition of Cell Division Cycle 25B (CDC25B, Accession NM_021874), a gene which is positively activated by dephosphorylation. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC25B. The function of CDC25B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM165.EPB72 (Accession NM_004099) is another VGAM2508 host target

gene. EPB72 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPB72, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPB72 BINDING SITE, designated SEQ ID:10304, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85010] Another function of VGAM2508 is therefore inhibition of EPB72 (Accession NM_004099), a gene which may regulate cation conductance. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB72. The function of EPB72 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1560.Epilepsy, Progressive Myoclonus Type 2, Lafora Disease (laforin) (EPM2A, Accession NM_005670) is another VGAM2508 host target gene. EPM2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPM2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPM2A BINDING SITE, designated SEQ ID:12227, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85011] Another function of VGAM2508 is therefore inhibition of Epilepsy, Progressive Myoclonus Type 2, Lafora Disease (laforin) (EPM2A, Accession NM_005670), a gene which Laforin; protein tyrosine phosphatase that may have role in glycogen metabolism. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPM2A. The function of EPM2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM470.Farnesyltransferase, CAAX Box, Beta (FNTB, Accession NM_002028) is another VGAM2508 host target gene. FNTB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FNTB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FNTB BINDING SITE, designated SEQ ID:7781,

to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85012] Another function of VGAM2508 is therefore inhibition of Farnesyltransferase, CAAX Box, Beta (FNTB, Accession NM_002028), a gene which transfers farnesyl groups to proteins. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FNTB. The function of FNTB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM615.Guanine Nucleotide-releasing Factor 2 (specific for crk proto-oncogene) (GRF2, Accession NM_005312) is another VGAM2508 host target gene. GRF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRF2 BINDING SITE, designated SEQ ID:11790, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85013] Another function of VGAM2508 is therefore inhibition of

Guanine Nucleotide-releasing Factor 2 (specific for crk proto-oncogene) (GRF2, Accession NM_005312), a gene which promotes the exchange of ras-bound gdp by gtp. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRF2. The function of GRF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Hepsin (transmembrane protease, serine 1) (HPN, Accession NM_002151) is another VGAM2508 host target gene. HPN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HPN BINDING SITE, designated SEQ ID:7932, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85014] Another function of VGAM2508 is therefore inhibition of Hepsin (transmembrane protease, serine 1) (HPN, Accession NM_002151), a gene which is a cell surface serine protease. Accordingly, utilities of VGAM2508 include di-

agnosis, prevention and treatment of diseases and clinical conditions associated with HPN. The function of HPN has been established by previous studies. Hepsin is a cell surface serine protease. From cDNA libraries prepared from human liver and hepatoma cell line mRNA, Leytus et al. (1988) isolated cDNA clones coding for a serine protease called hepsin. The proteolytic enzymes of the serine protease family exist as single- or 2-chain zymogenes that are activated by a specific and limited proteolytic cleavage. They contain 3 principal active-site amino acids, his, asp, and ser, that participate in peptide bond hydrolysis. Among the best-studied serine proteases are those found in plasma. These enzymes are involved in processes such as blood coagulation, fibrinolysis, and complement activation. Tsuji et al. (1991) showed that the hepsin mRNA is 1.85 kb in size and present in most tissues, with the highest level in liver. It is present in the plasma membrane in a molecular orientation of type II membrane-associated proteins, with its catalytic subunit (C-terminal half) at the cell surface and its N terminus facing the cytosol. Hepsin is not found in cytosol. See also TMPRSS2 (OMIM Ref. No. 602060), a related serine protease. Animal model experiments lend further support to the function of HPN. To de-

termine the functional importance of hepsin, Wu et al. (1998) generated hepsin-deficient mice by homologous recombination. The homozygous deficient mice were viable and fertile, and grew normally. In functional assays, including tail bleeding time, plasma clotting times, and tissue factor- or LPS-induced disseminated intravascular coagulation models, no significant difference was found between hepsin -/- and wildtype littermates. Liver weight and serum concentrations of liver-derived proteins and enzymes were similar. Serum concentrations of bone-derived alkaline phosphatase were approximately 2-fold higher in hepsin -/- mice of both sexes when compared with wildtype littermates. No obvious abnormalities were found in major organs in hepsin -/- mice on histologic examination. The results indicated that hepsin is not essential for embryonic development and normal hemostasis.

[85015] It is appreciated that the abovementioned animal model for HPN is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[85016] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[85017] Leytus, S. P.; Loeb, K. R.; Hagen, F. S.; Kurachi, K.; Davie, E. W. : A novel trypsin-like serine protease (hepsin) with a putative transmembrane domain expressed by human liver and hepatoma cells. Biochemistry 27: 1067-1074, 1988. ; and

[85018] Tsuji, A.; Torres-Rosado, A.; Arai, T.; Le Beau, M. M.; Lemons, R. S.; Chou, S.-H.; Kurachi, K. : Hepsin, a cell membrane-associated protease: characterization, tissue distribution, and.

[85019] Further studies establishing the function and utilities of HPN are found in John Hopkins OMIM database record ID 142440, and in sited publications numbered 11565-11568 listed in the bibliography section hereinbe-low, which are also hereby incorporated by refer-ence.Integral Membrane Protein 2B (ITM2B, Accession NM_021999) is another VGAM2508 host target gene. ITM2B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ITM2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-quences of ITM2B BINDING SITE, designated SEQ

ID:22539, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85020] Another function of VGAM2508 is therefore inhibition of Integral Membrane Protein 2B (ITM2B, Accession NM_021999), a gene which is a member of the type II integral membrane protein family. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITM2B. The function of ITM2B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM458.Membrane Protein, Palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2, Accession XM_008355) is another VGAM2508 host target gene. MPP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MPP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPP2 BINDING SITE, designated SEQ ID:30083, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85021] Another function of VGAM2508 is therefore inhibition of Membrane Protein, Palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2, Accession XM_008355). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPP2. Mucin and Cadherin-like (MUCDHL, Accession NM_031265) is another VGAM2508 host target gene. MUCDHL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MUCDHL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MUCDHL BINDING SITE, designated SEQ ID:25283, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85022] Another function of VGAM2508 is therefore inhibition of Mucin and Cadherin-like (MUCDHL, Accession NM_031265). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MUCDHL. Nuclear Receptor Co-repressor 2 (NCOR2, Accession NM_006312) is another VGAM2508 host target gene. NCOR2 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NCOR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOR2 BINDING SITE, designated SEQ ID:13003, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85023] Another function of VGAM2508 is therefore inhibition of Nuclear Receptor Co-repressor 2 (NCOR2, Accession NM_006312), a gene which mediates the transcriptional repression activity of some nuclear receptors by promoting chromatin condensation, thus preventing access of the basal transcription. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOR2. The function of NCOR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2346.Nuclear Factor I/A (NFIA, Accession XM_046827) is another VGAM2508 host target gene. NFIA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NFIA, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFIA BINDING SITE, designated SEQ ID:34842, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85024] Another function of VGAM2508 is therefore inhibition of Nuclear Factor I/A (NFIA, Accession XM_046827). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFIA. Ninjurin 1 (NINJ1, Accession NM_004148) is another VGAM2508 host target gene. NINJ1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NINJ1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NINJ1 BINDING SITE, designated SEQ ID:10351, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85025] Another function of VGAM2508 is therefore inhibition of Ninjurin 1 (NINJ1, Accession NM_004148), a gene which may play a role in nerve regeneration and in the formation

and function of other tissues. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NINJ1. The function of NINJ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1927.Neuronal Pentraxin I (NPTX1, Accession NM_002522) is another VGAM2508 host target gene. NPTX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPTX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPTX1 BINDING SITE, designated SEQ ID:8355, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85026] Another function of VGAM2508 is therefore inhibition of Neuronal Pentraxin I (NPTX1, Accession NM_002522), a gene which may be involved in synaptic uptake of extracellular material and is very strongly similar to rat NP1. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTX1. The function of NPTX1 and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.Paired Basic Amino Acid Cleaving System 4 (PACE4, Accession NM_002570) is another VGAM2508 host target gene. PACE4 BINDING SITE1 through PACE4 BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PACE4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PACE4 BINDING SITE1 through PACE4 BINDING SITE6, designated SEQ ID:8430, SEQ ID:28723, SEQ ID:28724, SEQ ID:28725, SEQ ID:28719 and SEQ ID:28722 respectively, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85027] Another function of VGAM2508 is therefore inhibition of Paired Basic Amino Acid Cleaving System 4 (PACE4, Accession NM_002570), a gene which processes hormone precursors by cleaving paired basic amino acids. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PACE4. The function of PACE4 and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1194.Plexin B2 (PLXNB2, Accession NM_012401) is another VGAM2508 host target gene. PLXNB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLXNB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLXNB2 BINDING SITE, designated SEQ ID:14777, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85028] Another function of VGAM2508 is therefore inhibition of Plexin B2 (PLXNB2, Accession NM_012401), a gene which is a novel member of the plexin family. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLXNB2. The function of PLXNB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM87.Retinoic Acid Induced 14 (RAI14, Accession NM_015577) is another VGAM2508

host target gene. RAI14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAI14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI14 BINDING SITE, designated SEQ ID:17845, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85029] Another function of VGAM2508 is therefore inhibition of Retinoic Acid Induced 14 (RAI14, Accession NM_015577), a gene which is required for protein transport from the er to the golgi complex. Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI14. The function of RAI14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1036.Sialic Acid Binding Ig-like Lectin 11 (SIGLEC11, Accession NM_052884) is another VGAM2508 host target gene. SIGLEC11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIGLEC11, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIGLEC11 BINDING SITE, designated SEQ ID:27465, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85030] Another function of VGAM2508 is therefore inhibition of Sialic Acid Binding Ig-like Lectin 11 (SIGLEC11, Accession NM_052884). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC11. Zinc Finger Protein 205 (ZNF205, Accession NM_003456) is another VGAM2508 host target gene. ZNF205 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF205 BINDING SITE, designated SEQ ID:9513, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85031] Another function of VGAM2508 is therefore inhibition of Zinc Finger Protein 205 (ZNF205, Accession NM_003456).

Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF205. DKFZp434E2220 (Accession NM_017612) is another VGAM2508 host target gene. DKFZp434E2220 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp434E2220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434E2220 BINDING SITE, designated SEQ ID:19110, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85032] Another function of VGAM2508 is therefore inhibition of DKFZp434E2220 (Accession NM_017612). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2220. Ets2 Repressor Factor (ERF, Accession NM_006494) is another VGAM2508 host target gene. ERF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of ERF BINDING SITE, designated SEQ ID:13236, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85033] Another function of VGAM2508 is therefore inhibition of Ets2 Repressor Factor (ERF, Accession NM_006494). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERF. Fer-1-like 4 (C. elegans) (FER1L4, Accession NM_025206) is another VGAM2508 host target gene. FER1L4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FER1L4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated SEQ ID:24873, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85034] Another function of VGAM2508 is therefore inhibition of Fer-1-like 4 (C. elegans) (FER1L4, Accession NM_025206). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with FER1L4. FLJ10709 (Accession NM_018188) is another VGAM2508 host target gene. FLJ10709 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10709, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10709 BINDING SITE, designated SEQ ID:20038, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85035] Another function of VGAM2508 is therefore inhibition of FLJ10709 (Accession NM_018188). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10709. FLJ10743 (Accession NM_018201) is another VGAM2508 host target gene. FLJ10743 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10743, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10743 BINDING SITE, designated SEQ ID:20078, to the nucleotide

sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85036] Another function of VGAM2508 is therefore inhibition of FLJ10743 (Accession NM_018201). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10743. FLJ12586 (Accession NM_024620) is another VGAM2508 host target gene. FLJ12586 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12586, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12586 BINDING SITE, designated SEQ ID:23882, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85037] Another function of VGAM2508 is therefore inhibition of FLJ12586 (Accession NM_024620). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12586. FLJ13710 (Accession NM_024817) is another VGAM2508 host target gene. FLJ13710 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ13710, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13710 BINDING SITE, designated SEQ ID:24207, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85038] Another function of VGAM2508 is therefore inhibition of FLJ13710 (Accession NM_024817). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13710. FLJ14327 (Accession NM_024912) is another VGAM2508 host target gene. FLJ14327 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14327, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14327 BINDING SITE, designated SEQ ID:24426, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85039] Another function of VGAM2508 is therefore inhibition of FLJ14327 (Accession NM_024912). Accordingly, utilities of

VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14327. FLJ14351 (Accession NM_024732) is another VGAM2508 host target gene. FLJ14351 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14351, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14351 BINDING SITE, designated SEQ ID:24070, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85040] Another function of VGAM2508 is therefore inhibition of FLJ14351 (Accession NM_024732). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14351. FLJ20647 (Accession NM_017918) is another VGAM2508 host target gene. FLJ20647 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20647, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20647

BINDING SITE, designated SEQ ID:19571, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85041] Another function of VGAM2508 is therefore inhibition of FLJ20647 (Accession NM_017918). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20647. FLJ21736 (Accession NM_024922) is another VGAM2508 host target gene. FLJ21736 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21736, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21736 BINDING SITE, designated SEQ ID:24461, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85042] Another function of VGAM2508 is therefore inhibition of FLJ21736 (Accession NM_024922). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21736. FLJ32884 (Accession NM_144702) is another VGAM2508 host target gene. FLJ32884 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ32884, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32884 BINDING SITE, designated SEQ ID:29528, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85043] Another function of VGAM2508 is therefore inhibition of FLJ32884 (Accession NM_144702). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32884. FXYD Domain Containing Ion Transport Regulator 3 (FXYD3, Accession NM_021910) is another VGAM2508 host target gene. FXYD3 BINDING SITE1 and FXYD3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FXYD3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FXYD3 BINDING SITE1 and FXYD3 BINDING SITE2, designated SEQ ID:22436 and SEQ ID:12593 respectively, to the nucleotide sequence of VGAM2508 RNA,

herein designated VGAM RNA, also designated SEQ ID:5219.

[85044] Another function of VGAM2508 is therefore inhibition of FXYD Domain Containing Ion Transport Regulator 3 (FXYD3, Accession NM_021910). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FXYD3. KIAA0481 (Accession XM_050144) is another VGAM2508 host target gene. KIAA0481 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0481, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0481 BINDING SITE, designated SEQ ID:35568, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85045] Another function of VGAM2508 is therefore inhibition of KIAA0481 (Accession XM_050144). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0481. KIAA1026 (Accession XM_048825) is another VGAM2508 host target gene. KIAA1026 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1026 BINDING SITE, designated SEQ ID:35275, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85046] Another function of VGAM2508 is therefore inhibition of KIAA1026 (Accession XM_048825). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1026. KIAA1126 (Accession XM_050325) is another VGAM2508 host target gene. KIAA1126 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1126, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1126 BINDING SITE, designated SEQ ID:35607, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85047] Another function of VGAM2508 is therefore inhibition of

KIAA1126 (Accession XM_050325). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1126. KIAA1344 (Accession XM_051699) is another VGAM2508 host target gene. KIAA1344 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1344, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1344 BINDING SITE, designated SEQ ID:35870, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85048] Another function of VGAM2508 is therefore inhibition of KIAA1344 (Accession XM_051699). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1344. KIAA1416 (Accession XM_098762) is another VGAM2508 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41808, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85049] Another function of VGAM2508 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. KIAA1538 (Accession XM_049474) is another VGAM2508 host target gene. KIAA1538 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1538 BINDING SITE, designated SEQ ID:35424, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85050] Another function of VGAM2508 is therefore inhibition of KIAA1538 (Accession XM_049474). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1538. KIAA1854 (Accession XM_049884) is another

VGAM2508 host target gene. KIAA1854 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1854, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1854 BINDING SITE, designated SEQ ID:35533, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85051] Another function of VGAM2508 is therefore inhibition of KIAA1854 (Accession XM_049884). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1854. KIAA1889 (Accession XM_056298) is another VGAM2508 host target gene. KIAA1889 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1889, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1889 BINDING SITE, designated SEQ ID:36388, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85052] Another function of VGAM2508 is therefore inhibition of KIAA1889 (Accession XM_056298). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1889. MGC13057 (Accession NM_032321) is another VGAM2508 host target gene. MGC13057 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC13057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13057 BINDING SITE, designated SEQ ID:26124, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85053] Another function of VGAM2508 is therefore inhibition of MGC13057 (Accession NM_032321). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13057. MGC21621 (Accession NM_145015) is another VGAM2508 host target gene. MGC21621 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC21621, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC21621 BINDING SITE, designated SEQ ID:29622, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85054] Another function of VGAM2508 is therefore inhibition of MGC21621 (Accession NM_145015). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21621. MGC2474 (Accession NM_023931) is another VGAM2508 host target gene. MGC2474 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE, designated SEQ ID:23416, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85055] Another function of VGAM2508 is therefore inhibition of MGC2474 (Accession NM_023931). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC2474. MGC2555 (Accession NM_032772) is another VGAM2508 host target gene. MGC2555 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC2555, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2555 BINDING SITE, designated SEQ ID:26519, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85056] Another function of VGAM2508 is therefore inhibition of MGC2555 (Accession NM_032772). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2555. moblak (Accession NM_130807) is another VGAM2508 host target gene. moblak BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by moblak, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of moblak BINDING SITE, designated SEQ ID:28304, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA,

also designated SEQ ID:5219.

[85057] Another function of VGAM2508 is therefore inhibition of moblak (Accession NM_130807). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with moblak. QKI (Accession XM_037438) is another VGAM2508 host target gene. QKI BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by QKI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of QKI BINDING SITE, designated SEQ ID:32618, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85058] Another function of VGAM2508 is therefore inhibition of QKI (Accession XM_037438). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with QKI. RoXaN (Accession NM_025013) is another VGAM2508 host target gene. RoXaN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RoXaN, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RoXaN BINDING SITE, designated SEQ ID:24602, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85059] Another function of VGAM2508 is therefore inhibition of RoXaN (Accession NM_025013). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RoXaN. SES2 (Accession NM_031459) is another VGAM2508 host target gene. SES2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SES2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SES2 BINDING SITE, designated SEQ ID:25482, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85060] Another function of VGAM2508 is therefore inhibition of SES2 (Accession NM_031459). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SES2. Serum Response Factor (c-fos serum response element-binding transcription factor) (SRF, Accession NM_003131) is another VGAM2508 host target gene. SRF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SRF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRF BINDING SITE, designated SEQ ID:9099, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85061] Another function of VGAM2508 is therefore inhibition of Serum Response Factor (c-fos serum response element-binding transcription factor) (SRF, Accession NM_003131). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRF. Upstream Binding Protein 1 (LBP-1a) (UBP1, Accession NM_014517) is another VGAM2508 host target gene. UBP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by UBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBP1 BINDING SITE, designated SEQ ID:15850, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85062] Another function of VGAM2508 is therefore inhibition of Upstream Binding Protein 1 (LBP-1a) (UBP1, Accession NM_014517). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBP1. Zinc Finger Protein 145 (Kruppel-like, expressed in promyelocytic leukemia) (ZNF145, Accession NM_006006) is another VGAM2508 host target gene. ZNF145 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF145, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF145 BINDING SITE, designated SEQ ID:12618, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85063] Another function of VGAM2508 is therefore inhibition of Zinc Finger Protein 145 (Kruppel-like, expressed in

promyelocytic leukemia) (ZNF145, Accession NM_006006). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF145. LOC124842 (Accession XM_064333) is another VGAM2508 host target gene. LOC124842 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124842, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124842 BINDING SITE, designated SEQ ID:37260, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85064] Another function of VGAM2508 is therefore inhibition of LOC124842 (Accession XM_064333). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124842. LOC145481 (Accession XM_085163) is another VGAM2508 host target gene. LOC145481 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145481, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145481 BINDING SITE, designated SEQ ID:37889, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85065] Another function of VGAM2508 is therefore inhibition of LOC145481 (Accession XM_085163). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145481. LOC147341 (Accession XM_097223) is another VGAM2508 host target gene. LOC147341 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147341, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147341 BINDING SITE, designated SEQ ID:40827, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85066] Another function of VGAM2508 is therefore inhibition of LOC147341 (Accession XM_097223). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC147341. LOC148809 (Accession XM_086325) is another VGAM2508 host target gene. LOC148809 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148809, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148809 BINDING SITE, designated SEQ ID:38594, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85067] Another function of VGAM2508 is therefore inhibition of LOC148809 (Accession XM_086325). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148809. LOC150319 (Accession XM_086816) is another VGAM2508 host target gene. LOC150319 BINDING SITE1 and LOC150319 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC150319, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150319 BINDING SITE1 and LOC150319 BINDING SITE2, designated SEQ ID:38893

and SEQ ID:38896 respectively, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85068] Another function of VGAM2508 is therefore inhibition of LOC150319 (Accession XM_086816). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150319. LOC157349 (Accession XM_088298) is another VGAM2508 host target gene. LOC157349 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157349, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157349 BINDING SITE, designated SEQ ID:39588, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85069] Another function of VGAM2508 is therefore inhibition of LOC157349 (Accession XM_088298). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157349. LOC157737 (Accession XM_098819) is another VGAM2508 host target gene. LOC157737 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157737, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157737 BINDING SITE, designated SEQ ID:41843, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85070] Another function of VGAM2508 is therefore inhibition of LOC157737 (Accession XM_098819). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157737. LOC166879 (Accession XM_106298) is another VGAM2508 host target gene. LOC166879 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC166879, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC166879 BINDING SITE, designated SEQ ID:42197, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85071] Another function of VGAM2508 is therefore inhibition of

LOC166879 (Accession XM_106298). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC166879. LOC196746 (Accession XM_113595) is another VGAM2508 host target gene. LOC196746 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196746, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196746 BINDING SITE, designated SEQ ID:42288, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85072] Another function of VGAM2508 is therefore inhibition of LOC196746 (Accession XM_113595). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196746. LOC197196 (Accession XM_117003) is another VGAM2508 host target gene. LOC197196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC197196 BINDING SITE, designated SEQ ID:43201, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85073] Another function of VGAM2508 is therefore inhibition of LOC197196 (Accession XM_117003). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197196. LOC199863 (Accession XM_117147) is another VGAM2508 host target gene. LOC199863 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199863, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199863 BINDING SITE, designated SEQ ID:43256, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85074] Another function of VGAM2508 is therefore inhibition of LOC199863 (Accession XM_117147). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199863. LOC203260 (Accession XM_114661) is an-

other VGAM2508 host target gene. LOC203260 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203260, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203260 BINDING SITE, designated SEQ ID:43022, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85075] Another function of VGAM2508 is therefore inhibition of LOC203260 (Accession XM_114661). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203260. LOC203378 (Accession XM_117541) is another VGAM2508 host target gene. LOC203378 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203378, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203378 BINDING SITE, designated SEQ ID:43552, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85076] Another function of VGAM2508 is therefore inhibition of LOC203378 (Accession XM_117541). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203378. LOC220021 (Accession XM_167814) is another VGAM2508 host target gene. LOC220021 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220021, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220021 BINDING SITE, designated SEQ ID:44850, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85077] Another function of VGAM2508 is therefore inhibition of LOC220021 (Accession XM_167814). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220021. LOC220776 (Accession XM_043388) is another VGAM2508 host target gene. LOC220776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220776, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220776 BINDING SITE, designated SEQ ID:33934, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85078] Another function of VGAM2508 is therefore inhibition of LOC220776 (Accession XM_043388). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220776. LOC254936 (Accession XM_170770) is another VGAM2508 host target gene. LOC254936 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254936, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254936 BINDING SITE, designated SEQ ID:45528, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85079] Another function of VGAM2508 is therefore inhibition of LOC254936 (Accession XM_170770). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC254936. LOC255271 (Accession XM_170945) is another VGAM2508 host target gene. LOC255271 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255271 BINDING SITE, designated SEQ ID:45727, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85080] Another function of VGAM2508 is therefore inhibition of LOC255271 (Accession XM_170945). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255271. LOC51008 (Accession NM_015947) is another VGAM2508 host target gene. LOC51008 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51008, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51008 BINDING SITE, designated SEQ ID:18062, to the nucleotide sequence of VGAM2508 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5219.

[85081] Another function of VGAM2508 is therefore inhibition of LOC51008 (Accession NM_015947). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51008. LOC81569 (Accession XM_030465) is another VGAM2508 host target gene. LOC81569 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC81569, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC81569 BINDING SITE, designated SEQ ID:31046, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85082] Another function of VGAM2508 is therefore inhibition of LOC81569 (Accession XM_030465). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC81569. LOC89919 (Accession XM_027244) is another VGAM2508 host target gene. LOC89919 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC89919, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89919 BINDING SITE, designated SEQ ID:30462, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85083] Another function of VGAM2508 is therefore inhibition of LOC89919 (Accession XM_027244). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC89919. LOC90019 (Accession NM_138567) is another VGAM2508 host target gene. LOC90019 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90019, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90019 BINDING SITE, designated SEQ ID:28873, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85084] Another function of VGAM2508 is therefore inhibition of LOC90019 (Accession NM_138567). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC90019. LOC90355 (Accession NM_033211) is another VGAM2508 host target gene. LOC90355 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90355, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90355 BINDING SITE, designated SEQ ID:27063, to the nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85085] Another function of VGAM2508 is therefore inhibition of LOC90355 (Accession NM_033211). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90355. LOC91252 (Accession XM_037173) is another VGAM2508 host target gene. LOC91252 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91252, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91252 BINDING SITE, designated SEQ ID:32554, to the

nucleotide sequence of VGAM2508 RNA, herein designated VGAM RNA, also designated SEQ ID:5219.

[85086] Another function of VGAM2508 is therefore inhibition of LOC91252 (Accession XM_037173). Accordingly, utilities of VGAM2508 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91252. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2509 (VGAM2509) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85087] VGAM2509 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2509 was detected is described hereinabove with reference to Figs. 1-8.

[85088] VGAM2509 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2509 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85089] VGAM2509 gene encodes a VGAM2509 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2509 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2509 precursor RNA is designated SEQ ID:2495, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2495 is located at position 220001 relative to the genome of Mouse Cytomegalovirus 1.

[85090] VGAM2509 precursor RNA folds onto itself, forming VGAM2509 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85091] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2509 folded precursor RNA into VGAM2509 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2509 RNA is designated SEQ ID:5220, and is provided hereinbelow with reference to the sequence listing part.

[85092] VGAM2509 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2509 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85093] VGAM2509 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2509 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2509 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85094] The complementary binding of VGAM2509 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2509 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2509 host target RNA into VGAM2509 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85095] It is appreciated that VGAM2509 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2509 host target genes. The mRNA of each one of this plurality of VGAM2509 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2509 RNA, herein designated VGAM RNA, and which when bound by VGAM2509 RNA causes inhibition of translation of respective one or more VGAM2509 host target proteins.

[85096] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2509 gene, herein designated VGAM GENE, on one or more VGAM2509 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85097] It is yet further appreciated that a function of VGAM2509 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2509 correlate with, and may be deduced from, the identity of the host target genes which VGAM2509 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85098] Nucleotide sequences of the VGAM2509 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2509 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2509 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2509 are further described hereinbelow with reference to Table 1.

[85099] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2509 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2509 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85100] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2509 gene, herein designated VGAM is inhibition of expression of VGAM2509 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2509 correlate with, and may be deduced from, the identity of the target genes which VGAM2509 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85101] S-adenosylmethionine Decarboxylase 1 (AMD1, Accession NM_001634) is a VGAM2509 host target gene. AMD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AMD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AMD1 BINDING SITE, designated SEQ ID:7347, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85102] A function of VGAM2509 is therefore inhibition of S-adenosylmethionine Decarboxylase 1 (AMD1, Accession

NM_001634), a gene which catalyzes the removal of the carboxylate group of S-adenosylmethionine in the polyamine biosynthesis pathway. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMD1. The function of AMD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1016.B-cell CLL/lymphoma 9 (BCL9, Accession NM_004326) is another VGAM2509 host target gene. BCL9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BCL9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL9 BINDING SITE, designated SEQ ID:10524, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85103] Another function of VGAM2509 is therefore inhibition of B-cell CLL/lymphoma 9 (BCL9, Accession NM_004326), a gene which recruits of PYGO to the nuclear beta-catenin-TCF complex in Wnt/Wingless signaling. Accordingly, utilities of VGAM2509 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with BCL9. The function of BCL9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Carbonic Anhydrase III, Muscle Specific (CA3, Accession NM_005181) is another VGAM2509 host target gene. CA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CA3 BINDING SITE, designated SEQ ID:11681, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85104] Another function of VGAM2509 is therefore inhibition of Carbonic Anhydrase III, Muscle Specific (CA3, Accession NM_005181), a gene which has a muscle-specific function of reversible hydratation of carbon dioxide. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CA3. The function of CA3 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM1911.Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116) is another VGAM2509 host target gene. CAPZA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAPZA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPZA1 BINDING SITE, designated SEQ ID:35950, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85105] Another function of VGAM2509 is therefore inhibition of Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116), a gene which is alpha 1 subunit of actin filament capping protein; binds actin, has roles in cell motility and actin assembly. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPZA1. The function of CAPZA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM547.Caspase Recruitment Domain

Family, Member 15 (CARD15, Accession NM_022162) is another VGAM2509 host target gene. CARD15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CARD15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARD15 BINDING SITE, designated SEQ ID:22718, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85106] Another function of VGAM2509 is therefore inhibition of Caspase Recruitment Domain Family, Member 15 (CARD15, Accession NM_022162), a gene which serves as an intracellular receptor for bacterial products in monocytes and transduces signals leading to NFKB activation. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD15. The function of CARD15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM126.Chemokine (C-C motif) Receptor 2 (CCR2, Accession NM_000647) is another VGAM2509 host target

gene. CCR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCR2 BINDING SITE, designated SEQ ID:6309, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85107] Another function of VGAM2509 is therefore inhibition of Chemokine (C-C motif) Receptor 2 (CCR2, Accession NM_000647), a gene which binds chemokines and transduces a signal by increasing the intracellular calcium ions level. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR2. The function of CCR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Cytochrome P450, Subfamily XXIV (vitamin D 24-hydroxylase) (CYP24, Accession NM_000782) is another VGAM2509 host target gene. CYP24 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CYP24, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP24 BINDING SITE, designated SEQ ID:6425, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85108] Another function of VGAM2509 is therefore inhibition of Cytochrome P450, Subfamily XXIV (vitamin D 24-hydroxylase) (CYP24, Accession NM_000782), a gene which induces the differentiation of promyelocytes into monocytes/macrophages. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP24. The function of CYP24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1204.Desmoglein 1 (DSG1, Accession NM_001942) is another VGAM2509 host target gene. DSG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DSG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of DSG1 BINDING SITE, designated SEQ ID:7657, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85109] Another function of VGAM2509 is therefore inhibition of Desmoglein 1 (DSG1, Accession NM_001942). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSG1. Ets Homologous Factor (EHF, Accession NM_012153) is another VGAM2509 host target gene. EHF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EHF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EHF BINDING SITE, designated SEQ ID:14452, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85110] Another function of VGAM2509 is therefore inhibition of Ets Homologous Factor (EHF, Accession NM_012153), a gene which is Member of the ESE subfamily of Ets transcription factors. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHF. The function of

EHF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM855.Integrin, Beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1, Accession NM_033666) is another VGAM2509 host target gene. ITGB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGB1 BINDING SITE, designated SEQ ID:27395, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85111] Another function of VGAM2509 is therefore inhibition of Integrin, Beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1, Accession NM_033666), a gene which acts as a fibronectin receptor. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGB1. The function of ITGB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to VGAM427.Meningioma Expressed Antigen 5 (hyaluronidase) (MGEA5, Accession NM_012215) is another VGAM2509 host target gene. MGEA5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGEA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGEA5 BINDING SITE, designated SEQ ID:14519, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85112] Another function of VGAM2509 is therefore inhibition of Meningioma Expressed Antigen 5 (hyaluronidase) (MGEA5, Accession NM_012215), a gene which has a hyaluronidase activity. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGEA5. The function of MGEA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM801.Mature T-cell Proliferation 1 (MTCP1, Accession NM_014221) is another VGAM2509 host target gene. MTCP1 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MTCP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTCP1 BINDING SITE, designated SEQ ID:15490, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85113] Another function of VGAM2509 is therefore inhibition of Mature T-cell Proliferation 1 (MTCP1, Accession NM_014221). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTCP1. poly(A) Binding Protein, Nuclear 1 (PABPN1, Accession NM_004643) is another VGAM2509 host target gene. PABPN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PABPN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PABPN1 BINDING SITE, designated SEQ ID:11019, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85114] Another function of VGAM2509 is therefore inhibition of poly(A) Binding Protein, Nuclear 1 (PABPN1, Accession NM_004643), a gene which binds to Poly(A). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PABPN1. The function of PABPN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1968.Proteasome (prosome, macropain) Activator Subunit 3 (PA28 gamma; Ki) (PSME3, Accession NM_005789) is another VGAM2509 host target gene. PSME3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PSME3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSME3 BINDING SITE, designated SEQ ID:12373, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85115] Another function of VGAM2509 is therefore inhibition of Proteasome (prosome, macropain) Activator Subunit 3 (PA28 gamma; Ki) (PSME3, Accession NM_005789), a gene

which is the activator subunit of the proteasome (prosome macropain). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSME3. The function of PSME3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1498.Spastic Paraplegia 3A (autosomal dominant) (SPG3A, Accession NM_015915) is another VGAM2509 host target gene. SPG3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPG3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPG3A BINDING SITE, designated SEQ ID:18047, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85116] Another function of VGAM2509 is therefore inhibition of Spastic Paraplegia 3A (autosomal dominant) (SPG3A, Accession NM_015915). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPG3A. Structure

Specific Recognition Protein 1 (SSRP1, Accession NM_003146) is another VGAM2509 host target gene. SSRP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SSRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSRP1 BINDING SITE, designated SEQ ID:9116, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85117] Another function of VGAM2509 is therefore inhibition of Structure Specific Recognition Protein 1 (SSRP1, Accession NM_003146), a gene which has specific affinity for DNA modified with cisplatin and has a region of homology to HMG-box DNA binding proteins. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSRP1. The function of SSRP1 has been established by previous studies. Members of the high mobility group (HMG) protein family (see OMIM Ref. No. HMG1, 163905) recognize specific DNA structures. By expression screening of a human B cell cDNA library, Bruhn et al. (1992) isolated cDNAs encoding a structure-specific recognition protein,

SSRP1, that binds specifically to DNA structurally modified by the antitumor drug cisplatin. The SSRP1 cDNA predicts a 709-amino acid protein with M(r) 81,068. The protein has a high percentage (36%) of charged residues grouped into several highly charged domains. SSRP1 has an HMG box located between amino acids 539-614. The SSRP1 protein shows homology to HMG1 and HMG2 (OMIM Ref. No. 163906) proteins from several species and to a transcription factor, UBF (OMIM Ref. No. 600673), which also has an HMG-box domain. Northern blot analysis identified a 2.8-kb transcript in all tissues examined. Northern blot analysis of mRNA from testicular and bladder cancer cell lines showed no correlation between SSRP1 mRNA levels and antitumor activity of cisplatin for these tissues. SSRP1 mRNA was not inducible by cisplatin in HeLa cells. Transcription of naked DNA in eukaryotic cells minimally requires the general transcription factors (see OMIM Ref. No. GTF2E1; 189962) and RNA polymerase II (see OMIM Ref. No. POLR2A; 180660). This minimal set of factors is not sufficient for transcription by RNA polymerase II in vivo, where DNA is packaged into chromatin by histone octamers (see OMIM Ref. No. 142711). One set of accessory factors involved in chromatin remodeling is the SWI/SNF

complex (see OMIM Ref. No. SMARCC1; 601732). By sequential chromatography, Orphanides et al. (1998) purified FACT (facilitates chromatin remodeling), an accessory factor required for transcript elongation after chromatin remodeling, from HeLa cell nuclear extracts. After the initiation of transcription, FACT acts to release RNA polymerase II from a nucleosome-induced block to allow productive transcription. SDS-PAGE and chromatographic analyses showed that FACT activity is present in an approximately 230-kD protein composed of 140-kD (FACTp140, or SPT16; 605012) and 80-kD (FACTp80) subunits.

[85118] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[85119] Bruhn, S. L.; Pil, P. M.; Essigmann, J. M.; Housman, D. E.; Lippard, S. J. : Isolation and characterization of human cDNA clones encoding a high mobility group box protein that recognizes structural distortions to DNA caused by binding of the anticancer agent cisplatin. Proc. Nat. Acad. Sci. 89: 2307-2311, 1992. ; and

[85120] Orphanides, G.; LeRoy, G.; Chang, C.-H.; Luse, D. S.; Reinberg, D. : FACT, a factor that facilitates transcript elonga-

tion through nucleosomes. Cell 92: 105-116, 1998.

[85121] Further studies establishing the function and utilities of SSRP1 are found in John Hopkins OMIM database record ID 604328, and in sited publications numbered 7468, 1035 and 7469 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.T-box 3 (ulnar mammary syndrome) (TBX3, Accession NM_016569) is another VGAM2509 host target gene. TBX3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBX3 BINDING SITE, designated SEQ ID:18641, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85122] Another function of VGAM2509 is therefore inhibition of T-box 3 (ulnar mammary syndrome) (TBX3, Accession NM_016569). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX3. Tumor Necrosis Factor Receptor Superfamily, Member 1B (TNFRSF1B, Accession NM_001066) is another VGAM2509 host target gene.

TNFRSF1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF1B BINDING SITE, designated SEQ ID:6735, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85123] Another function of VGAM2509 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 1B (TNFRSF1B, Accession NM_001066), a gene which mediates proinflammatory cellular responses. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF1B. The function of TNFRSF1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM939.Tripartite Motif-containing 37 (TRIM37, Accession NM_015294) is another VGAM2509 host target gene. TRIM37 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM37, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM37 BINDING SITE, designated SEQ ID:17617, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85124] Another function of VGAM2509 is therefore inhibition of Tripartite Motif-containing 37 (TRIM37, Accession NM_015294). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM37. TSLP (Accession NM_138551) is another VGAM2509 host target gene. TSLP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TSLP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSLP BINDING SITE, designated SEQ ID:28850, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85125] Another function of VGAM2509 is therefore inhibition of TSLP (Accession NM_138551), a gene which may contribute directly to the activation of Langerhans cells and

inhibit apoptosis. Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSLP. The function of TSLP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM558.Adaptor-related Protein Complex 4, Mu 1 Subunit (AP4M1, Accession NM_004722) is another VGAM2509 host target gene. AP4M1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AP4M1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP4M1 BINDING SITE, designated SEQ ID:11088, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85126] Another function of VGAM2509 is therefore inhibition of Adaptor-related Protein Complex 4, Mu 1 Subunit (AP4M1, Accession NM_004722). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP4M1. ATPase, (Na+)/K+ Transporting, Beta 4 Polypeptide

(ATP1B4, Accession NM_012069) is another VGAM2509 host target gene. ATP1B4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP1B4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1B4 BINDING SITE, designated SEQ ID:14328, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85127] Another function of VGAM2509 is therefore inhibition of ATPase, (Na+)/K+ Transporting, Beta 4 Polypeptide (ATP1B4, Accession NM_012069). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B4. Basic Helix-loop-helix Domain Containing, Class B, 2 (BHLHB2, Accession NM_003670) is another VGAM2509 host target gene. BHLHB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BHLHB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BHLHB2

BINDING SITE, designated SEQ ID:9756, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85128] Another function of VGAM2509 is therefore inhibition of Basic Helix-loop-helix Domain Containing, Class B, 2 (BHLHB2, Accession NM_003670). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHLHB2. Chromosome 7 Open Reading Frame 13 (C7orf13, Accession NM_032625) is another VGAM2509 host target gene. C7orf13 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C7orf13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C7orf13 BINDING SITE, designated SEQ ID:26343, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85129] Another function of VGAM2509 is therefore inhibition of Chromosome 7 Open Reading Frame 13 (C7orf13, Accession NM_032625). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with C7orf13. DCOHM (Accession NM_032151) is another VGAM2509 host target gene. DCOHM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCOHM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCOHM BINDING SITE, designated SEQ ID:25847, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85130] Another function of VGAM2509 is therefore inhibition of DCOHM (Accession NM_032151). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCOHM. DKFZp762A227 (Accession NM_014096) is another VGAM2509 host target gene. DKFZp762A227 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp762A227, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp762A227 BINDING SITE, designated SEQ

ID:15321, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85131] Another function of VGAM2509 is therefore inhibition of DKFZp762A227 (Accession NM_014096). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762A227. Cyclin D Binding Myb-like Transcription Factor 1 (DMTF1, Accession NM_021145) is another VGAM2509 host target gene. DMTF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DMTF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMTF1 BINDING SITE, designated SEQ ID:22117, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85132] Another function of VGAM2509 is therefore inhibition of Cyclin D Binding Myb-like Transcription Factor 1 (DMTF1, Accession NM_021145). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMTF1.

Extra Spindle Poles Like 1 (S. cerevisiae) (ESPL1, Accession NM_012291) is another VGAM2509 host target gene. ESPL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ESPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESPL1 BINDING SITE, designated SEQ ID:14631, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85133] Another function of VGAM2509 is therefore inhibition of Extra Spindle Poles Like 1 (S. cerevisiae) (ESPL1, Accession NM_012291). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESPL1. FLJ00060 (Accession XM_028154) is another VGAM2509 host target gene. FLJ00060 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00060, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00060 BINDING SITE, designated SEQ ID:30630, to the nucleotide sequence of VGAM2509 RNA,

herein designated VGAM RNA, also designated SEQ ID:5220.

[85134] Another function of VGAM2509 is therefore inhibition of FLJ00060 (Accession XM_028154). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00060. FLJ12484 (Accession XM_045681) is another VGAM2509 host target gene. FLJ12484 BINDING SITE1 and FLJ12484 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ12484, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12484 BINDING SITE1 and FLJ12484 BINDING SITE2, designated SEQ ID:34517 and SEQ ID:23019 respectively, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85135] Another function of VGAM2509 is therefore inhibition of FLJ12484 (Accession XM_045681). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12484. FLJ12875 (Accession NM_024544) is another

VGAM2509 host target gene. FLJ12875 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12875, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12875 BINDING SITE, designated SEQ ID:23756, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85136] Another function of VGAM2509 is therefore inhibition of FLJ12875 (Accession NM_024544). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12875. FLJ12975 (Accession XM_045522) is another VGAM2509 host target gene. FLJ12975 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12975, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12975 BINDING SITE, designated SEQ ID:34481, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85137] Another function of VGAM2509 is therefore inhibition of FLJ12975 (Accession XM_045522). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12975. FLJ13081 (Accession NM_024834) is another VGAM2509 host target gene. FLJ13081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13081 BINDING SITE, designated SEQ ID:24237, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85138] Another function of VGAM2509 is therefore inhibition of FLJ13081 (Accession NM_024834). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13081. HHGP (Accession NM_020200) is another VGAM2509 host target gene. HHGP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HHGP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HHGP BINDING SITE, designated SEQ ID:21435, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85139] Another function of VGAM2509 is therefore inhibition of HHGP (Accession NM_020200). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HHGP. KIAA1204 (Accession XM_045011) is another VGAM2509 host target gene. KIAA1204 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1204, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1204 BINDING SITE, designated SEQ ID:34317, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85140] Another function of VGAM2509 is therefore inhibition of KIAA1204 (Accession XM_045011). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1204. KIAA1463 (Accession XM_051160) is another VGAM2509 host target gene. KIAA1463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1463 BINDING SITE, designated SEQ ID:35772, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85141] Another function of VGAM2509 is therefore inhibition of KIAA1463 (Accession XM_051160). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1463. KIAA1549 (Accession XM_045127) is another VGAM2509 host target gene. KIAA1549 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1549, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1549 BINDING SITE, designated SEQ ID:34371, to the nucleotide sequence of VGAM2509 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5220.

[85142] Another function of VGAM2509 is therefore inhibition of KIAA1549 (Accession XM_045127). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1549. KIAA1576 (Accession XM_038186) is another VGAM2509 host target gene. KIAA1576 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1576 BINDING SITE, designated SEQ ID:32776, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85143] Another function of VGAM2509 is therefore inhibition of KIAA1576 (Accession XM_038186). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1576. KIAA1908 (Accession XM_055834) is another VGAM2509 host target gene. KIAA1908 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1908, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1908 BINDING SITE, designated SEQ ID:36341, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85144] Another function of VGAM2509 is therefore inhibition of KIAA1908 (Accession XM_055834). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1908. MGC22014 (Accession XM_035307) is another VGAM2509 host target gene. MGC22014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC22014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC22014 BINDING SITE, designated SEQ ID:32221, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85145] Another function of VGAM2509 is therefore inhibition of MGC22014 (Accession XM_035307). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC22014. MGC32043 (Accession NM_144582) is another VGAM2509 host target gene. MGC32043 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC32043, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC32043 BINDING SITE, designated SEQ ID:29393, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85146] Another function of VGAM2509 is therefore inhibition of MGC32043 (Accession NM_144582). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC32043. Neuronal Pentraxin Receptor (NPTXR, Accession NM_058178) is another VGAM2509 host target gene. NPTXR BINDING SITE1 and NPTXR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NPTXR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE1 and

NPTXR BINDING SITE2, designated SEQ ID:27735 and SEQ ID:15587 respectively, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85147] Another function of VGAM2509 is therefore inhibition of Neuronal Pentraxin Receptor (NPTXR, Accession NM_058178). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR. Smith-Magenis Syndrome Chromosome Region, Candidate 8 (SMCR8, Accession NM_144775) is another VGAM2509 host target gene. SMCR8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SMCR8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMCR8 BINDING SITE, designated SEQ ID:29567, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85148] Another function of VGAM2509 is therefore inhibition of Smith-Magenis Syndrome Chromosome Region, Candidate 8 (SMCR8, Accession NM_144775). Accordingly, utilities of

VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCR8. LOC126302 (Accession XM_059020) is another VGAM2509 host target gene. LOC126302 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126302, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126302 BINDING SITE, designated SEQ ID:36827, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85149] Another function of VGAM2509 is therefore inhibition of LOC126302 (Accession XM_059020). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126302. LOC126353 (Accession XM_059034) is another VGAM2509 host target gene. LOC126353 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126353, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC126353 BINDING SITE, designated SEQ ID:36831, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85150] Another function of VGAM2509 is therefore inhibition of LOC126353 (Accession XM_059034). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126353. LOC130535 (Accession XM_072244) is another VGAM2509 host target gene. LOC130535 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130535, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130535 BINDING SITE, designated SEQ ID:37477, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85151] Another function of VGAM2509 is therefore inhibition of LOC130535 (Accession XM_072244). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130535. LOC144363 (Accession XM_084843) is another VGAM2509 host target gene. LOC144363 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144363, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144363 BINDING SITE, designated SEQ ID:37730, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85152] Another function of VGAM2509 is therefore inhibition of LOC144363 (Accession XM_084843). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144363. LOC146229 (Accession XM_085387) is another VGAM2509 host target gene. LOC146229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE, designated SEQ ID:38113, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85153] Another function of VGAM2509 is therefore inhibition of

LOC146229 (Accession XM_085387). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229. LOC147976 (Accession XM_085980) is another VGAM2509 host target gene. LOC147976 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147976, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147976 BINDING SITE, designated SEQ ID:38430, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85154] Another function of VGAM2509 is therefore inhibition of LOC147976 (Accession XM_085980). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147976. LOC150095 (Accession XM_097805) is another VGAM2509 host target gene. LOC150095 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150095, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC150095 BINDING SITE, designated SEQ ID:41132, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85155] Another function of VGAM2509 is therefore inhibition of LOC150095 (Accession XM_097805). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150095. LOC157753 (Accession XM_088381) is another VGAM2509 host target gene. LOC157753 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157753, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157753 BINDING SITE, designated SEQ ID:39663, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85156] Another function of VGAM2509 is therefore inhibition of LOC157753 (Accession XM_088381). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157753. LOC157858 (Accession XM_098833) is an-

other VGAM2509 host target gene. LOC157858 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157858, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157858 BINDING SITE, designated SEQ ID:41870, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85157] Another function of VGAM2509 is therefore inhibition of LOC157858 (Accession XM_098833). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157858. LOC163882 (Accession XM_089211) is another VGAM2509 host target gene. LOC163882 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC163882, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163882 BINDING SITE, designated SEQ ID:39974, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85158] Another function of VGAM2509 is therefore inhibition of LOC163882 (Accession XM_089211). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163882. LOC196205 (Accession XM_113676) is another VGAM2509 host target gene. LOC196205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196205 BINDING SITE, designated SEQ ID:42326, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85159] Another function of VGAM2509 is therefore inhibition of LOC196205 (Accession XM_113676). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196205. LOC200339 (Accession XM_117226) is another VGAM2509 host target gene. LOC200339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200339, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200339 BINDING SITE, designated SEQ ID:43300, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85160] Another function of VGAM2509 is therefore inhibition of LOC200339 (Accession XM_117226). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200339. LOC201245 (Accession XM_113326) is another VGAM2509 host target gene. LOC201245 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201245, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201245 BINDING SITE, designated SEQ ID:42231, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85161] Another function of VGAM2509 is therefore inhibition of LOC201245 (Accession XM_113326). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC201245. LOC202934 (Accession XM_117486) is another VGAM2509 host target gene. LOC202934 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, designated SEQ ID:43465, to the nucleotide sequence of VGAM2509 RNA, herein designated VGAM RNA, also designated SEQ ID:5220.

[85162] Another function of VGAM2509 is therefore inhibition of LOC202934 (Accession XM_117486). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934. LOC255465 (Accession XM_173206) is another VGAM2509 host target gene. LOC255465 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255465 BINDING SITE, designated SEQ ID:46457, to the nucleotide sequence of VGAM2509 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5220.

[85163] Another function of VGAM2509 is therefore inhibition of LOC255465 (Accession XM_173206). Accordingly, utilities of VGAM2509 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255465. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2510 (VGAM2510) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85164] VGAM2510 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2510 was detected is described hereinabove with reference to Figs. 1-8.

[85165] VGAM2510 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2510 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85166] VGAM2510 gene encodes a VGAM2510 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2510 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2510 precursor RNA is designated SEQ ID:2496, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2496 is located at position 226893 relative to the genome of Mouse Cytomegalovirus 1.

[85167] VGAM2510 precursor RNA folds onto itself, forming VGAM2510 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85168] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2510 folded precursor RNA into VGAM2510 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2510 RNA is designated SEQ ID:5221, and is provided hereinbelow with reference to the sequence listing part.

[85169] VGAM2510 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2510 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85170] VGAM2510 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2510 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2510 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85171] The complementary binding of VGAM2510 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2510 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2510 host target RNA into VGAM2510 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85172] It is appreciated that VGAM2510 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2510 host target genes. The mRNA of

each one of this plurality of VGAM2510 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2510 RNA, herein designated VGAM RNA, and which when bound by VGAM2510 RNA causes inhibition of translation of respective one or more VGAM2510 host target proteins.

[85173] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2510 gene, herein designated VGAM GENE, on one or more VGAM2510 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[85174] It is yet further appreciated that a function of VGAM2510 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2510 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2510 correlate with, and may be deduced from, the identity of the host target genes which VGAM2510 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85175] Nucleotide sequences of the VGAM2510 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2510 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2510 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2510 are further described hereinbelow with reference to Table 1.

[85176] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2510 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2510 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85177] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2510 gene, herein designated VGAM is inhibition of expression of VGAM2510 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2510 correlate with, and may be deduced from, the identity of the target genes which VGAM2510 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85178] Ephrin-B1 (EFNB1, Accession NM_004429) is a VGAM2510 host target gene. EFNB1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EFNB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFNB1 BINDING SITE, designated SEQ ID:10704, to the nucleotide sequence of VGAM2510 RNA, herein designated VGAM RNA, also designated SEQ ID:5221.

[85179] A function of VGAM2510 is therefore inhibition of Ephrin-B1 (EFNB1, Accession NM_004429), a gene which is a transmembrane ligand of Eph-related receptor tyrosine

kinases, has a role in cell adhesion. Accordingly, utilities of VGAM2510 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFNB1. The function of EFNB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM390.Cleavage Stimulation Factor, 3' Pre-RNA, Subunit 1, 50kDa (CSTF1, Accession NM_001324) is another VGAM2510 host target gene. CSTF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CSTF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSTF1 BINDING SITE, designated SEQ ID:7008, to the nucleotide sequence of VGAM2510 RNA, herein designated VGAM RNA, also designated SEQ ID:5221.

[85180] Another function of VGAM2510 is therefore inhibition of Cleavage Stimulation Factor, 3' Pre-RNA, Subunit 1, 50kDa (CSTF1, Accession NM_001324). Accordingly, utilities of VGAM2510 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSTF1. FLJ22794 (Accession XM_166220) is another VGAM2510

host target gene. FLJ22794 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:44022, to the nucleotide sequence of VGAM2510 RNA, herein designated VGAM RNA, also designated SEQ ID:5221.

[85181] Another function of VGAM2510 is therefore inhibition of FLJ22794 (Accession XM_166220). Accordingly, utilities of VGAM2510 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22794. KIAA1977 (Accession XM_058800) is another VGAM2510 host target gene. KIAA1977 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1977, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1977 BINDING SITE, designated SEQ ID:36744, to the nucleotide sequence of VGAM2510 RNA, herein designated VGAM RNA, also designated SEQ ID:5221.

[85182] Another function of VGAM2510 is therefore inhibition of KIAA1977 (Accession XM_058800). Accordingly, utilities of VGAM2510 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1977. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2511 (VGAM2511) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85183] VGAM2511 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2511 was detected is described hereinabove with reference to Figs. 1-8.

[85184] VGAM2511 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2511 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85185] VGAM2511 gene encodes a VGAM2511 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2511 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2511 precursor RNA is designated SEQ ID:2497, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2497 is located at position 36653 relative to the genome of Mouse Cytomegalovirus 1.

[85186] VGAM2511 precursor RNA folds onto itself, forming VGAM2511 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85187] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2511 folded precursor RNA into VGAM2511 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2511 RNA is designated SEQ ID:5222, and is provided hereinbelow with reference to the sequence listing part.

[85188] VGAM2511 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2511 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85189] VGAM2511 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2511 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2511 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85190] The complementary binding of VGAM2511 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2511 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2511 host target RNA into VGAM2511 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85191] It is appreciated that VGAM2511 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2511 host target genes. The mRNA of each one of this plurality of VGAM2511 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2511 RNA, herein designated VGAM RNA, and which when bound by VGAM2511 RNA causes inhibition of translation of respective one or more VGAM2511 host target proteins.

[85192] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2511 gene, herein designated VGAM GENE, on one or more VGAM2511 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85193] It is yet further appreciated that a function of VGAM2511 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2511 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2511 correlate with, and may be deduced from, the identity of the host target genes which VGAM2511 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85194] Nucleotide sequences of the VGAM2511 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2511 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2511 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2511 are further described hereinbelow with reference to Table 1.

[85195] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2511 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2511 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[85196] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2511 gene, herein designated VGAM is inhibition of expression of VGAM2511 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2511 correlate with, and may be deduced from, the identity of the target genes which VGAM2511 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85197] APACD (Accession NM_005783) is a VGAM2511 host target gene. APACD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APACD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APACD BINDING SITE, designated SEQ ID:12363, to the nucleotide sequence of VGAM2511 RNA, herein designated VGAM RNA, also designated SEQ ID:5222.

[85198] A function of VGAM2511 is therefore inhibition of APACD (Accession NM_005783). Accordingly, utilities of VGAM2511 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APACD.

COP9 Constitutive Photomorphogenic Homolog Subunit 7A (Arabidopsis) (COPS7A, Accession NM_016319) is another VGAM2511 host target gene. COPS7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COPS7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COPS7A BINDING SITE, designated SEQ ID:18437, to the nucleotide sequence of VGAM2511 RNA, herein designated VGAM RNA, also designated SEQ ID:5222.

[85199] Another function of VGAM2511 is therefore inhibition of COP9 Constitutive Photomorphogenic Homolog Subunit 7A (Arabidopsis) (COPS7A, Accession NM_016319). Accordingly, utilities of VGAM2511 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COPS7A. FLJ10702 (Accession NM_018184) is another VGAM2511 host target gene. FLJ10702 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10702, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of FLJ10702 BINDING SITE, designated SEQ ID:20028, to the nucleotide sequence of VGAM2511 RNA, herein designated VGAM RNA, also designated SEQ ID:5222.

[85200] Another function of VGAM2511 is therefore inhibition of FLJ10702 (Accession NM_018184). Accordingly, utilities of VGAM2511 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10702. Sphingomyelin Phosphodiesterase 2, Neutral Membrane (neutral sphingomyelinase) (SMPD2, Accession NM_003080) is another VGAM2511 host target gene. SMPD2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SMPD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMPD2 BINDING SITE, designated SEQ ID:9053, to the nucleotide sequence of VGAM2511 RNA, herein designated VGAM RNA, also designated SEQ ID:5222.

[85201] Another function of VGAM2511 is therefore inhibition of Sphingomyelin Phosphodiesterase 2, Neutral Membrane (neutral sphingomyelinase) (SMPD2, Accession

NM_003080). Accordingly, utilities of VGAM2511 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMPD2. LOC254251 (Accession XM_171088) is another VGAM2511 host target gene. LOC254251 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254251, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254251 BINDING SITE, designated SEQ ID:45898, to the nucleotide sequence of VGAM2511 RNA, herein designated VGAM RNA, also designated SEQ ID:5222.

[85202] Another function of VGAM2511 is therefore inhibition of LOC254251 (Accession XM_171088). Accordingly, utilities of VGAM2511 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254251. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2512 (VGAM2512) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[85203] VGAM2512 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2512 was detected is described hereinabove with reference to Figs. 1-8.

[85204] VGAM2512 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2512 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85205] VGAM2512 gene encodes a VGAM2512 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2512 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2512 precursor RNA is designated SEQ ID:2498, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2498 is located at position 84643 relative to the genome of Mouse Cytomegalovirus 1.

[85206] VGAM2512 precursor RNA folds onto itself, forming VGAM2512 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85207] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2512 folded precursor RNA into VGAM2512 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2512 RNA is designated SEQ ID:5223, and is provided hereinbelow with reference to the sequence listing part.

[85208] VGAM2512 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2512 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85209] VGAM2512 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2512 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2512 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[85210] The complementary binding of VGAM2512 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2512 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2512 host target RNA into VGAM2512 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85211] It is appreciated that VGAM2512 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2512 host target genes. The mRNA of each one of this plurality of VGAM2512 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2512 RNA, herein designated VGAM RNA, and which when bound by VGAM2512 RNA causes inhibition of translation of respective one or more VGAM2512 host target proteins.

[85212] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2512 gene, herein designated VGAM GENE, on one

or more VGAM2512 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85213] It is yet further appreciated that a function of VGAM2512 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2512 correlate with, and may be deduced from, the identity of the host target genes which VGAM2512 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85214] Nucleotide sequences of the VGAM2512 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2512 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2512 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2512 are further described hereinbelow with reference to Table 1.

[85215] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2512 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2512 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85216] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2512 gene, herein designated VGAM is inhibition of expression of VGAM2512 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2512 correlate with, and may be deduced from, the identity of the target genes which VGAM2512 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85217] ATPase, Aminophospholipid Transporter-like, Class I,

Type 8A, Member 2 (ATP8A2, Accession XM_167916) is a VGAM2512 host target gene. ATP8A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP8A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8A2 BINDING SITE, designated SEQ ID:44914, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85218] A function of VGAM2512 is therefore inhibition of ATPase, Aminophospholipid Transporter-like, Class I, Type 8A, Member 2 (ATP8A2, Accession XM_167916). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8A2. DMC1 Dosage Suppressor of Mck1 Homolog, Meiosis-specific Homologous Recombination (yeast) (DMC1, Accession NM_007068) is another VGAM2512 host target gene. DMC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DMC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of DMC1 BINDING SITE, designated SEQ ID:13932, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85219] Another function of VGAM2512 is therefore inhibition of DMC1 Dosage Suppressor of Mck1 Homolog, Meiosis-specific Homologous Recombination (yeast) (DMC1, Accession NM_007068). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMC1. Glutamate Receptor, Metabotropic 7 (GRM7, Accession NM_000844) is another VGAM2512 host target gene. GRM7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRM7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRM7 BINDING SITE, designated SEQ ID:6515, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85220] Another function of VGAM2512 is therefore inhibition of Glutamate Receptor, Metabotropic 7 (GRM7, Accession NM_000844), a gene which is mediated by a g-protein

that inhibits adenylate cyclase activity. Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM7. The function of GRM7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM746.Potassium Inwardly-rectifying Channel, Subfamily J, Member 1 (KCNJ1, Accession NM_000220) is another VGAM2512 host target gene. KCNJ1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNJ1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ1 BINDING SITE, designated SEQ ID:5728, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85221] Another function of VGAM2512 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 1 (KCNJ1, Accession NM_000220). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ1. Solute Carrier Family 11 (proton-coupled di-

valent metal ion transporters), Member 3 (SLC11A3, Accession NM_014585) is another VGAM2512 host target gene. SLC11A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC11A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC11A3 BINDING SITE, designated SEQ ID:15941, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85222] Another function of VGAM2512 is therefore inhibition of Solute Carrier Family 11 (proton-coupled divalent metal ion transporters), Member 3 (SLC11A3, Accession NM_014585). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC11A3. DKFZP586F1318 (Accession NM_015677) is another VGAM2512 host target gene. DKFZP586F1318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586F1318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of DKFZP586F1318 BINDING SITE, designated SEQ ID:17903, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85223] Another function of VGAM2512 is therefore inhibition of DKFZP586F1318 (Accession NM_015677). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586F1318. DKFZp761N1114 (Accession XM_086327) is another VGAM2512 host target gene. DKFZp761N1114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761N1114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761N1114 BINDING SITE, designated SEQ ID:38607, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85224] Another function of VGAM2512 is therefore inhibition of DKFZp761N1114 (Accession XM_086327). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZp761N1114. FLJ32784 (Accession NM_144623) is another VGAM2512 host target gene. FLJ32784 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32784, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32784 BINDING SITE, designated SEQ ID:29442, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85225] Another function of VGAM2512 is therefore inhibition of FLJ32784 (Accession NM_144623). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32784. INSM2 (Accession NM_032594) is another VGAM2512 host target gene. INSM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by INSM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of INSM2 BINDING SITE, designated SEQ ID:26327, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5223.

[85226] Another function of VGAM2512 is therefore inhibition of INSM2 (Accession NM_032594). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INSM2. KIAA0332 (Accession XM_031553) is another VGAM2512 host target gene. KIAA0332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0332 BINDING SITE, designated SEQ ID:31420, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85227] Another function of VGAM2512 is therefore inhibition of KIAA0332 (Accession XM_031553). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0332. KIAA0376 (Accession XM_037759) is another VGAM2512 host target gene. KIAA0376 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0376, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0376 BINDING SITE, designated SEQ ID:32671, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85228] Another function of VGAM2512 is therefore inhibition of KIAA0376 (Accession XM_037759). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0376. KIAA0788 (Accession XM_049108) is another VGAM2512 host target gene. KIAA0788 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0788, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0788 BINDING SITE, designated SEQ ID:35343, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85229] Another function of VGAM2512 is therefore inhibition of KIAA0788 (Accession XM_049108). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0788. Suppression of Tumorigenicity 7 Like (ST7L, Accession NM_138727) is another VGAM2512 host target gene. ST7L BINDING SITE1 through ST7L BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ST7L, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ST7L BINDING SITE1 through ST7L BINDING SITE3, designated SEQ ID:28978, SEQ ID:29208 and SEQ ID:19336 respectively, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85230] Another function of VGAM2512 is therefore inhibition of Suppression of Tumorigenicity 7 Like (ST7L, Accession NM_138727). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ST7L. Serine/threonine Kinase 38 Like (STK38L, Accession XM_044823) is another VGAM2512 host target gene. STK38L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STK38L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK38L BINDING SITE, designated SEQ ID:34292, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85231] Another function of VGAM2512 is therefore inhibition of Serine/threonine Kinase 38 Like (STK38L, Accession XM_044823). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK38L. Succinate-CoA Ligase, GDP-forming, Beta Subunit (SUCLG2, Accession XM_037772) is another VGAM2512 host target gene. SUCLG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUCLG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUCLG2 BINDING SITE, designated SEQ ID:32677, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85232] Another function of VGAM2512 is therefore inhibition of Succinate-CoA Ligase, GDP-forming, Beta Subunit

(SUCLG2, Accession XM_037772). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUCLG2. Tripartite Motif-containing 2 (TRIM2, Accession NM_015271) is another VGAM2512 host target gene. TRIM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM2 BINDING SITE, designated SEQ ID:17602, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85233] Another function of VGAM2512 is therefore inhibition of Tripartite Motif-containing 2 (TRIM2, Accession NM_015271). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM2. LOC149506 (Accession XM_097661) is another VGAM2512 host target gene. LOC149506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149506, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE, designated SEQ ID:40999, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85234] Another function of VGAM2512 is therefore inhibition of LOC149506 (Accession XM_097661). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506. LOC153914 (Accession XM_087799) is another VGAM2512 host target gene. LOC153914 BINDING SITE1 and LOC153914 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC153914, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153914 BINDING SITE1 and LOC153914 BINDING SITE2, designated SEQ ID:39437 and SEQ ID:39435 respectively, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85235] Another function of VGAM2512 is therefore inhibition of

LOC153914 (Accession XM_087799). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153914. LOC222031 (Accession XM_168371) is another VGAM2512 host target gene. LOC222031 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222031, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222031 BINDING SITE, designated SEQ ID:45129, to the nucleotide sequence of VGAM2512 RNA, herein designated VGAM RNA, also designated SEQ ID:5223.

[85236] Another function of VGAM2512 is therefore inhibition of LOC222031 (Accession XM_168371). Accordingly, utilities of VGAM2512 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222031. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2513 (VGAM2513) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[85237] VGAM2513 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2513 was detected is described hereinabove with reference to Figs. 1-8.

[85238] VGAM2513 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2513 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85239] VGAM2513 gene encodes a VGAM2513 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2513 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2513 precursor RNA is designated SEQ ID:2499, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2499 is located at position 157900 relative to the genome of Mouse Cytomegalovirus 1.

[85240] VGAM2513 precursor RNA folds onto itself, forming VGAM2513 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85241] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2513 folded precursor RNA into VGAM2513 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2513 RNA is designated SEQ ID:5224, and is provided hereinbelow with reference to the sequence listing part.

[85242] VGAM2513 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2513 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85243] VGAM2513 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2513 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2513 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[85244] The complementary binding of VGAM2513 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2513 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2513 host target RNA into VGAM2513 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85245] It is appreciated that VGAM2513 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2513 host target genes. The mRNA of each one of this plurality of VGAM2513 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2513 RNA, herein designated VGAM RNA, and which when bound by VGAM2513 RNA causes inhibition of translation of respective one or more VGAM2513 host target proteins.

[85246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2513 gene, herein designated VGAM GENE, on one

or more VGAM2513 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85247] It is yet further appreciated that a function of VGAM2513 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2513 correlate with, and may be deduced from, the identity of the host target genes which VGAM2513 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85248] Nucleotide sequences of the VGAM2513 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2513 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2513 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2513 are further described hereinbelow with reference to Table 1.

[85249] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2513 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2513 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85250] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2513 gene, herein designated VGAM is inhibition of expression of VGAM2513 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2513 correlate with, and may be deduced from, the identity of the target genes which VGAM2513 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85251] Stromal Interaction Molecule 1 (STIM1, Accession

XM_011967) is a VGAM2513 host target gene. STIM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STIM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STIM1 BINDING SITE, designated SEQ ID:30202, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85252] A function of VGAM2513 is therefore inhibition of Stromal Interaction Molecule 1 (STIM1, Accession XM_011967), a gene which is very strongly similar to murine Stim1 and may be a transmembrane stromal cell protein. Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STIM1. The function of STIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1191.CAT56 (Accession NM_025263) is another VGAM2513 host target gene. CAT56 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAT56, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAT56 BINDING SITE, designated SEQ ID:24930, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85253] Another function of VGAM2513 is therefore inhibition of CAT56 (Accession NM_025263). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAT56. FLJ23598 (Accession NM_024783) is another VGAM2513 host target gene. FLJ23598 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23598, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23598 BINDING SITE, designated SEQ ID:24155, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85254] Another function of VGAM2513 is therefore inhibition of FLJ23598 (Accession NM_024783). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ23598. FLJ32332 (Accession NM_144641) is another VGAM2513 host target gene. FLJ32332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32332 BINDING SITE, designated SEQ ID:29469, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85255] Another function of VGAM2513 is therefore inhibition of FLJ32332 (Accession NM_144641). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32332. KIAA0022 (Accession NM_014880) is another VGAM2513 host target gene. KIAA0022 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0022, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0022 BINDING SITE, designated SEQ ID:17029, to the

nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85256] Another function of VGAM2513 is therefore inhibition of KIAA0022 (Accession NM_014880). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0022. KIAA1211 (Accession XM_044178) is another VGAM2513 host target gene. KIAA1211 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1211, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1211 BINDING SITE, designated SEQ ID:34162, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85257] Another function of VGAM2513 is therefore inhibition of KIAA1211 (Accession XM_044178). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1211. KIAA1522 (Accession XM_036299) is another VGAM2513 host target gene. KIAA1522 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1522, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1522 BINDING SITE, designated SEQ ID:32414, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85258] Another function of VGAM2513 is therefore inhibition of KIAA1522 (Accession XM_036299). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1522. KIAA1866 (Accession XM_027658) is another VGAM2513 host target gene. KIAA1866 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1866 BINDING SITE, designated SEQ ID:30552, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85259] Another function of VGAM2513 is therefore inhibition of KIAA1866 (Accession XM_027658). Accordingly, utilities

of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1866. Purinergic Receptor P2X, Ligand-gated Ion Channel, 1 (P2RX1, Accession XM_040635) is another VGAM2513 host target gene. P2RX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P2RX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RX1 BINDING SITE, designated SEQ ID:33350, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85260] Another function of VGAM2513 is therefore inhibition of Purinergic Receptor P2X, Ligand-gated Ion Channel, 1 (P2RX1, Accession XM_040635). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RX1. Pleiomorphic Adenoma Gene-like 2 (PLAGL2, Accession XM_047007) is another VGAM2513 host target gene. PLAGL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLAGL2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAGL2 BINDING SITE, designated SEQ ID:34876, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85261] Another function of VGAM2513 is therefore inhibition of Pleiomorphic Adenoma Gene-like 2 (PLAGL2, Accession XM_047007). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAGL2. Transient Receptor Potential Cation Channel, Subfamily V, Member 5 (TRPV5, Accession NM_019841) is another VGAM2513 host target gene. TRPV5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TRPV5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPV5 BINDING SITE, designated SEQ ID:21247, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85262] Another function of VGAM2513 is therefore inhibition of

Transient Receptor Potential Cation Channel, Subfamily V, Member 5 (TRPV5, Accession NM_019841). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV5. LOC219397 (Accession XM_167889) is another VGAM2513 host target gene. LOC219397 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219397 BINDING SITE, designated SEQ ID:44897, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85263] Another function of VGAM2513 is therefore inhibition of LOC219397 (Accession XM_167889). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219397. LOC221322 (Accession XM_166323) is another VGAM2513 host target gene. LOC221322 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221322, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221322 BINDING SITE, designated SEQ ID:44151, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85264] Another function of VGAM2513 is therefore inhibition of LOC221322 (Accession XM_166323). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221322. LOC222060 (Accession XM_168427) is another VGAM2513 host target gene. LOC222060 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222060, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222060 BINDING SITE, designated SEQ ID:45158, to the nucleotide sequence of VGAM2513 RNA, herein designated VGAM RNA, also designated SEQ ID:5224.

[85265] Another function of VGAM2513 is therefore inhibition of LOC222060 (Accession XM_168427). Accordingly, utilities of VGAM2513 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC222060. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2514 (VGAM2514) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85266] VGAM2514 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2514 was detected is described hereinabove with reference to Figs. 1-8.

[85267] VGAM2514 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2514 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85268] VGAM2514 gene encodes a VGAM2514 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2514 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2514 precursor RNA is designated SEQ ID:2500, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2500 is located at position 127106 relative to the genome of Mouse Cytomegalovirus 1.

[85269] VGAM2514 precursor RNA folds onto itself, forming VGAM2514 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85270] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2514 folded precursor RNA into VGAM2514 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2514 RNA is designated SEQ ID:5225, and is provided hereinbelow with reference to the sequence listing part.

[85271] VGAM2514 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2514 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85272] VGAM2514 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2514 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2514 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85273] The complementary binding of VGAM2514 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2514 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2514 host target RNA into VGAM2514 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85274] It is appreciated that VGAM2514 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2514 host target genes. The mRNA of each one of this plurality of VGAM2514 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2514 RNA, herein designated VGAM RNA, and which when bound by VGAM2514 RNA causes

inhibition of translation of respective one or more VGAM2514 host target proteins.

[85275] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2514 gene, herein designated VGAM GENE, on one or more VGAM2514 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85276] It is yet further appreciated that a function of VGAM2514 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2514 include diagnosis, prevention and

treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2514 correlate with, and may be deduced from, the identity of the host target genes which VGAM2514 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85277] Nucleotide sequences of the VGAM2514 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2514 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2514 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2514 are further described hereinbelow with reference to Table 1.

[85278] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2514 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2514 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85279] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2514 gene, herein designated VGAM is inhibition of expression of VGAM2514 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2514 correlate with, and may be deduced from, the identity of the target genes which VGAM2514 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85280] Aryl Hydrocarbon Receptor (AHR, Accession NM_001621) is a VGAM2514 host target gene. AHR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AHR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AHR BINDING SITE, designated SEQ ID:7332, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85281] A function of VGAM2514 is therefore inhibition of Aryl Hydrocarbon Receptor (AHR, Accession NM_001621), a gene which plays a role in modulating carcinogenesis through the induction of xenobiotic-metabolizing enzymes. Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AHR. The function of AHR and its association with various diseases and clinical condi-

tions, has been established by previous studies, as described hereinabove with reference to VGAM368.Ectodysplasin 1, Anhidrotic Receptor (EDAR, Accession NM_022336) is another VGAM2514 host target gene. EDAR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EDAR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EDAR BINDING SITE, designated SEQ ID:22745, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85282] Another function of VGAM2514 is therefore inhibition of Ectodysplasin 1, Anhidrotic Receptor (EDAR, Accession NM_022336). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDAR. Fibulin 5 (FBLN5, Accession NM_006329) is another VGAM2514 host target gene. FBLN5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBLN5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of FBLN5 BINDING SITE, designated SEQ ID:13026, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85283] Another function of VGAM2514 is therefore inhibition of Fibulin 5 (FBLN5, Accession NM_006329), a gene which promotes adhesion of endothelial cells through interaction of integrins and the rgd motif. Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBLN5. The function of FBLN5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1127.Gamma-aminobutyric Acid (GABA) A Receptor, Epsilon (GABRE, Accession NM_021990) is another VGAM2514 host target gene. GABRE BINDING SITE1 through GABRE BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GABRE, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABRE BINDING SITE1 through GABRE BINDING SITE4, designated SEQ ID:22528, SEQ ID:22513, SEQ

ID:22509 and SEQ ID:11407 respectively, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85284] Another function of VGAM2514 is therefore inhibition of Gamma-aminobutyric Acid (GABA) A Receptor, Epsilon (GABRE, Accession NM_021990), a gene which mediates neuronal inhibition by binding to the gaba/benzodiazepine receptor and opening an integral chloride channel. Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABRE. The function of GABRE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM259.Nephronophthisis 1 (juvenile) (NPHP1, Accession XM_031236) is another VGAM2514 host target gene. NPHP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPHP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPHP1 BINDING SITE, designated SEQ ID:31315, to the nucleotide sequence of VGAM2514 RNA,

herein designated VGAM RNA, also designated SEQ ID:5225.

[85285] Another function of VGAM2514 is therefore inhibition of Nephronophthisis 1 (juvenile) (NPHP1, Accession XM_031236). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPHP1. Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695) is another VGAM2514 host target gene. VANGL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VANGL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VANGL2 BINDING SITE, designated SEQ ID:35477, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85286] Another function of VGAM2514 is therefore inhibition of Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695), a gene which may take part in defining the lateral boundary of floorplate differentiation. Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with VANGL2. The function of VANGL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.CHFR (Accession NM_018223) is another VGAM2514 host target gene. CHFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHFR BINDING SITE, designated SEQ ID:20149, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85287] Another function of VGAM2514 is therefore inhibition of CHFR (Accession NM_018223). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHFR. DKFZp586I021 (Accession NM_032271) is another VGAM2514 host target gene. DKFZp586I021 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp586I021, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates

the complementarity of the nucleotide sequences of DKFZp586I021 BINDING SITE, designated SEQ ID:26020, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85288] Another function of VGAM2514 is therefore inhibition of DKFZp586I021 (Accession NM_032271). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp586I021. DKFZP761I2123 (Accession NM_031449) is another VGAM2514 host target gene. DKFZP761I2123 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761I2123, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761I2123 BINDING SITE, designated SEQ ID:25463, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85289] Another function of VGAM2514 is therefore inhibition of DKFZP761I2123 (Accession NM_031449). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP761I2123. FLJ14855 (Accession NM_033210) is another VGAM2514 host target gene. FLJ14855 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14855, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14855 BINDING SITE, designated SEQ ID:27060, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85290] Another function of VGAM2514 is therefore inhibition of FLJ14855 (Accession NM_033210). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14855. FLJ20069 (Accession NM_017651) is another VGAM2514 host target gene. FLJ20069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20069 BINDING SITE, designated SEQ ID:19157, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM

RNA, also designated SEQ ID:5225.

[85291] Another function of VGAM2514 is therefore inhibition of FLJ20069 (Accession NM_017651). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20069. FLJ21140 (Accession NM_024776) is another VGAM2514 host target gene. FLJ21140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21140 BINDING SITE, designated SEQ ID:24140, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85292] Another function of VGAM2514 is therefore inhibition of FLJ21140 (Accession NM_024776). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21140. PNPASE (Accession XM_048088) is another VGAM2514 host target gene. PNPASE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PNPASE, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PNPASE BINDING SITE, designated SEQ ID:35101, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85293] Another function of VGAM2514 is therefore inhibition of PNPASE (Accession XM_048088). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNPASE. PRO1914 (Accession NM_014106) is another VGAM2514 host target gene. PRO1914 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1914, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1914 BINDING SITE, designated SEQ ID:15328, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85294] Another function of VGAM2514 is therefore inhibition of PRO1914 (Accession NM_014106). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PRO1914. TERA (Accession NM_021238) is another VGAM2514 host target gene. TERA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TERA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TERA BINDING SITE, designated SEQ ID:22206, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85295] Another function of VGAM2514 is therefore inhibition of TERA (Accession NM_021238). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERA. LOC196283 (Accession XM_113684) is another VGAM2514 host target gene. LOC196283 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196283, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196283 BINDING SITE, designated SEQ ID:42340, to

the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85296] Another function of VGAM2514 is therefore inhibition of LOC196283 (Accession XM_113684). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196283. LOC202451 (Accession XM_117401) is another VGAM2514 host target gene. LOC202451 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202451, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202451 BINDING SITE, designated SEQ ID:43436, to the nucleotide sequence of VGAM2514 RNA, herein designated VGAM RNA, also designated SEQ ID:5225.

[85297] Another function of VGAM2514 is therefore inhibition of LOC202451 (Accession XM_117401). Accordingly, utilities of VGAM2514 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202451. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2515 (VGAM2515) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85298] VGAM2515 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2515 was detected is described hereinabove with reference to Figs. 1-8.

[85299] VGAM2515 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2515 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85300] VGAM2515 gene encodes a VGAM2515 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2515 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2515 precursor RNA is designated SEQ ID:2501, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2501 is located at position 35144 relative to the genome of Mouse Cytomegalovirus 1.

[85301] VGAM2515 precursor RNA folds onto itself, forming VGAM2515 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85302] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2515 folded precursor RNA into VGAM2515 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2515 RNA is designated SEQ ID:5226, and is provided hereinbelow with reference to the sequence listing part.

[85303] VGAM2515 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2515 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2515 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85304] VGAM2515 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2515 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2515 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85305] The complementary binding of VGAM2515 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2515 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2515 host target RNA into VGAM2515 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85306] It is appreciated that VGAM2515 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2515 host target genes. The mRNA of each one of this plurality of VGAM2515 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2515 RNA, herein designated VGAM RNA, and which when bound by VGAM2515 RNA causes inhibition of translation of respective one or more VGAM2515 host target proteins.

[85307] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2515 gene, herein designated VGAM GENE, on one or more VGAM2515 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85308] It is yet further appreciated that a function of VGAM2515 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2515 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2515 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85309] Nucleotide sequences of the VGAM2515 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2515 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2515 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2515 are further described hereinbelow with reference to Table 1.

[85310] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2515 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2515 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85311] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2515 gene, herein designated VGAM is inhibition of expression of VGAM2515 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2515 correlate with, and may be deduced from, the identity of the target genes which VGAM2515

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85312] Protein Tyrosine Phosphatase, Non-receptor Type 1 (PTPN1, Accession NM_002827) is a VGAM2515 host target gene. PTPN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPN1 BINDING SITE, designated SEQ ID:8703, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85313] A function of VGAM2515 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type 1 (PTPN1, Accession NM_002827), a gene which is a non-receptor type 1 protein tyrosine phosphatase and inhibits insulin signaling. Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN1. The function of PTPN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM327.Zinc Fin-

ger Protein 2 (A1-5) (ZNF2, Accession NM_021088) is another VGAM2515 host target gene. ZNF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF2 BINDING SITE, designated SEQ ID:22070, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85314] Another function of VGAM2515 is therefore inhibition of Zinc Finger Protein 2 (A1-5) (ZNF2, Accession NM_021088). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF2. D2S448 (Accession XM_056455) is another VGAM2515 host target gene. D2S448 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by D2S448, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of D2S448 BINDING SITE, designated SEQ ID:36396, to the nucleotide sequence of VGAM2515 RNA,

herein designated VGAM RNA, also designated SEQ ID:5226.

[85315] Another function of VGAM2515 is therefore inhibition of D2S448 (Accession XM_056455). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D2S448. FLJ13102 (Accession NM_024887) is another VGAM2515 host target gene. FLJ13102 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13102, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13102 BINDING SITE, designated SEQ ID:24345, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85316] Another function of VGAM2515 is therefore inhibition of FLJ13102 (Accession NM_024887). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13102. KIAA0418 (Accession NM_014631) is another VGAM2515 host target gene. KIAA0418 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0418, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0418 BINDING SITE, designated SEQ ID:15998, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85317] Another function of VGAM2515 is therefore inhibition of KIAA0418 (Accession NM_014631). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0418. MAGE-E1 (Accession NM_030801) is another VGAM2515 host target gene. MAGE-E1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAGE-E1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAGE-E1 BINDING SITE, designated SEQ ID:25107, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85318] Another function of VGAM2515 is therefore inhibition of MAGE-E1 (Accession NM_030801). Accordingly, utilities of

VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGE-E1. Melanoma Antigen, Family E, 1, Cancer/testis Specific (MAGEE1, Accession NM_016249) is another VGAM2515 host target gene. MAGEE1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAGEE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAGEE1 BINDING SITE, designated SEQ ID:18377, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85319] Another function of VGAM2515 is therefore inhibition of Melanoma Antigen, Family E, 1, Cancer/testis Specific (MAGEE1, Accession NM_016249). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGEE1. Mesoderm Development Candidate 1 (MESDC1, Accession NM_022566) is another VGAM2515 host target gene. MESDC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MESDC1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MESDC1 BINDING SITE, designated SEQ ID:22884, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85320] Another function of VGAM2515 is therefore inhibition of Mesoderm Development Candidate 1 (MESDC1, Accession NM_022566). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MESDC1. MGC11335 (Accession NM_030819) is another VGAM2515 host target gene. MGC11335 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC11335, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11335 BINDING SITE, designated SEQ ID:25148, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85321] Another function of VGAM2515 is therefore inhibition of MGC11335 (Accession NM_030819). Accordingly, utilities

of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11335. OS4 (Accession NM_005730) is another VGAM2515 host target gene. OS4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OS4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OS4 BINDING SITE, designated SEQ ID:12291, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85322] Another function of VGAM2515 is therefore inhibition of OS4 (Accession NM_005730). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OS4. PP1665 (Accession NM_030792) is another VGAM2515 host target gene. PP1665 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PP1665, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP1665 BINDING SITE, des-

ignated SEQ ID:25092, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85323] Another function of VGAM2515 is therefore inhibition of PP1665 (Accession NM_030792). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1665. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840) is another VGAM2515 host target gene. PPP1R16B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R16B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R16B BINDING SITE, designated SEQ ID:30778, to the nucleotide sequence of VGAM2515 RNA, herein designated VGAM RNA, also designated SEQ ID:5226.

[85324] Another function of VGAM2515 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840). Accordingly, utilities of VGAM2515 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

PPP1R16B. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2516 (VGAM2516) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85325] VGAM2516 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2516 was detected is described hereinabove with reference to Figs. 1-8.

[85326] VGAM2516 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2516 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85327] VGAM2516 gene encodes a VGAM2516 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2516 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2516 precursor RNA is designated SEQ ID:2502, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2502 is located at position 84255 relative to the genome of Mouse Cytomegalovirus 1.

[85328] VGAM2516 precursor RNA folds onto itself, forming VGAM2516 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85329] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2516 folded precursor RNA into VGAM2516 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2516 RNA is designated SEQ ID:5227, and is provided hereinbelow with reference to the sequence listing part.

[85330] VGAM2516 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2516 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85331] VGAM2516 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2516 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2516 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85332] The complementary binding of VGAM2516 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2516 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2516 host target RNA into VGAM2516 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85333] It is appreciated that VGAM2516 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2516 host target genes. The mRNA of each one of this plurality of VGAM2516 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2516 RNA, herein designated VGAM RNA, and which when bound by VGAM2516 RNA causes

inhibition of translation of respective one or more VGAM2516 host target proteins.

[85334] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2516 gene, herein designated VGAM GENE, on one or more VGAM2516 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85335] It is yet further appreciated that a function of VGAM2516 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2516 include diagnosis, prevention and

treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2516 correlate with, and may be deduced from, the identity of the host target genes which VGAM2516 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85336] Nucleotide sequences of the VGAM2516 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2516 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2516 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2516 are further described hereinbelow with reference to Table 1.

[85337] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2516 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2516 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85338] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2516 gene, herein designated VGAM is inhibition of expression of VGAM2516 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2516 correlate with, and may be deduced from, the identity of the target genes which VGAM2516 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85339] FLJ14442 (Accession NM_032785) is a VGAM2516 host target gene. FLJ14442 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14442, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14442 BINDING SITE, designated SEQ ID:26534, to the nucleotide sequence of VGAM2516 RNA, herein designated VGAM RNA, also designated SEQ ID:5227.

[85340] A function of VGAM2516 is therefore inhibition of FLJ14442 (Accession NM_032785). Accordingly, utilities of VGAM2516 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14442. ISL2 Transcription Factor, LIM/homeodomain, (islet-2) (ISL2, Accession XM_047951) is another VGAM2516 host target gene. ISL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by ISL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ISL2 BINDING SITE, designated SEQ ID:35081, to the nucleotide sequence of VGAM2516 RNA, herein designated VGAM RNA, also designated SEQ ID:5227.

[85341] Another function of VGAM2516 is therefore inhibition of ISL2 Transcription Factor, LIM/homeodomain, (islet-2) (ISL2, Accession XM_047951). Accordingly, utilities of VGAM2516 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ISL2. KIAA1915 (Accession XM_055481) is another VGAM2516 host target gene. KIAA1915 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1915, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1915 BINDING SITE, designated SEQ ID:36273, to the nucleotide sequence of VGAM2516 RNA, herein designated VGAM RNA, also designated SEQ ID:5227.

[85342] Another function of VGAM2516 is therefore inhibition of

KIAA1915 (Accession XM_055481). Accordingly, utilities of VGAM2516 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1915. PLPL (Accession NM_020181) is another VGAM2516 host target gene. PLPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLPL BINDING SITE, designated SEQ ID:21400, to the nucleotide sequence of VGAM2516 RNA, herein designated VGAM RNA, also designated SEQ ID:5227.

[85343] Another function of VGAM2516 is therefore inhibition of PLPL (Accession NM_020181). Accordingly, utilities of VGAM2516 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLPL. LOC256639 (Accession XM_171241) is another VGAM2516 host target gene. LOC256639 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256639, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC256639 BINDING SITE, designated SEQ ID:46029, to the nucleotide sequence of VGAM2516 RNA, herein designated VGAM RNA, also designated SEQ ID:5227.

[85344] Another function of VGAM2516 is therefore inhibition of LOC256639 (Accession XM_171241). Accordingly, utilities of VGAM2516 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256639. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2517 (VGAM2517) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85345] VGAM2517 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2517 was detected is described hereinabove with reference to Figs. 1-8.

[85346] VGAM2517 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2517 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[85347] VGAM2517 gene encodes a VGAM2517 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2517 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2517 precursor RNA is designated SEQ ID:2503, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2503 is located at position 158132 relative to the genome of Mouse Cytomegalovirus 1.

[85348] VGAM2517 precursor RNA folds onto itself, forming VGAM2517 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85349] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2517 folded precursor RNA into VGAM2517 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2517 RNA is designated SEQ ID:5228, and is provided hereinbelow with reference to the sequence listing part.

[85350] VGAM2517 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2517 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85351] VGAM2517 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2517 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2517 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85352] The complementary binding of VGAM2517 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2517 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2517 host target RNA into VGAM2517 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85353] It is appreciated that VGAM2517 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2517 host target genes. The mRNA of each one of this plurality of VGAM2517 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2517 RNA, herein designated VGAM RNA, and which when bound by VGAM2517 RNA causes inhibition of translation of respective one or more VGAM2517 host target proteins.

[85354] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2517 gene, herein designated VGAM GENE, on one or more VGAM2517 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85355] It is yet further appreciated that a function of VGAM2517 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2517 correlate with, and may be deduced from, the identity of the host target genes which VGAM2517 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85356] Nucleotide sequences of the VGAM2517 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2517 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2517 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2517 are further described hereinbelow with reference to Table 1.

[85357] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2517 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2517 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85358] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2517 gene, herein designated VGAM is inhibition of expression of VGAM2517 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2517 correlate with, and may be deduced from, the identity of the target genes which VGAM2517 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85359] Complement Component 5 Receptor 1 (C5a ligand) (C5R1, Accession NM_001736) is a VGAM2517 host target gene. C5R1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5R1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5R1 BINDING SITE, designated SEQ ID:7472, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85360] A function of VGAM2517 is therefore inhibition of Complement Component 5 Receptor 1 (C5a ligand) (C5R1, Accession NM_001736), a gene which has a nonredundant function and is required for mucosal host cell defense in the lung. Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5R1. The function of C5R1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM484.Phosphoenolpyruvate Carboxykinase 1 (soluble) (PCK1, Accession XM_009672) is another VGAM2517 host target gene. PCK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCK1 BINDING SITE, designated SEQ ID:30117, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85361] Another function of VGAM2517 is therefore inhibition of Phosphoenolpyruvate Carboxykinase 1 (soluble) (PCK1,

Accession XM_009672), a gene which forms phosphoenolpyruvate by decarboxylation of oxaloacetate. Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCK1. The function of PCK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2341.HERV-H LTR-associating 2 (HHLA2, Accession NM_007072) is another VGAM2517 host target gene. HHLA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HHLA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HHLA2 BINDING SITE, designated SEQ ID:13936, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85362] Another function of VGAM2517 is therefore inhibition of HERV-H LTR-associating 2 (HHLA2, Accession NM_007072). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HHLA2. KIAA1559

(Accession XM_054472) is another VGAM2517 host target gene. KIAA1559 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:36161, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85363] Another function of VGAM2517 is therefore inhibition of KIAA1559 (Accession XM_054472). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559. Ras Protein-specific Guanine Nucleotide-releasing Factor 2 (RASGRF2, Accession XM_027943) is another VGAM2517 host target gene. RASGRF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASGRF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASGRF2 BINDING SITE, designated SEQ ID:30598, to the nucleotide

sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85364] Another function of VGAM2517 is therefore inhibition of Ras Protein-specific Guanine Nucleotide-releasing Factor 2 (RASGRF2, Accession XM_027943). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASGRF2. LOC124460 (Accession XM_071892) is another VGAM2517 host target gene. LOC124460 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124460, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124460 BINDING SITE, designated SEQ ID:37443, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85365] Another function of VGAM2517 is therefore inhibition of LOC124460 (Accession XM_071892). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124460. LOC147817 (Accession XM_085903) is another VGAM2517 host target gene. LOC147817 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE, designated SEQ ID:38383, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85366] Another function of VGAM2517 is therefore inhibition of LOC147817 (Accession XM_085903). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817. LOC164397 (Accession XM_092780) is another VGAM2517 host target gene. LOC164397 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC164397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164397 BINDING SITE, designated SEQ ID:40152, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85367] Another function of VGAM2517 is therefore inhibition of

LOC164397 (Accession XM_092780). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164397. LOC201294 (Accession XM_113950) is another VGAM2517 host target gene. LOC201294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201294 BINDING SITE, designated SEQ ID:42566, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85368] Another function of VGAM2517 is therefore inhibition of LOC201294 (Accession XM_113950). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201294. LOC245728 (Accession XM_165922) is another VGAM2517 host target gene. LOC245728 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC245728, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC245728 BINDING SITE, designated SEQ ID:43801, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85369] Another function of VGAM2517 is therefore inhibition of LOC245728 (Accession XM_165922). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC245728. LOC253038 (Accession XM_174524) is another VGAM2517 host target gene. LOC253038 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253038, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253038 BINDING SITE, designated SEQ ID:46595, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85370] Another function of VGAM2517 is therefore inhibition of LOC253038 (Accession XM_174524). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253038. LOC253776 (Accession XM_173240) is an-

other VGAM2517 host target gene. LOC253776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253776 BINDING SITE, designated SEQ ID:46525, to the nucleotide sequence of VGAM2517 RNA, herein designated VGAM RNA, also designated SEQ ID:5228.

[85371] Another function of VGAM2517 is therefore inhibition of LOC253776 (Accession XM_173240). Accordingly, utilities of VGAM2517 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253776. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2518 (VGAM2518) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85372] VGAM2518 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2518 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[85373] VGAM2518 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2518 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85374] VGAM2518 gene encodes a VGAM2518 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2518 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2518 precursor RNA is designated SEQ ID:2504, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2504 is located at position 3872 relative to the genome of Mouse Cytomegalovirus 1.

[85375] VGAM2518 precursor RNA folds onto itself, forming VGAM2518 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85376] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2518 folded precursor RNA into VGAM2518 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2518 RNA is designated SEQ ID:5229, and is provided hereinbelow with reference to the sequence listing part.

[85377] VGAM2518 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2518 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2518 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85378] VGAM2518 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2518 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2518 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2518 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2518 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85379] The complementary binding of VGAM2518 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2518 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2518 host target RNA into VGAM2518 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85380] It is appreciated that VGAM2518 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2518 host target genes. The mRNA of each one of this plurality of VGAM2518 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2518 RNA, herein designated VGAM RNA, and which when bound by VGAM2518 RNA causes inhibition of translation of respective one or more VGAM2518 host target proteins.

[85381] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2518 gene, herein designated VGAM GENE, on one or more VGAM2518 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85382] It is yet further appreciated that a function of VGAM2518 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2518 correlate with, and may be deduced from, the identity of the host target genes which VGAM2518 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85383] Nucleotide sequences of the VGAM2518 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2518 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2518 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2518 are further described hereinbelow with reference to Table 1.

[85384] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2518 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2518 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85385] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2518 gene, herein designated VGAM is inhibition of expression of VGAM2518 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2518 correlate with, and may be deduced from, the identity of the target genes which VGAM2518 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85386] Kallmann Syndrome 1 Sequence (KAL1, Accession NM_000216) is a VGAM2518 host target gene. KAL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KAL1, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KAL1 BINDING SITE, designated SEQ ID:5718, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85387] A function of VGAM2518 is therefore inhibition of Kallmann Syndrome 1 Sequence (KAL1, Accession NM_000216). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KAL1. Basic, Immunoglobulin-like Variable Motif Containing (BIVM, Accession NM_017693) is another VGAM2518 host target gene. BIVM BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BIVM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIVM BINDING SITE, designated SEQ ID:19251, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85388] Another function of VGAM2518 is therefore inhibition of Basic, Immunoglobulin-like Variable Motif Containing (BIVM, Accession NM_017693). Accordingly, utilities of

VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIVM. BOP (Accession XM_097915) is another VGAM2518 host target gene. BOP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BOP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BOP BINDING SITE, designated SEQ ID:41208, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85389] Another function of VGAM2518 is therefore inhibition of BOP (Accession XM_097915). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BOP. KIAA1458 (Accession XM_044434) is another VGAM2518 host target gene. KIAA1458 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1458, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1458 BINDING SITE,

designated SEQ ID:34207, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85390] Another function of VGAM2518 is therefore inhibition of KIAA1458 (Accession XM_044434). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1458. KIAA1829 (Accession XM_030378) is another VGAM2518 host target gene. KIAA1829 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1829 BINDING SITE, designated SEQ ID:31035, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85391] Another function of VGAM2518 is therefore inhibition of KIAA1829 (Accession XM_030378). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829. MGC11082 (Accession NM_032691) is another VGAM2518 host target gene. MGC11082 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC11082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11082 BINDING SITE, designated SEQ ID:26412, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85392] Another function of VGAM2518 is therefore inhibition of MGC11082 (Accession NM_032691). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11082. MGC4663 (Accession NM_024514) is another VGAM2518 host target gene. MGC4663 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4663, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4663 BINDING SITE, designated SEQ ID:23718, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85393] Another function of VGAM2518 is therefore inhibition of

MGC4663 (Accession NM_024514). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4663. Phosphodiesterase 4D Interacting Protein (myomegalin) (PDE4DIP, Accession NM_014644) is another VGAM2518 host target gene. PDE4DIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4DIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4DIP BINDING SITE, designated SEQ ID:16050, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85394] Another function of VGAM2518 is therefore inhibition of Phosphodiesterase 4D Interacting Protein (myomegalin) (PDE4DIP, Accession NM_014644). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4DIP. LOC120227 (Accession XM_058459) is another VGAM2518 host target gene. LOC120227 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC120227, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120227 BINDING SITE, designated SEQ ID:36620, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85395] Another function of VGAM2518 is therefore inhibition of LOC120227 (Accession XM_058459). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120227. LOC158318 (Accession XM_098925) is another VGAM2518 host target gene. LOC158318 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158318 BINDING SITE, designated SEQ ID:41957, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85396] Another function of VGAM2518 is therefore inhibition of LOC158318 (Accession XM_098925). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158318. LOC158857 (Accession XM_098997) is another VGAM2518 host target gene. LOC158857 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158857, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158857 BINDING SITE, designated SEQ ID:42031, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85397] Another function of VGAM2518 is therefore inhibition of LOC158857 (Accession XM_098997). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158857. LOC159049 (Accession XM_099020) is another VGAM2518 host target gene. LOC159049 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159049, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159049 BINDING SITE, designated SEQ ID:42057, to

the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85398] Another function of VGAM2518 is therefore inhibition of LOC159049 (Accession XM_099020). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159049. LOC200310 (Accession XM_037840) is another VGAM2518 host target gene. LOC200310 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200310, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200310 BINDING SITE, designated SEQ ID:32710, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85399] Another function of VGAM2518 is therefore inhibition of LOC200310 (Accession XM_037840). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200310. LOC257443 (Accession XM_171072) is another VGAM2518 host target gene. LOC257443 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC257443, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257443 BINDING SITE, designated SEQ ID:45875, to the nucleotide sequence of VGAM2518 RNA, herein designated VGAM RNA, also designated SEQ ID:5229.

[85400] Another function of VGAM2518 is therefore inhibition of LOC257443 (Accession XM_171072). Accordingly, utilities of VGAM2518 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257443. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2519 (VGAM2519) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85401] VGAM2519 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2519 was detected is described hereinabove with reference to Figs. 1-8.

[85402] VGAM2519 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2519 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85403] VGAM2519 gene encodes a VGAM2519 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2519 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2519 precursor RNA is designated SEQ ID:2505, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2505 is located at position 59910 relative to the genome of Mouse Cytomegalovirus 1.

[85404] VGAM2519 precursor RNA folds onto itself, forming VGAM2519 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85405] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2519 folded precursor RNA into VGAM2519 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2519 RNA is designated SEQ ID:5230, and is provided hereinbelow with reference to the sequence listing part.

[85406] VGAM2519 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2519 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85407] VGAM2519 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2519 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2519 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85408] The complementary binding of VGAM2519 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2519 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2519

host target RNA into VGAM2519 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85409] It is appreciated that VGAM2519 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2519 host target genes. The mRNA of each one of this plurality of VGAM2519 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2519 RNA, herein designated VGAM RNA, and which when bound by VGAM2519 RNA causes inhibition of translation of respective one or more VGAM2519 host target proteins.

[85410] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2519 gene, herein designated VGAM GENE, on one or more VGAM2519 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85411] It is yet further appreciated that a function of VGAM2519 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2519 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2519 correlate with, and may be deduced from, the identity of the host target genes which VGAM2519 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85412] Nucleotide sequences of the VGAM2519 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2519 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2519 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2519 are further

described hereinbelow with reference to Table 1.

[85413] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2519 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2519 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85414] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2519 gene, herein designated VGAM is inhibition of expression of VGAM2519 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2519 correlate with, and may be deduced from, the identity of the target genes which VGAM2519 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85415] KIAA0356 (Accession XM_038655) is a VGAM2519 host target gene. KIAA0356 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0356, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0356 BINDING SITE,

designated SEQ ID:32892, to the nucleotide sequence of VGAM2519 RNA, herein designated VGAM RNA, also designated SEQ ID:5230.

[85416] A function of VGAM2519 is therefore inhibition of KIAA0356 (Accession XM_038655). Accordingly, utilities of VGAM2519 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0356. LOC150295 (Accession XM_097868) is another VGAM2519 host target gene. LOC150295 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150295, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150295 BINDING SITE, designated SEQ ID:41178, to the nucleotide sequence of VGAM2519 RNA, herein designated VGAM RNA, also designated SEQ ID:5230.

[85417] Another function of VGAM2519 is therefore inhibition of LOC150295 (Accession XM_097868). Accordingly, utilities of VGAM2519 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150295. LOC219513 (Accession XM_169166) is another VGAM2519 host target gene. LOC219513 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219513, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219513 BINDING SITE, designated SEQ ID:45292, to the nucleotide sequence of VGAM2519 RNA, herein designated VGAM RNA, also designated SEQ ID:5230.

[85418] Another function of VGAM2519 is therefore inhibition of LOC219513 (Accession XM_169166). Accordingly, utilities of VGAM2519 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219513. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2520 (VGAM2520) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85419] VGAM2520 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2520 was detected is described hereinabove with reference to Figs. 1-8.

[85420] VGAM2520 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2520 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85421] VGAM2520 gene encodes a VGAM2520 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2520 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2520 precursor RNA is designated SEQ ID:2506, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2506 is located at position 173931 relative to the genome of Mouse Cytomegalovirus 1.

[85422] VGAM2520 precursor RNA folds onto itself, forming VGAM2520 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[85423] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2520 folded precursor RNA into VGAM2520 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2520 RNA is designated SEQ ID:5231, and is provided hereinbelow with reference to the sequence listing part.

[85424] VGAM2520 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2520 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85425] VGAM2520 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2520 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2520 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2520 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85426] The complementary binding of VGAM2520 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2520 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2520 host target RNA into VGAM2520 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85427] It is appreciated that VGAM2520 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2520 host target genes. The mRNA of each one of this plurality of VGAM2520 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2520 RNA, herein designated VGAM RNA, and which when bound by VGAM2520 RNA causes inhibition of translation of respective one or more VGAM2520 host target proteins.

[85428] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2520 gene, herein designated VGAM GENE, on one or more VGAM2520 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85429] It is yet further appreciated that a function of VGAM2520 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2520 correlate with, and may be deduced from, the identity of the host target genes which VGAM2520 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85430] Nucleotide sequences of the VGAM2520 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2520 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2520 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2520 are further described hereinbelow with reference to Table 1.

[85431] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2520 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2520 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85432] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2520 gene, herein designated VGAM is inhibition of expression of VGAM2520 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2520 correlate with, and may be deduced from, the identity of the target genes which VGAM2520 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85433] Breast Cancer 1, Early Onset (BRCA1, Accession NM_007295) is a VGAM2520 host target gene. BRCA1 BINDING SITE1 through BRCA1 BINDING SITE10 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BRCA1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II

or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRCA1 BINDING SITE1 through BRCA1 BINDING SITE10, designated SEQ ID:14171, SEQ ID:14177, SEQ ID:14184, SEQ ID:14190, SEQ ID:14196, SEQ ID:14204, SEQ ID:14210, SEQ ID:14216, SEQ ID:14222 and SEQ ID:14165 respectively, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85434] A function of VGAM2520 is therefore inhibition of Breast Cancer 1, Early Onset (BRCA1, Accession NM_007295). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRCA1. Heat Shock 70kDa Protein 4 (HSPA4, Accession XM_114482) is another VGAM2520 host target gene. HSPA4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSPA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPA4 BINDING SITE, designated SEQ ID:42978, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85435] Another function of VGAM2520 is therefore inhibition of Heat Shock 70kDa Protein 4 (HSPA4, Accession XM_114482). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPA4. Regulatory Factor X, 5 (influences HLA class II expression) (RFX5, Accession NM_000449) is another VGAM2520 host target gene. RFX5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RFX5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RFX5 BINDING SITE, designated SEQ ID:6044, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85436] Another function of VGAM2520 is therefore inhibition of Regulatory Factor X, 5 (influences HLA class II expression) (RFX5, Accession NM_000449), a gene which activates transcription from class ii mhc promoters. Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFX5. The function of RFX5 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM55.Reticulon 3 (RTN3, Accession XM_058207) is another VGAM2520 host target gene. RTN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RTN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RTN3 BINDING SITE, designated SEQ ID:36585, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85437] Another function of VGAM2520 is therefore inhibition of Reticulon 3 (RTN3, Accession XM_058207), a gene which is a member of the reticulon (neuroendocrine-specific, NSP) family. Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RTN3. The function of RTN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM596.Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 5 (SLC7A5, Accession NM_003486) is another VGAM2520 host target gene. SLC7A5 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC7A5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC7A5 BINDING SITE, designated SEQ ID:9578, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85438] Another function of VGAM2520 is therefore inhibition of Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 5 (SLC7A5, Accession NM_003486), a gene which mediates transport of large and small neutral amino acids. Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A5. The function of SLC7A5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM430.Mitogen-activated Protein Kinase Kinase 5 (MAP2K5, Accession NM_002757) is another VGAM2520 host target gene. MAP2K5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAP2K5, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP2K5 BINDING SITE, designated SEQ ID:8638, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85439] Another function of VGAM2520 is therefore inhibition of Mitogen-activated Protein Kinase Kinase 5 (MAP2K5, Accession NM_002757). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP2K5.

LOC132001 (Accession NM_138807) is another VGAM2520 host target gene. LOC132001 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132001, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132001 BINDING SITE, designated SEQ ID:29030, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85440] Another function of VGAM2520 is therefore inhibition of LOC132001 (Accession NM_138807). Accordingly, utilities

of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132001. LOC138050 (Accession XM_059937) is another VGAM2520 host target gene. LOC138050 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC138050, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138050 BINDING SITE, designated SEQ ID:37116, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85441] Another function of VGAM2520 is therefore inhibition of LOC138050 (Accession XM_059937). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138050. LOC146901 (Accession XM_097121) is another VGAM2520 host target gene. LOC146901 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146901, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC146901 BINDING SITE, designated SEQ ID:40762, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85442] Another function of VGAM2520 is therefore inhibition of LOC146901 (Accession XM_097121). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146901. LOC151516 (Accession XM_087229) is another VGAM2520 host target gene. LOC151516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151516 BINDING SITE, designated SEQ ID:39130, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85443] Another function of VGAM2520 is therefore inhibition of LOC151516 (Accession XM_087229). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151516. LOC165741 (Accession XM_105272) is another VGAM2520 host target gene. LOC165741 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC165741, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC165741 BINDING SITE, designated SEQ ID:42190, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85444] Another function of VGAM2520 is therefore inhibition of LOC165741 (Accession XM_105272). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165741. LOC222008 (Accession XM_168361) is another VGAM2520 host target gene. LOC222008 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222008, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222008 BINDING SITE, designated SEQ ID:45124, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85445] Another function of VGAM2520 is therefore inhibition of

LOC222008 (Accession XM_168361). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222008. LOC253461 (Accession XM_172341) is another VGAM2520 host target gene. LOC253461 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253461, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253461 BINDING SITE, designated SEQ ID:46074, to the nucleotide sequence of VGAM2520 RNA, herein designated VGAM RNA, also designated SEQ ID:5231.

[85446] Another function of VGAM2520 is therefore inhibition of LOC253461 (Accession XM_172341). Accordingly, utilities of VGAM2520 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253461. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2521 (VGAM2521) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[85447] VGAM2521 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2521 was detected is described hereinabove with reference to Figs. 1-8.

[85448] VGAM2521 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2521 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85449] VGAM2521 gene encodes a VGAM2521 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2521 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2521 precursor RNA is designated SEQ ID:2507, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2507 is located at position 9443 relative to the genome of Mouse Cytomegalovirus 1.

[85450] VGAM2521 precursor RNA folds onto itself, forming VGAM2521 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85451] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2521 folded precursor RNA into VGAM2521 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2521 RNA is designated SEQ ID:5232, and is provided hereinbelow with reference to the sequence listing part.

[85452] VGAM2521 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2521 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85453] VGAM2521 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2521 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2521 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[85454] The complementary binding of VGAM2521 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2521 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2521 host target RNA into VGAM2521 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85455] It is appreciated that VGAM2521 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2521 host target genes. The mRNA of each one of this plurality of VGAM2521 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2521 RNA, herein designated VGAM RNA, and which when bound by VGAM2521 RNA causes inhibition of translation of respective one or more VGAM2521 host target proteins.

[85456] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2521 gene, herein designated VGAM GENE, on one

or more VGAM2521 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85457] It is yet further appreciated that a function of VGAM2521 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2521 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2521 correlate with, and may be deduced from, the identity of the host target genes which VGAM2521 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85458] Nucleotide sequences of the VGAM2521 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2521 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2521 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2521 are further described hereinbelow with reference to Table 1.

[85459] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2521 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2521 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85460] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2521 gene, herein designated VGAM is inhibition of expression of VGAM2521 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2521 correlate with, and may be deduced from, the identity of the target genes which VGAM2521 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85461] SEC22 Vesicle Trafficking Protein-like 1 (S. cerevisiae)

(SEC22L1, Accession NM_004892) is a VGAM2521 host target gene. SEC22L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC22L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC22L1 BINDING SITE, designated SEQ ID:11319, to the nucleotide sequence of VGAM2521 RNA, herein designated VGAM RNA, also designated SEQ ID:5232.

[85462] A function of VGAM2521 is therefore inhibition of SEC22 Vesicle Trafficking Protein-like 1 (S. cerevisiae) (SEC22L1, Accession NM_004892), a gene which may be involved in vesicle docking during transport between the ER and the Golgi apparatus. Accordingly, utilities of VGAM2521 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC22L1. The function of SEC22L1 has been established by previous studies. In S. cerevisiae, the vesicle trafficking protein complexes directing transport between the endoplasmic reticulum (ER) and Golgi appear to include Sed5 (see OMIM Ref. No. syntaxin-5; 603189), proposed to be a cis-Golgi receptor protein, and Sec22 and Bet1 (OMIM Ref. No. 605456), po-

tential Sed5 docking partners localized on ER-derived vesicles. The Sly1 protein may bind to and regulate the activity of Sed5 for docking with ER-derived vesicle proteins. See membrin (GOSR2; 604027). Hay et al. (1997) isolated a rat liver protein complex representing an intermediate in ER-to-Golgi transfer reactions. The complex contained syntaxin-5, GOS28 (OMIM Ref. No. 604026), the rat homologs of Bet1 and Sly1, and 2 novel proteins, rat sec22b and membrin. The authors isolated mouse sec22b cDNAs and determined that the sec22b protein is distinct from the previously identified rat sec22a protein. Sequence analysis revealed that mouse sec22b is a cytoplasmically oriented, C-terminally anchored integral membrane protein. By immunofluorescence of mammalian cells expressing epitope-tagged sec22b, Hay et al. (1997) found that sec22b and membrin accumulated primarily at the ER. Other members of the complex localized to Golgi membranes, indicating that the complex recapitulates vesicle docking between distinct organelles in the ER/Golgi transport cycle. Expression of recombinant membrin and sec22b disrupted normal trafficking, demonstrating that these proteins regulate ER-to-Golgi trafficking. Mao et al. (1998) identified an umbilical cord blood

CD34-positive cell cDNA encoding the human homolog of sec22b. The predicted human protein contains 215 amino acids. To fuse transport vesicles with target membranes, proteins of the SNARE complex must be located on both the vesicle and the target membrane. In yeast, 4 integral membrane proteins, Sed5, Bos1, Sec22, and Bet1 each are believed to contribute a single helix to form the SNARE complex that is needed for transport from endoplasmic reticulum to Golgi. This generates a 4-helix bundle, which ultimately mediates the actual fusion event. Parlati et al. (2000) explored how the anchoring arrangement of the 4 helices affects their ability to mediate fusion. Parlati et al. (2000) reconstituted 2 populations of phospholipid bilayer vesicles, with the individual SNARE proteins distributed in all possible combinations between them. Of the 8 nonredundant permutations of 4 subunits distributed over 2 vesicle populations, only 1 resulted in membrane fusion. Fusion occurred only when the v-SNARE Bet1 is on 1 membrane and the syntaxin heavy chain Sed5 and its 2 light chains, Bos1 and Sec22, are on the other membrane, where they form a functional t-SNARE. Thus, each SNARE protein is topologically restricted by design to function either as a v-SNARE or as part of a t-SNARE complex.

[85463] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[85464] Mao, M.; Fu, G.; Wu, J.-S.; Zhang, Q.-H.; Zhou, J.; Kan, L.-X.; Huang, Q.-H.; He, K.-L.; Gu, B.-W.; Han, Z.-G.; Shen, Y.; Gu, J.; Yu, Y.-P.; Xu, S.-H.; Wang, Y.-X.; Chen, S.-J.; Chen, Z. : Identification of genes expressed in human CD34+ hematopoietic stem/progenitor cells by expressed sequence tags and efficient full-length cDNA cloning. Proc. Nat. Acad. Sci. 95: 8175-8180, 1998. ; and

[85465] Parlati, F.; McNew, J. A.; Fukuda, R.; Miller, R.; Sollner, T. H.; Rothman, J. E. : Topological restriction of SNARE-dependent membrane fusion. Nature 407: 194-198, 2000.

[85466] Further studies establishing the function and utilities of SEC22L1 are found in John Hopkins OMIM database record ID 604029, and in sited publications numbered 763 and 8801 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.KIAA0189 (Accession NM_014725) is another VGAM2521 host target gene. KIAA0189 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0189, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0189 BINDING SITE, designated SEQ ID:16315, to the nucleotide sequence of VGAM2521 RNA, herein designated VGAM RNA, also designated SEQ ID:5232.

[85467] Another function of VGAM2521 is therefore inhibition of KIAA0189 (Accession NM_014725). Accordingly, utilities of VGAM2521 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0189. PRO1598 (Accession NM_018503) is another VGAM2521 host target gene. PRO1598 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1598, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1598 BINDING SITE, designated SEQ ID:20570, to the nucleotide sequence of VGAM2521 RNA, herein designated VGAM RNA, also designated SEQ ID:5232.

[85468] Another function of VGAM2521 is therefore inhibition of PRO1598 (Accession NM_018503). Accordingly, utilities of VGAM2521 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PRO1598. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2522 (VGAM2522) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85469] VGAM2522 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2522 was detected is described hereinabove with reference to Figs. 1-8.

[85470] VGAM2522 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2522 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85471] VGAM2522 gene encodes a VGAM2522 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2522 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2522 precursor RNA is desig-

nated SEQ ID:2508, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2508 is located at position 116189 relative to the genome of Mouse Cytomegalovirus 1.

[85472] VGAM2522 precursor RNA folds onto itself, forming VGAM2522 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85473] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2522 folded precursor RNA into VGAM2522 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2522 RNA is designated SEQ ID:5233, and is provided hereinbelow with reference to the sequence

listing part.

[85474] VGAM2522 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2522 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85475] VGAM2522 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2522 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2522 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85476] The complementary binding of VGAM2522 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2522 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2522 host target RNA into VGAM2522 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85477] It is appreciated that VGAM2522 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2522 host target genes. The mRNA of each one of this plurality of VGAM2522 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2522 RNA, herein designated VGAM

RNA, and which when bound by VGAM2522 RNA causes inhibition of translation of respective one or more VGAM2522 host target proteins.

[85478] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2522 gene, herein designated VGAM GENE, on one or more VGAM2522 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85479] It is yet further appreciated that a function of VGAM2522 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2522 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2522 correlate with, and may be deduced from, the identity of the host target genes which VGAM2522 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85480] Nucleotide sequences of the VGAM2522 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2522 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2522 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2522 are further described hereinbelow with reference to Table 1.

[85481] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2522 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2522 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85482] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2522 gene, herein designated VGAM is

inhibition of expression of VGAM2522 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2522 correlate with, and may be deduced from, the identity of the target genes which VGAM2522 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85483] Cullin 4B (CUL4B, Accession NM_003588) is a VGAM2522 host target gene. CUL4B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CUL4B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CUL4B BINDING SITE, designated SEQ ID:9641, to the nucleotide sequence of VGAM2522 RNA, herein designated VGAM RNA, also designated SEQ ID:5233.

[85484] A function of VGAM2522 is therefore inhibition of Cullin 4B (CUL4B, Accession NM_003588), a gene which is a negative regulator of the cell cycle in C. elegans. Accordingly, utilities of VGAM2522 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CUL4B. The function of CUL4B and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM140.Protein Tyrosine Phosphatase, Non-receptor Type 9 (PTPN9, Accession NM_002833) is another VGAM2522 host target gene. PTPN9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPN9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPN9 BINDING SITE, designated SEQ ID:8711, to the nucleotide sequence of VGAM2522 RNA, herein designated VGAM RNA, also designated SEQ ID:5233.

[85485] Another function of VGAM2522 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type 9 (PTPN9, Accession NM_002833). Accordingly, utilities of VGAM2522 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN9. Synaptosomal-associated Protein, 29kDa (SNAP29, Accession NM_004782) is another VGAM2522 host target gene. SNAP29 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNAP29, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of SNAP29 BINDING SITE, designated SEQ ID:11184, to the nucleotide sequence of VGAM2522 RNA, herein designated VGAM RNA, also designated SEQ ID:5233.

[85486] Another function of VGAM2522 is therefore inhibition of Synaptosomal-associated Protein, 29kDa (SNAP29, Accession NM_004782). Accordingly, utilities of VGAM2522 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP29. LOC254559 (Accession XM_172931) is another VGAM2522 host target gene. LOC254559 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254559, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254559 BINDING SITE, designated SEQ ID:46196, to the nucleotide sequence of VGAM2522 RNA, herein designated VGAM RNA, also designated SEQ ID:5233.

[85487] Another function of VGAM2522 is therefore inhibition of LOC254559 (Accession XM_172931). Accordingly, utilities of VGAM2522 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC254559. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2523 (VGAM2523) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85488] VGAM2523 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2523 was detected is described hereinabove with reference to Figs. 1-8.

[85489] VGAM2523 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2523 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85490] VGAM2523 gene encodes a VGAM2523 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2523 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2523 precursor RNA is desig-

nated SEQ ID:2509, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2509 is located at position 122311 relative to the genome of Mouse Cytomegalovirus 1.

[85491] VGAM2523 precursor RNA folds onto itself, forming VGAM2523 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85492] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2523 folded precursor RNA into VGAM2523 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2523 RNA is designated SEQ ID:5234, and is provided hereinbelow with reference to the sequence

listing part.

[85493] VGAM2523 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2523 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85494] VGAM2523 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2523 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2523 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85495] The complementary binding of VGAM2523 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2523 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2523 host target RNA into VGAM2523 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85496] It is appreciated that VGAM2523 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2523 host target genes. The mRNA of each one of this plurality of VGAM2523 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2523 RNA, herein designated VGAM

RNA, and which when bound by VGAM2523 RNA causes inhibition of translation of respective one or more VGAM2523 host target proteins.

[85497] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2523 gene, herein designated VGAM GENE, on one or more VGAM2523 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85498] It is yet further appreciated that a function of VGAM2523 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2523 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2523 correlate with, and may be deduced from, the identity of the host target genes which VGAM2523 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85499] Nucleotide sequences of the VGAM2523 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2523 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2523 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2523 are further described hereinbelow with reference to Table 1.

[85500] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2523 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2523 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85501] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2523 gene, herein designated VGAM is

inhibition of expression of VGAM2523 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2523 correlate with, and may be deduced from, the identity of the target genes which VGAM2523 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85502] Proteoglycan 2, Bone Marrow (natural killer cell activator, eosinophil granule major basic protein) (PRG2, Accession NM_002728) is a VGAM2523 host target gene. PRG2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRG2 BINDING SITE, designated SEQ ID:8593, to the nucleotide sequence of VGAM2523 RNA, herein designated VGAM RNA, also designated SEQ ID:5234.

[85503] A function of VGAM2523 is therefore inhibition of Proteoglycan 2, Bone Marrow (natural killer cell activator, eosinophil granule major basic protein) (PRG2, Accession NM_002728), a gene which Myelin basic protein; a constituent of myelin, plays a role in nerve function. Accordingly, utilities of VGAM2523 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with PRG2. The function of PRG2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1845.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2524 (VGAM2524) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85504] VGAM2524 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2524 was detected is described hereinabove with reference to Figs. 1-8.

[85505] VGAM2524 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2524 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85506] VGAM2524 gene encodes a VGAM2524 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2524 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2524 precursor RNA is designated SEQ ID:2510, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2510 is located at position 180093 relative to the genome of Mouse Cytomegalovirus 1.

[85507] VGAM2524 precursor RNA folds onto itself, forming VGAM2524 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85508] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2524 folded precursor RNA into VGAM2524 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2524 RNA is designated SEQ ID:5235, and is provided hereinbelow with reference to the sequence listing part.

[85509] VGAM2524 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2524 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85510] VGAM2524 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2524 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2524 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85511] The complementary binding of VGAM2524 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2524 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2524 host target RNA into VGAM2524 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85512] It is appreciated that VGAM2524 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2524 host target genes. The mRNA of each one of this plurality of VGAM2524 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2524 RNA, herein designated VGAM RNA, and which when bound by VGAM2524 RNA causes inhibition of translation of respective one or more VGAM2524 host target proteins.

[85513] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2524 gene, herein designated VGAM GENE, on one or more VGAM2524 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85514] It is yet further appreciated that a function of VGAM2524 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2524 correlate with, and may be deduced from, the identity of the host target genes which VGAM2524 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85515] Nucleotide sequences of the VGAM2524 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2524 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2524 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2524 are further described hereinbelow with reference to Table 1.

[85516] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2524 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2524 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[85517] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2524 gene, herein designated VGAM is inhibition of expression of VGAM2524 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2524 correlate with, and may be deduced from, the identity of the target genes which VGAM2524 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85518] Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858) is a VGAM2524 host target gene. COL19A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL19A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL19A1 BINDING SITE, designated SEQ ID:7597, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85519] A function of VGAM2524 is therefore inhibition of Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858), a gene which may act as a cross-bridge between fibrils

and other extracellular matrix molecules. Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL19A1. The function of COL19A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM19.Endoglin (Osler-Rendu-Weber syndrome 1) (ENG, Accession NM_000118) is another VGAM2524 host target gene. ENG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENG BINDING SITE, designated SEQ ID:5595, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85520] Another function of VGAM2524 is therefore inhibition of Endoglin (Osler-Rendu-Weber syndrome 1) (ENG, Accession NM_000118). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENG. High-mobility Group Nucleosomal Binding Domain 2 (HMGN2, Accession

NM_005517) is another VGAM2524 host target gene. HMGN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMGN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGN2 BINDING SITE, designated SEQ ID:12041, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85521] Another function of VGAM2524 is therefore inhibition of High-mobility Group Nucleosomal Binding Domain 2 (HMGN2, Accession NM_005517), a gene which binds HMG proteins and may confer specific conformations to transcriptionally active regions of chromatin. Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGN2. The function of HMGN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2461.Interleukin 1 Family, Member 5 (delta) (IL1F5, Accession NM_012275) is another VGAM2524 host target gene. IL1F5 BINDING SITE1 and

IL1F5 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by IL1F5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1F5 BINDING SITE1 and IL1F5 BINDING SITE2, designated SEQ ID:14601 and SEQ ID:14602 respectively, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85522] Another function of VGAM2524 is therefore inhibition of Interleukin 1 Family, Member 5 (delta) (IL1F5, Accession NM_012275), a gene which is a novel interleukin-1 receptor antagonist gene. Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1F5. The function of IL1F5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM263.Activator of Basal Transcription 1 (ABT1, Accession NM_013375) is another VGAM2524 host target gene. ABT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABT1, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABT1 BINDING SITE, designated SEQ ID:15030, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85523] Another function of VGAM2524 is therefore inhibition of Activator of Basal Transcription 1 (ABT1, Accession NM_013375). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABT1. DKFZP434K1421 (Accession NM_032141) is another VGAM2524 host target gene. DKFZP434K1421 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434K1421, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434K1421 BINDING SITE, designated SEQ ID:25823, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85524] Another function of VGAM2524 is therefore inhibition of DKFZP434K1421 (Accession NM_032141). Accordingly, utilities of VGAM2524 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP434K1421. DKFZP761F241 (Accession NM_031455) is another VGAM2524 host target gene. DKFZP761F241 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761F241, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761F241 BINDING SITE, designated SEQ ID:25477, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85525] Another function of VGAM2524 is therefore inhibition of DKFZP761F241 (Accession NM_031455). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761F241. FLJ12903 (Accession NM_022753) is another VGAM2524 host target gene. FLJ12903 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12903, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

FLJ12903 BINDING SITE, designated SEQ ID:22980, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85526] Another function of VGAM2524 is therefore inhibition of FLJ12903 (Accession NM_022753). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903. KIAA0430 (Accession NM_019081) is another VGAM2524 host target gene. KIAA0430 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0430, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0430 BINDING SITE, designated SEQ ID:21149, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85527] Another function of VGAM2524 is therefore inhibition of KIAA0430 (Accession NM_019081). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0430. KIAA0676 (Accession NM_015043) is another VGAM2524 host target gene. KIAA0676 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0676 BINDING SITE, designated SEQ ID:17393, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85528] Another function of VGAM2524 is therefore inhibition of KIAA0676 (Accession NM_015043). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0676. KIAA1036 (Accession NM_014909) is another VGAM2524 host target gene. KIAA1036 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1036, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1036 BINDING SITE, designated SEQ ID:17132, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85529] Another function of VGAM2524 is therefore inhibition of

KIAA1036 (Accession NM_014909). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1036. KIAA1393 (Accession XM_050793) is another VGAM2524 host target gene. KIAA1393 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:35688, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85530] Another function of VGAM2524 is therefore inhibition of KIAA1393 (Accession XM_050793). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393. Postmeiotic Segregation Increased 2-like 3 (PMS2L3, Accession XM_049100) is another VGAM2524 host target gene. PMS2L3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PMS2L3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMS2L3 BINDING SITE, designated SEQ ID:35342, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85531] Another function of VGAM2524 is therefore inhibition of Postmeiotic Segregation Increased 2-like 3 (PMS2L3, Accession XM_049100). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMS2L3. Uronyl-2-sulfotransferase (UST, Accession NM_005715) is another VGAM2524 host target gene. UST BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UST, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UST BINDING SITE, designated SEQ ID:12271, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85532] Another function of VGAM2524 is therefore inhibition of Uronyl-2-sulfotransferase (UST, Accession NM_005715). Accordingly, utilities of VGAM2524 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with UST. LOC115343 (Accession XM_050640) is another VGAM2524 host target gene. LOC115343 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC115343, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115343 BINDING SITE, designated SEQ ID:35667, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85533] Another function of VGAM2524 is therefore inhibition of LOC115343 (Accession XM_050640). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115343. LOC145268 (Accession XM_085072) is another VGAM2524 host target gene. LOC145268 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC145268 BINDING SITE, designated SEQ ID:37811, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85534] Another function of VGAM2524 is therefore inhibition of LOC145268 (Accession XM_085072). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145268. LOC152212 (Accession XM_096198) is another VGAM2524 host target gene. LOC152212 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152212, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152212 BINDING SITE, designated SEQ ID:40308, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85535] Another function of VGAM2524 is therefore inhibition of LOC152212 (Accession XM_096198). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152212. LOC152267 (Accession XM_017070) is another VGAM2524 host target gene. LOC152267 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152267 BINDING SITE, designated SEQ ID:30295, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85536] Another function of VGAM2524 is therefore inhibition of LOC152267 (Accession XM_017070). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152267. LOC158382 (Accession XM_098931) is another VGAM2524 host target gene. LOC158382 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158382, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158382 BINDING SITE, designated SEQ ID:41963, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85537] Another function of VGAM2524 is therefore inhibition of

LOC158382 (Accession XM_098931). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158382. LOC220926 (Accession XM_166128) is another VGAM2524 host target gene. LOC220926 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220926, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220926 BINDING SITE, designated SEQ ID:43917, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85538] Another function of VGAM2524 is therefore inhibition of LOC220926 (Accession XM_166128). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220926. LOC222189 (Accession XM_168447) is another VGAM2524 host target gene. LOC222189 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC222189 BINDING SITE, designated SEQ ID:45188, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85539] Another function of VGAM2524 is therefore inhibition of LOC222189 (Accession XM_168447). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222189. LOC90371 (Accession XM_031261) is another VGAM2524 host target gene. LOC90371 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90371, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90371 BINDING SITE, designated SEQ ID:31322, to the nucleotide sequence of VGAM2524 RNA, herein designated VGAM RNA, also designated SEQ ID:5235.

[85540] Another function of VGAM2524 is therefore inhibition of LOC90371 (Accession XM_031261). Accordingly, utilities of VGAM2524 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90371. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2525 (VGAM2525) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85541] VGAM2525 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2525 was detected is described hereinabove with reference to Figs. 1-8.

[85542] VGAM2525 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2525 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85543] VGAM2525 gene encodes a VGAM2525 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2525 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2525 precursor RNA is designated SEQ ID:2511, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2511 is located at position 213327 relative to the genome of Mouse Cytomegalovirus 1.

[85544] VGAM2525 precursor RNA folds onto itself, forming VGAM2525 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85545] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2525 folded precursor RNA into VGAM2525 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2525 RNA is designated SEQ ID:5236, and is provided hereinbelow with reference to the sequence listing part.

[85546] VGAM2525 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2525 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2525 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85547] VGAM2525 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2525 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2525 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2525 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2525 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85548] The complementary binding of VGAM2525 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2525 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2525 host target RNA into VGAM2525 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85549] It is appreciated that VGAM2525 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2525 host target genes. The mRNA of each one of this plurality of VGAM2525 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2525 RNA, herein designated VGAM RNA, and which when bound by VGAM2525 RNA causes inhibition of translation of respective one or more

VGAM2525 host target proteins.

[85550] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2525 gene, herein designated VGAM GENE, on one or more VGAM2525 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85551] It is yet further appreciated that a function of VGAM2525 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2525 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2525 correlate with, and may be deduced from, the identity of the host target genes which VGAM2525 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85552] Nucleotide sequences of the VGAM2525 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2525 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2525 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2525 are further described hereinbelow with reference to Table 1.

[85553] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2525 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2525 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85554] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2525 gene, herein designated VGAM is inhibition of expression of VGAM2525 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2525 correlate with, and may be deduced from, the identity of the target genes which VGAM2525 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85555] Dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1, Accession NM_004393) is a VGAM2525 host target gene. DAG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAG1 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of VGAM2525 RNA, herein designated VGAM RNA, also designated SEQ ID:5236.

[85556] A function of VGAM2525 is therefore inhibition of Dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1, Accession NM_004393), a gene which may provide linkage between the sarcolemma and extracellular matrix (ECM). Accordingly, utilities of VGAM2525 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAG1. The function of DAG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to VGAM1095.Diacylglycerol Kinase, Delta 130kDa (DGKD, Accession XM_002384) is another VGAM2525 host target gene. DGKD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGKD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKD BINDING SITE, designated SEQ ID:29876, to the nucleotide sequence of VGAM2525 RNA, herein designated VGAM RNA, also designated SEQ ID:5236.

[85557] Another function of VGAM2525 is therefore inhibition of Diacylglycerol Kinase, Delta 130kDa (DGKD, Accession XM_002384). Accordingly, utilities of VGAM2525 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKD. KIAA0746 (Accession XM_045277) is another VGAM2525 host target gene. KIAA0746 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0746, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0746 BINDING SITE, designated

SEQ ID:34413, to the nucleotide sequence of VGAM2525 RNA, herein designated VGAM RNA, also designated SEQ ID:5236.

[85558] Another function of VGAM2525 is therefore inhibition of KIAA0746 (Accession XM_045277). Accordingly, utilities of VGAM2525 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0746. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2526 (VGAM2526) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85559] VGAM2526 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2526 was detected is described hereinabove with reference to Figs. 1-8.

[85560] VGAM2526 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2526 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85561] VGAM2526 gene encodes a VGAM2526 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2526 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2526 precursor RNA is designated SEQ ID:2512, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2512 is located at position 85449 relative to the genome of Mouse Cytomegalovirus 1.

[85562] VGAM2526 precursor RNA folds onto itself, forming VGAM2526 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85563] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2526 folded precursor RNA into VGAM2526 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2526 RNA is designated SEQ ID:5237, and is provided hereinbelow with reference to the sequence listing part.

[85564] VGAM2526 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2526 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85565] VGAM2526 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2526 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2526 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85566] The complementary binding of VGAM2526 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2526 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2526 host target RNA into VGAM2526 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85567] It is appreciated that VGAM2526 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2526 host target genes. The mRNA of each one of this plurality of VGAM2526 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2526 RNA, herein designated VGAM RNA, and which when bound by VGAM2526 RNA causes inhibition of translation of respective one or more VGAM2526 host target proteins.

[85568] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2526 gene, herein designated VGAM GENE, on one or more VGAM2526 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85569] It is yet further appreciated that a function of VGAM2526 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2526 correlate with, and may be deduced from, the identity of the host target genes which VGAM2526 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85570] Nucleotide sequences of the VGAM2526 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2526 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2526 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2526 are further described hereinbelow with reference to Table 1.

[85571] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2526 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2526 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85572] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2526 gene, herein designated VGAM is inhibition of expression of VGAM2526 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2526 correlate with, and may be deduced from, the identity of the target genes which VGAM2526 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85573] Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 2 (MLLT2, Accession NM_005935) is a VGAM2526 host target gene. MLLT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MLLT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLLT2 BINDING SITE, designated SEQ ID:12566, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85574] A function of VGAM2526 is therefore inhibition of Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 2 (MLLT2, Accession NM_005935), a gene which is a Putative transcription factor. Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLLT2. The function of MLLT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM57.SH3-domain GRB2-like 1 (SH3GL1, Accession NM_003025) is another VGAM2526 host target gene. SH3GL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3GL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3GL1 BINDING SITE, designated SEQ ID:8959, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85575] Another function of VGAM2526 is therefore inhibition of SH3-domain GRB2-like 1 (SH3GL1, Accession

NM_003025). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3GL1. FLJ13576 (Accession NM_022484) is another VGAM2526 host target gene. FLJ13576 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13576 BINDING SITE, designated SEQ ID:22860, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85576] Another function of VGAM2526 is therefore inhibition of FLJ13576 (Accession NM_022484). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13576. FLJ13769 (Accession NM_025012) is another VGAM2526 host target gene. FLJ13769 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ13769 BINDING SITE, designated SEQ ID:24594, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85577] Another function of VGAM2526 is therefore inhibition of FLJ13769 (Accession NM_025012). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13769. PRO2964 (Accession NM_018547) is another VGAM2526 host target gene. PRO2964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2964 BINDING SITE, designated SEQ ID:20629, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85578] Another function of VGAM2526 is therefore inhibition of PRO2964 (Accession NM_018547). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2964. LOC145368 (Accession XM_085112) is another

VGAM2526 host target gene. LOC145368 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145368, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145368 BINDING SITE, designated SEQ ID:37825, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85579] Another function of VGAM2526 is therefore inhibition of LOC145368 (Accession XM_085112). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145368. LOC150423 (Accession XM_086912) is another VGAM2526 host target gene. LOC150423 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150423 BINDING SITE, designated SEQ ID:38966, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85580] Another function of VGAM2526 is therefore inhibition of LOC150423 (Accession XM_086912). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150423. LOC158055 (Accession XM_088453) is another VGAM2526 host target gene. LOC158055 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158055, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158055 BINDING SITE, designated SEQ ID:39701, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85581] Another function of VGAM2526 is therefore inhibition of LOC158055 (Accession XM_088453). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158055. LOC197117 (Accession XM_116989) is another VGAM2526 host target gene. LOC197117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197117, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197117 BINDING SITE, designated SEQ ID:43191, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85582] Another function of VGAM2526 is therefore inhibition of LOC197117 (Accession XM_116989). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197117. LOC220164 (Accession XM_166294) is another VGAM2526 host target gene. LOC220164 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220164, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220164 BINDING SITE, designated SEQ ID:44108, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85583] Another function of VGAM2526 is therefore inhibition of LOC220164 (Accession XM_166294). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC220164. LOC255481 (Accession XM_170489) is another VGAM2526 host target gene. LOC255481 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255481, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255481 BINDING SITE, designated SEQ ID:45331, to the nucleotide sequence of VGAM2526 RNA, herein designated VGAM RNA, also designated SEQ ID:5237.

[85584] Another function of VGAM2526 is therefore inhibition of LOC255481 (Accession XM_170489). Accordingly, utilities of VGAM2526 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255481. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2527 (VGAM2527) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85585] VGAM2527 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2527 was detected is described hereinabove with reference to Figs. 1-8.

[85586] VGAM2527 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2527 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85587] VGAM2527 gene encodes a VGAM2527 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2527 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2527 precursor RNA is designated SEQ ID:2513, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2513 is located at position 157147 relative to the genome of Mouse Cytomegalovirus 1.

[85588] VGAM2527 precursor RNA folds onto itself, forming VGAM2527 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85589] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2527 folded precursor RNA into VGAM2527 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2527 RNA is designated SEQ ID:5238, and is provided hereinbelow with reference to the sequence listing part.

[85590] VGAM2527 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2527 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85591] VGAM2527 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2527 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2527 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85592] The complementary binding of VGAM2527 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2527 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2527 host target RNA into VGAM2527 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85593] It is appreciated that VGAM2527 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2527 host target genes. The mRNA of each one of this plurality of VGAM2527 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2527 RNA, herein designated VGAM RNA, and which when bound by VGAM2527 RNA causes inhibition of translation of respective one or more VGAM2527 host target proteins.

[85594] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2527 gene, herein designated VGAM GENE, on one or more VGAM2527 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85595] It is yet further appreciated that a function of VGAM2527 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2527 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2527 correlate with, and may be deduced from, the identity of the host target genes which VGAM2527 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85596] Nucleotide sequences of the VGAM2527 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2527 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2527 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2527 are further described hereinbelow with reference to Table 1.

[85597] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2527 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2527 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85598] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2527 gene, herein designated VGAM is inhibition of expression of VGAM2527 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2527 correlate with, and may be deduced from, the identity of the target genes which VGAM2527 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85599] Leucine-zipper-like Transcriptional Regulator, 1 (LZTR1, Accession NM_006767) is a VGAM2527 host target gene. LZTR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LZTR1,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LZTR1 BINDING SITE, designated SEQ ID:13638, to the nucleotide sequence of VGAM2527 RNA, herein designated VGAM RNA, also designated SEQ ID:5238.

[85600] A function of VGAM2527 is therefore inhibition of Leucine-zipper-like Transcriptional Regulator, 1 (LZTR1, Accession NM_006767). Accordingly, utilities of VGAM2527 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTR1. KIAA1643 (Accession XM_035371) is another VGAM2527 host target gene. KIAA1643 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1643, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1643 BINDING SITE, designated SEQ ID:32241, to the nucleotide sequence of VGAM2527 RNA, herein designated VGAM RNA, also designated SEQ ID:5238.

[85601] Another function of VGAM2527 is therefore inhibition of

KIAA1643 (Accession XM_035371). Accordingly, utilities of VGAM2527 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1643. LOC164395 (Accession XM_092778) is another VGAM2527 host target gene. LOC164395 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC164395, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164395 BINDING SITE, designated SEQ ID:40144, to the nucleotide sequence of VGAM2527 RNA, herein designated VGAM RNA, also designated SEQ ID:5238.

[85602] Another function of VGAM2527 is therefore inhibition of LOC164395 (Accession XM_092778). Accordingly, utilities of VGAM2527 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164395. LOC255177 (Accession XM_172941) is another VGAM2527 host target gene. LOC255177 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255177, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC255177 BINDING SITE, designated SEQ ID:46200, to the nucleotide sequence of VGAM2527 RNA, herein designated VGAM RNA, also designated SEQ ID:5238.

[85603] Another function of VGAM2527 is therefore inhibition of LOC255177 (Accession XM_172941). Accordingly, utilities of VGAM2527 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255177. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2528 (VGAM2528) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85604] VGAM2528 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2528 was detected is described hereinabove with reference to Figs. 1-8.

[85605] VGAM2528 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2528 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[85606] VGAM2528 gene encodes a VGAM2528 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2528 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2528 precursor RNA is designated SEQ ID:2514, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2514 is located at position 17101 relative to the genome of Cowpox Virus.

[85607] VGAM2528 precursor RNA folds onto itself, forming VGAM2528 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85608] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2528 folded precursor RNA into VGAM2528 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2528 RNA is designated SEQ ID:5239, and is provided hereinbelow with reference to the sequence listing part.

[85609] VGAM2528 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2528 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85610] VGAM2528 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2528 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2528 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85611] The complementary binding of VGAM2528 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2528 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2528 host target RNA into VGAM2528 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85612] It is appreciated that VGAM2528 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2528 host target genes. The mRNA of each one of this plurality of VGAM2528 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2528 RNA, herein designated VGAM RNA, and which when bound by VGAM2528 RNA causes inhibition of translation of respective one or more VGAM2528 host target proteins.

[85613] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2528 gene, herein designated VGAM GENE, on one or more VGAM2528 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85614] It is yet further appreciated that a function of VGAM2528 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2528 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2528 correlate with, and may be deduced from, the identity of the host target genes which VGAM2528 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85615] Nucleotide sequences of the VGAM2528 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2528 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2528 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2528 are further described hereinbelow with reference to Table 1.

[85616] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2528 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2528 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85617] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2528 gene, herein designated VGAM is inhibition of expression of VGAM2528 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2528 correlate with, and may be deduced from, the identity of the target genes which VGAM2528 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85618] Chloride Channel 6 (CLCN6, Accession NM_001286) is a VGAM2528 host target gene. CLCN6 BINDING SITE1 through CLCN6 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CLCN6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE1 through CLCN6 BINDING SITE3, designated SEQ ID:6960, SEQ ID:22342 and SEQ ID:22337 respectively, to the nucleotide sequence of

VGAM2528 RNA, herein designated VGAM RNA, also designated SEQ ID:5239.

[85619] A function of VGAM2528 is therefore inhibition of Chloride Channel 6 (CLCN6, Accession NM_001286), a gene which is a voltage-gated chloride channel. Accordingly, utilities of VGAM2528 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN6. The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM599.KIAA0319 (Accession NM_014809) is another VGAM2528 host target gene. KIAA0319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0319 BINDING SITE, designated SEQ ID:16761, to the nucleotide sequence of VGAM2528 RNA, herein designated VGAM RNA, also designated SEQ ID:5239.

[85620] Another function of VGAM2528 is therefore inhibition of KIAA0319 (Accession NM_014809). Accordingly, utilities

of VGAM2528 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0319. RAB40A, Member RAS Oncogene Family (RAB40A, Accession XM_088733) is another VGAM2528 host target gene. RAB40A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAB40A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB40A BINDING SITE, designated SEQ ID:39930, to the nucleotide sequence of VGAM2528 RNA, herein designated VGAM RNA, also designated SEQ ID:5239.

[85621] Another function of VGAM2528 is therefore inhibition of RAB40A, Member RAS Oncogene Family (RAB40A, Accession XM_088733). Accordingly, utilities of VGAM2528 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB40A. LOC123264 (Accession XM_058693) is another VGAM2528 host target gene. LOC123264 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC123264, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC123264 BINDING SITE, designated SEQ ID:36723, to the nucleotide sequence of VGAM2528 RNA, herein designated VGAM RNA, also designated SEQ ID:5239.

[85622] Another function of VGAM2528 is therefore inhibition of LOC123264 (Accession XM_058693). Accordingly, utilities of VGAM2528 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC123264. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2529 (VGAM2529) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85623] VGAM2529 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2529 was detected is described hereinabove with reference to Figs. 1-8.

[85624] VGAM2529 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pepper Ringspot Virus. VGAM2529 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[85625] VGAM2529 gene encodes a VGAM2529 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2529 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2529 precursor RNA is designated SEQ ID:2515, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2515 is located at position 4230 relative to the genome of Pepper Ringspot Virus.

[85626] VGAM2529 precursor RNA folds onto itself, forming VGAM2529 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85627] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2529 folded precursor RNA into VGAM2529

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2529 RNA is designated SEQ ID:5240, and is provided hereinbelow with reference to the sequence listing part.

[85628] VGAM2529 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2529 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85629] VGAM2529 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2529 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2529 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85630] The complementary binding of VGAM2529 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2529 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2529 host target RNA into VGAM2529 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[85631] It is appreciated that VGAM2529 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2529 host target genes. The mRNA of each one of this plurality of VGAM2529 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2529 RNA, herein designated VGAM RNA, and which when bound by VGAM2529 RNA causes inhibition of translation of respective one or more VGAM2529 host target proteins.

[85632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2529 gene, herein designated VGAM GENE, on one or more VGAM2529 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85633] It is yet further appreciated that a function of VGAM2529 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2529 include diagnosis, prevention and treatment of viral infection by Pepper Ringspot Virus. Specific functions, and accordingly utilities, of VGAM2529 correlate with, and may be deduced from, the identity of the host target genes which VGAM2529 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85634] Nucleotide sequences of the VGAM2529 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2529 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2529 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2529 are further described hereinbelow with reference to Table 1.

[85635] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2529 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2529 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85636] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2529 gene, herein designated VGAM is inhibition of expression of VGAM2529 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2529 correlate with, and may be deduced from, the identity of the target genes which VGAM2529 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85637] SH2 Domain Containing Phosphatase Anchor Protein 1 (SPAP1, Accession NM_030764) is a VGAM2529 host target gene. SPAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPAP1 BINDING SITE, designated SEQ ID:25048, to the nucleotide sequence of VGAM2529 RNA,

herein designated VGAM RNA, also designated SEQ ID:5240.

[85638] A function of VGAM2529 is therefore inhibition of SH2 Domain Containing Phosphatase Anchor Protein 1 (SPAP1, Accession NM_030764), a gene which regulation of immunologic function. Accordingly, utilities of VGAM2529 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPAP1. The function of SPAP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM672.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2530 (VGAM2530) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85639] VGAM2530 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2530 was detected is described hereinabove with reference to Figs. 1-8.

[85640] VGAM2530 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Pepper Ringspot Virus. VGAM2530 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85641] VGAM2530 gene encodes a VGAM2530 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2530 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2530 precursor RNA is designated SEQ ID:2516, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2516 is located at position 1886 relative to the genome of Pepper Ringspot Virus.

[85642] VGAM2530 precursor RNA folds onto itself, forming VGAM2530 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85643] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2530 folded precursor RNA into VGAM2530 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2530 RNA is designated SEQ ID:5241, and is provided hereinbelow with reference to the sequence listing part.

[85644] VGAM2530 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2530 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85645] VGAM2530 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2530 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2530 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85646] The complementary binding of VGAM2530 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2530 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2530

host target RNA into VGAM2530 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85647] It is appreciated that VGAM2530 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2530 host target genes. The mRNA of each one of this plurality of VGAM2530 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2530 RNA, herein designated VGAM RNA, and which when bound by VGAM2530 RNA causes inhibition of translation of respective one or more VGAM2530 host target proteins.

[85648] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2530 gene, herein designated VGAM GENE, on one or more VGAM2530 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85649] It is yet further appreciated that a function of VGAM2530 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of viral infection by Pepper Ringspot Virus. Specific functions, and accordingly utilities, of VGAM2530 correlate with, and may be deduced from, the identity of the host target genes which VGAM2530 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85650] Nucleotide sequences of the VGAM2530 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2530 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2530 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2530 are further

described hereinbelow with reference to Table 1.

[85651] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2530 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2530 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85652] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2530 gene, herein designated VGAM is inhibition of expression of VGAM2530 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2530 correlate with, and may be deduced from, the identity of the target genes which VGAM2530 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85653] B-cell CLL/lymphoma 9 (BCL9, Accession NM_004326) is a VGAM2530 host target gene. BCL9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL9 BINDING SITE,

designated SEQ ID:10525, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85654] A function of VGAM2530 is therefore inhibition of B-cell CLL/lymphoma 9 (BCL9, Accession NM_004326), a gene which recruits of PYGO to the nuclear beta-catenin-TCF complex in Wnt/Wingless signaling. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL9. The function of BCL9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Calpain 10 (CAPN10, Accession NM_023089) is another VGAM2530 host target gene. CAPN10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAPN10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPN10 BINDING SITE, designated SEQ ID:23359, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85655] Another function of VGAM2530 is therefore inhibition of Calpain 10 (CAPN10, Accession NM_023089), a gene which catalyzes limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPN10. The function of CAPN10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.Coproporphyrinogen Oxidase (coproporphyria, harderoporphyria) (CPO, Accession NM_000097) is another VGAM2530 host target gene. CPO BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPO BINDING SITE, designated SEQ ID:5557, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85656] Another function of VGAM2530 is therefore inhibition of Coproporphyrinogen Oxidase (coproporphyria, hardero-

porphyria) (CPO, Accession NM_000097), a gene which Coproporphyrinogen; catalyzes oxidative decarboxylation in sixth step of heme biosynthesis. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPO. The function of CPO has been established by previous studies. Brewer et al. (1999) presented clinical, cytogenetic, molecular, and statistical evidence for the existence of a novel locus for isolated CP at 2q32. They studied 2 unrelated children with strikingly similar clinical features, in whom there were apparently balanced, de novo cytogenetic rearrangements involving the same region of 2q. Both children had cleft palate, facial dysmorphism, and mild learning disability. Molecular cytogenetic analyses localized both translocation breakpoints between markers D2S311 and D2S116 on chromosome 2. This suggested that the true location of these breakpoints was 2q32 rather than 2q33, as had been suggested on cytogenetic grounds alone. To obtain independent support for the existence of a CP locus at 2q32, the authors performed a detailed statistical analysis for all cases in the human cytogenetics database of nonmosaic, single, contiguous autosomal deletions associated with orofacial clefting; see

Brewer et al. (1998). This analysis showed 2q32 to be 1 of only 3 chromosomal regions in which haploinsufficiency is significantly associated with isolated CP. Thus, the data provided strong evidence for the existence at 2q32 of a gene that is critical for the development of the secondary palate. The close proximity of the 2 translocation breakpoints should allow rapid progress toward positional cloning of this CP gene Van den Boogaard et al. (2000) identified a stop codon in the MSX1 gene (142983.0002) in a 3-generation Dutch family with tooth agenesis and combinations of cleft palate only and cleft lip and cleft palate, providing further evidence for this gene in orofacial clefting.

[85657] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[85658] Brewer, C. M.; Leek, J. P.; Green, A. J.; Holloway, S.; Bonthron, D. T.; Markham, A. F.; FitzPatrick, D. R. : A locus for isolated cleft palate, located on human chromosome 2q32. Am. J. Hum. Genet. 65: 387-396, 1999. ; and

[85659] van den Boogaard, M.-J. H.; Dorland, M.; Beemer, F. A.; Ploos van Amstel, H. K. : MSX1 mutation is associated with orofacial clefting and tooth agenesis in humans. (Letter)

Nature Gene.

[85660] Further studies establishing the function and utilities of CPO are found in John Hopkins OMIM database record ID 119540, and in sited publications numbered 3721-3725, 3584, 3728, 3778-3779, 372 and 11320 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Cardiotrophin 1 (CTF1, Accession NM_001330) is another VGAM2530 host target gene. CTF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTF1 BINDING SITE, designated SEQ ID:7013, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85661] Another function of VGAM2530 is therefore inhibition of Cardiotrophin 1 (CTF1, Accession NM_001330), a gene which may play a role in cardiac hypertrophy. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTF1. The function of CTF1 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM71.Cystathionase (cystathionine gamma-lyase) (CTH, Accession NM_001902) is another VGAM2530 host target gene. CTH BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CTH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTH BINDING SITE, designated SEQ ID:7626, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85662] Another function of VGAM2530 is therefore inhibition of Cystathionase (cystathionine gamma-lyase) (CTH, Accession NM_001902), a gene which catalyzes removal of ammonia, cleaves cystathionine to yield free cys. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTH. The function of CTH has been established by previous studies. The rate of glutathione synthesis in the liver is limited by the availability of cysteine which is provided either in the diet or by the trans-sulfuration pathway in which cystathionine derived from methionine

is transformed into cysteine by cystathionase (cystathionine gamma-lyase; EC 4.4.1.1). Lu et al. (1992) found and sequenced a 1,083-bp cDNA encoding the human liver cystathionine gamma-lyase. The human sequence presented a deletion of 132 bases (44 amino acids) compared to the cystathionase sequence reported for the rat, and a deletion of 135 bases (45 amino acids) compared to the sequence reported for yeast. After realignment for the missing nucleotides, the human cDNA sequence showed significant amino acid homology to the rat (85%) and yeast (50%) enzymes. Using the polymerase chain reaction, Lu et al. (1992) isolated a second clone which contained the missing 132 bases. Flanking nucleotides in the latter clone were identical to those in the cDNA clone containing the deletion. Alternative splicing as the basis of the 2 forms of cystathionase is plausible During a survey by paper chromatography of amino acids in the urine of patients in an institution for mental defectives, Harris et al. (1959) discovered a case with abnormal excretion of cystathionine. An inborn error involving the cleavage of cystathionine to give cysteine and homoserine was suggested. The subject was a severely retarded female, aged 64 years at the time of study. Another case

was studied at The New York Hospital. Other clinical manifestations have been clubfoot, developmental defects about the ears, convulsions, and thrombocytopenia. Urinary lithiasis also occurs. Frimpter (1965) has shown that the defect involves cystathionase that does not properly bind its coenzyme, pyridoxal phosphate. In vitro studies suggested that high pyridoxine would be therapeutically beneficial. Mongeau et al. (1967) described the case of a 2-year-old boy with normal mentality, thrombocytopenia, and urinary calculi. The relation of the latter two features to the metabolic defect was problematical. Both parents (who were apparently unrelated) showed cystathioninuria after methionine loading test. With administration of pyridoxine, cystathioninuria was diminished in the proband. Schneiderman (1967) studied 2 mentally retarded brothers who excreted large amounts of cystathionine after methionine ingestion. The mother and another brother excreted lesser but abnormal amounts after methionine loading. The father was not tested. Perry et al. (1968) discovered cystathioninuria in a brother and sister when the brother's urine was by chance subjected to 2-dimensional paper chromatography for amino acids. Both children were normal. The parents excreted cystathionine only af-

ter methionine loading. The authors suggested that mental defect and other disorders reported in association with cystathioninuria may have been coincidental. Whelan and Scriver (1968) also found cystathioninuria as an apparently benign inborn error. The case of Tada et al. (1968) did not respond to vitamin

[85663] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[85664] Lu, Y.; O'Dowd, B. F.; Orrego, H.; Israel, Y. : Cloning and nucleotide sequence of human liver cDNA encoding for cystathionine gamma-lyase. Biochem. Biophys. Res. Commun. 189: 749-758, 1992. ; and

[85665] Whelan, D. T.; Scriver, C. R. : Cystathioninuria and renal iminoglycinuria in a pedigree: a perspective on counseling. New Eng. J. Med. 278: 924-927, 1968.

[85666] Further studies establishing the function and utilities of CTH are found in John Hopkins OMIM database record ID 219500, and in sited publications numbered 9352-9366 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Diaphanous Homolog 2 (Drosophila) (DIAPH2, Accession NM_006729) is another VGAM2530 host target gene. DIAPH2 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DIAPH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIAPH2 BINDING SITE, designated SEQ ID:13562, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85667] Another function of VGAM2530 is therefore inhibition of Diaphanous Homolog 2 (Drosophila) (DIAPH2, Accession NM_006729), a gene which may affect in oogenesis. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIAPH2. The function of DIAPH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM129.Deoxyribonuclease I (DNASE1, Accession NM_005223) is another VGAM2530 host target gene. DNASE1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DNASE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of DNASE1 BINDING SITE, designated SEQ ID:11713, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85668] Another function of VGAM2530 is therefore inhibition of Deoxyribonuclease I (DNASE1, Accession NM_005223), a gene which seems to be involved in cell death. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNASE1. The function of DNASE1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM492.Fatty-acid-Coenzyme A Ligase, Long-chain 5 (FACL5, Accession XM_034424) is another VGAM2530 host target gene. FACL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FACL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FACL5 BINDING SITE, designated SEQ ID:32107, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA,

also designated SEQ ID:5241.

[85669] Another function of VGAM2530 is therefore inhibition of Fatty-acid-Coenzyme A Ligase, Long-chain 5 (FACL5, Accession XM_034424), a gene which may be involved in fatty acid metabolism; contains an AMP-binding domain. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FACL5. The function of FACL5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM357.Flap Structure-specific Endonuclease 1 (FEN1, Accession NM_004111) is another VGAM2530 host target gene. FEN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FEN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FEN1 BINDING SITE, designated SEQ ID:10321, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85670] Another function of VGAM2530 is therefore inhibition of Flap Structure-specific Endonuclease 1 (FEN1, Accession

NM_004111), a gene which Flap endonuclease; double-stranded DNA 5'-3' exonuclease. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEN1. The function of FEN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1217.Farnesyltransferase, CAAX Box, Beta (FNTB, Accession NM_002028) is another VGAM2530 host target gene. FNTB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FNTB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FNTB BINDING SITE, designated SEQ ID:7784, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85671] Another function of VGAM2530 is therefore inhibition of Farnesyltransferase, CAAX Box, Beta (FNTB, Accession NM_002028), a gene which transfers farnesyl groups to proteins. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FNTB. The function of FNTB

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM615.Glycine Receptor, Alpha 3 (GLRA3, Accession XM_011092) is another VGAM2530 host target gene. GLRA3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GLRA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GLRA3 BINDING SITE, designated SEQ ID:30169, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85672] Another function of VGAM2530 is therefore inhibition of Glycine Receptor, Alpha 3 (GLRA3, Accession XM_011092), a gene which increases the chloride conductance and thus produces hyperpolarization (inhibition of neuronal firing). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLRA3. The function of GLRA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM602.GSBS

(Accession XM_165869) is another VGAM2530 host target gene. GSBS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GSBS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GSBS BINDING SITE, designated SEQ ID:43787, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85673] Another function of VGAM2530 is therefore inhibition of GSBS (Accession XM_165869). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSBS. Huntingtin-associated Protein 1 (neuroan 1) (HAP1, Accession NM_003949) is another VGAM2530 host target gene. HAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HAP1 BINDING SITE, designated SEQ ID:10077, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85674] Another function of VGAM2530 is therefore inhibition of Huntingtin-associated Protein 1 (neuroan 1) (HAP1, Accession NM_003949), a gene which functions as an adaptor protein using coiled coils to mediate interactions among cytoskeletal, vascular, and motor proteins. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAP1. The function of HAP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM126.Heterogeneous Nuclear Ribonucleoprotein D-like (HNRPDL, Accession NM_005463) is another VGAM2530 host target gene. HNRPDL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HNRPDL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPDL BINDING SITE, designated SEQ ID:11953, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85675] Another function of VGAM2530 is therefore inhibition of

Heterogeneous Nuclear Ribonucleoprotein D-like (HNRPDL, Accession NM_005463), a gene which binds to rna molecules that contain au-rich elements. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPDL. The function of HNRPDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM144.NGFI-A Binding Protein 1 (EGR1 binding protein 1) (NAB1, Accession NM_005966) is another VGAM2530 host target gene. NAB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAB1 BINDING SITE, designated SEQ ID:12588, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85676] Another function of VGAM2530 is therefore inhibition of NGFI-A Binding Protein 1 (EGR1 binding protein 1) (NAB1, Accession NM_005966), a gene which acts as a transcriptional repressor for zinc finger transcription factors egr1

and egr2 (by similarity). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAB1. The function of NAB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1074.Orthopedia Homolog (Drosophila) (OTP, Accession NM_032109) is another VGAM2530 host target gene. OTP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OTP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OTP BINDING SITE, designated SEQ ID:25802, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85677] Another function of VGAM2530 is therefore inhibition of Orthopedia Homolog (Drosophila) (OTP, Accession NM_032109), a gene which involves in the development of the forebrain and spinal cord. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTP. The function of OTP and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM183.P53AIP1 (Accession NM_022112) is another VGAM2530 host target gene. P53AIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P53AIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P53AIP1 BINDING SITE, designated SEQ ID:22660, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85678] Another function of VGAM2530 is therefore inhibition of P53AIP1 (Accession NM_022112). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P53AIP1. Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 2 (p85 beta) (PIK3R2, Accession NM_005027) is another VGAM2530 host target gene. PIK3R2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIK3R2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of PIK3R2 BINDING SITE, designated SEQ ID:11467, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85679] Another function of VGAM2530 is therefore inhibition of Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 2 (p85 beta) (PIK3R2, Accession NM_005027), a gene which acts as an adapter and is regulatory subunit (p85 beta) of phosphatidylinositol 3-kinase. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3R2. The function of PIK3R2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM647.Protein Phosphatase 1, Regulatory (inhibitor) Subunit 12B (PPP1R12B, Accession NM_032104) is another VGAM2530 host target gene. PPP1R12B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R12B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE, designated SEQ

ID:25798, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85680] Another function of VGAM2530 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 12B (PPP1R12B, Accession NM_032104). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B. RIG (Accession NM_006394) is another VGAM2530 host target gene. RIG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RIG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RIG BINDING SITE, designated SEQ ID:13109, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85681] Another function of VGAM2530 is therefore inhibition of RIG (Accession NM_006394), a gene which is ribosomal protein S15. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIG. The function of RIG

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Sine Oculis Homeobox Homolog 2 (Drosophila) (SIX2, Accession NM_016932) is another VGAM2530 host target gene. SIX2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIX2 BINDING SITE, designated SEQ ID:18851, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85682] Another function of VGAM2530 is therefore inhibition of Sine Oculis Homeobox Homolog 2 (Drosophila) (SIX2, Accession NM_016932), a gene which may be involved in limb tendon and ligament development (by similarity). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIX2. The function of SIX2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.SRY (sex determin-

ing region Y)-box 13 (SOX13, Accession NM_005686) is another VGAM2530 host target gene. SOX13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX13 BINDING SITE, designated SEQ ID:12246, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85683] Another function of VGAM2530 is therefore inhibition of SRY (sex determining region Y)-box 13 (SOX13, Accession NM_005686). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX13. Transgelin 2 (TAGLN2, Accession NM_003564) is another VGAM2530 host target gene. TAGLN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAGLN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAGLN2 BINDING SITE, designated SEQ ID:9621, to the nucleotide sequence of

VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85684] Another function of VGAM2530 is therefore inhibition of Transgelin 2 (TAGLN2, Accession NM_003564), a gene which is similar to transgelins and may be an actin-binding proteins. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAGLN2. The function of TAGLN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM144.Transporter 2, ATP-binding Cassette, Sub-family B (MDR/TAP) (TAP2, Accession NM_000544) is another VGAM2530 host target gene. TAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAP2 BINDING SITE, designated SEQ ID:6144, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85685] Another function of VGAM2530 is therefore inhibition of

Transporter 2, ATP-binding Cassette, Sub-family B (MDR/TAP) (TAP2, Accession NM_000544), a gene which is involved in the transport of antigens from the cytoplasm to a membrane-bound compartment for association with mhc class i molecules. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAP2. The function of TAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Transforming Growth Factor, Beta Receptor III (betaglycan, 300kDa) (TGFBR3, Accession NM_003243) is another VGAM2530 host target gene. TGFBR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TGFBR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGFBR3 BINDING SITE, designated SEQ ID:9250, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85686] Another function of VGAM2530 is therefore inhibition of Transforming Growth Factor, Beta Receptor III (betaglycan,

300kDa) (TGFBR3, Accession NM_003243), a gene which involves in capturing and retaining TGF-beta for presentation to the signaling receptors. Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFBR3. The function of TGFBR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM139.Wingless-type MMTV Integration Site Family, Member 1 (WNT1, Accession NM_005430) is another VGAM2530 host target gene. WNT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WNT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT1 BINDING SITE, designated SEQ ID:11898, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85687] Another function of VGAM2530 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 1 (WNT1, Accession NM_005430), a gene which may have a role in development of the central nervous system. Ac-

cordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT1. The function of WNT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Zinc Finger Protein 137 (clone pHZ-30) (ZNF137, Accession NM_003438) is another VGAM2530 host target gene. ZNF137 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF137, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF137 BINDING SITE, designated SEQ ID:9494, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85688] Another function of VGAM2530 is therefore inhibition of Zinc Finger Protein 137 (clone pHZ-30) (ZNF137, Accession NM_003438). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF137. Arachidonate Lipoxygenase 3 (ALOXE3, Accession NM_021628) is another VGAM2530 host target gene. ALOXE3 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALOXE3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALOXE3 BINDING SITE, designated SEQ ID:22266, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85689] Another function of VGAM2530 is therefore inhibition of Arachidonate Lipoxygenase 3 (ALOXE3, Accession NM_021628). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOXE3. Chromosome 11 Open Reading Frame 25 (C11orf25, Accession NM_031418) is another VGAM2530 host target gene. C11orf25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf25 BINDING SITE, designated SEQ ID:25402, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ

ID:5241.

[85690] Another function of VGAM2530 is therefore inhibition of Chromosome 11 Open Reading Frame 25 (C11orf25, Accession NM_031418). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf25. DKFZp434K2435 (Accession NM_032256) is another VGAM2530 host target gene. DKFZp434K2435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434K2435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434K2435 BINDING SITE, designated SEQ ID:25999, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85691] Another function of VGAM2530 is therefore inhibition of DKFZp434K2435 (Accession NM_032256). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434K2435. DKFZp761D0614 (Accession XM_113634) is another VGAM2530 host target gene. DK-

FZp761D0614 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761D0614, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761D0614 BINDING SITE, designated SEQ ID:42312, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85692] Another function of VGAM2530 is therefore inhibition of DKFZp761D0614 (Accession XM_113634). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761D0614. Dynamin 1-like (DNM1L, Accession NM_012062) is another VGAM2530 host target gene. DNM1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNM1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNM1L BINDING SITE, designated SEQ ID:14318, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ

ID:5241.

[85693] Another function of VGAM2530 is therefore inhibition of Dynamin 1-like (DNM1L, Accession NM_012062). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNM1L. FLJ10482 (Accession NM_018107) is another VGAM2530 host target gene. FLJ10482 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10482, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10482 BINDING SITE, designated SEQ ID:19877, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85694] Another function of VGAM2530 is therefore inhibition of FLJ10482 (Accession NM_018107). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10482. FLJ11142 (Accession NM_018338) is another VGAM2530 host target gene. FLJ11142 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11142, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11142 BINDING SITE, designated SEQ ID:20345, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85695] Another function of VGAM2530 is therefore inhibition of FLJ11142 (Accession NM_018338). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11142. FLJ11722 (Accession NM_024970) is another VGAM2530 host target gene. FLJ11722 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11722, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11722 BINDING SITE, designated SEQ ID:24520, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85696] Another function of VGAM2530 is therefore inhibition of FLJ11722 (Accession NM_024970). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ11722. FLJ23322 (Accession XM_114207) is another VGAM2530 host target gene. FLJ23322 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23322, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23322 BINDING SITE, designated SEQ ID:42800, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85697] Another function of VGAM2530 is therefore inhibition of FLJ23322 (Accession XM_114207). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23322. FLJ32356 (Accession NM_144671) is another VGAM2530 host target gene. FLJ32356 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32356, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32356 BINDING SITE, designated SEQ ID:29494, to the nucleotide

sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85698] Another function of VGAM2530 is therefore inhibition of FLJ32356 (Accession NM_144671). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32356. Forkhead Box O3A (FOXO3A, Accession NM_001455) is another VGAM2530 host target gene. FOXO3A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FOXO3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXO3A BINDING SITE, designated SEQ ID:7191, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85699] Another function of VGAM2530 is therefore inhibition of Forkhead Box O3A (FOXO3A, Accession NM_001455). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXO3A. GREB1 (Accession XM_051545) is another VGAM2530 host target gene. GREB1 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GREB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE, designated SEQ ID:35854, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85700] Another function of VGAM2530 is therefore inhibition of GREB1 (Accession XM_051545). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GREB1. H11 (Accession NM_014365) is another VGAM2530 host target gene. H11 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by H11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H11 BINDING SITE, designated SEQ ID:15694, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85701] Another function of VGAM2530 is therefore inhibition of

H11 (Accession NM_014365). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H11. HERV-H LTR-associating 2 (HHLA2, Accession NM_007072) is another VGAM2530 host target gene. HHLA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HHLA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HHLA2 BINDING SITE, designated SEQ ID:13940, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85702] Another function of VGAM2530 is therefore inhibition of HERV-H LTR-associating 2 (HHLA2, Accession NM_007072). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HHLA2. HSGP25L2G (Accession XM_030771) is another VGAM2530 host target gene. HSGP25L2G BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSGP25L2G, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSGP25L2G BINDING SITE, designated SEQ ID:31136, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85703] Another function of VGAM2530 is therefore inhibition of HSGP25L2G (Accession XM_030771). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSGP25L2G. Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 1 (KCNS1, Accession NM_002251) is another VGAM2530 host target gene. KCNS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNS1 BINDING SITE, designated SEQ ID:8046, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85704] Another function of VGAM2530 is therefore inhibition of

Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 1 (KCNS1, Accession NM_002251). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNS1. KIAA0747 (Accession NM_015292) is another VGAM2530 host target gene. KIAA0747 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0747, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0747 BINDING SITE, designated SEQ ID:17613, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85705] Another function of VGAM2530 is therefore inhibition of KIAA0747 (Accession NM_015292). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0747. KIAA1190 (Accession XM_048695) is another VGAM2530 host target gene. KIAA1190 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1190, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1190 BINDING SITE, designated SEQ ID:35225, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85706] Another function of VGAM2530 is therefore inhibition of KIAA1190 (Accession XM_048695). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1190. KIAA1456 (Accession XM_040100) is another VGAM2530 host target gene. KIAA1456 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1456, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1456 BINDING SITE, designated SEQ ID:33265, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85707] Another function of VGAM2530 is therefore inhibition of KIAA1456 (Accession XM_040100). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1456. KIAA1813 (Accession XM_046743) is another VGAM2530 host target gene. KIAA1813 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1813 BINDING SITE, designated SEQ ID:34812, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85708] Another function of VGAM2530 is therefore inhibition of KIAA1813 (Accession XM_046743). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1813. MGC20255 (Accession NM_052848) is another VGAM2530 host target gene. MGC20255 BINDING SITE1 and MGC20255 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MGC20255, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC20255 BINDING SITE1 and MGC20255 BINDING SITE2, designated SEQ ID:27431 and SEQ

ID:27430 respectively, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85709] Another function of VGAM2530 is therefore inhibition of MGC20255 (Accession NM_052848). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20255. MGC5590 (Accession NM_024058) is another VGAM2530 host target gene. MGC5590 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC5590, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5590 BINDING SITE, designated SEQ ID:23496, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85710] Another function of VGAM2530 is therefore inhibition of MGC5590 (Accession NM_024058). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5590. NK4 (Accession NM_004221) is another VGAM2530 host target gene. NK4 BINDING SITE is HOST

TARGET binding site found in the 5` untranslated region of mRNA encoded by NK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NK4 BINDING SITE, designated SEQ ID:10418, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85711] Another function of VGAM2530 is therefore inhibition of NK4 (Accession NM_004221). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NK4. PB1 (Accession NM_018165) is another VGAM2530 host target gene. PB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PB1 BINDING SITE, designated SEQ ID:19979, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85712] Another function of VGAM2530 is therefore inhibition of PB1 (Accession NM_018165). Accordingly, utilities of

VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PB1. PP3501 (Accession NM_021731) is another VGAM2530 host target gene. PP3501 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PP3501, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP3501 BINDING SITE, designated SEQ ID:22334, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85713] Another function of VGAM2530 is therefore inhibition of PP3501 (Accession NM_021731). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP3501. PRO0659 (Accession NM_014138) is another VGAM2530 host target gene. PRO0659 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO0659, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0659

BINDING SITE, designated SEQ ID:15406, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85714] Another function of VGAM2530 is therefore inhibition of PRO0659 (Accession NM_014138). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0659. R3H Domain (binds single-stranded nucleic acids) Containing (R3HDM, Accession NM_015361) is another VGAM2530 host target gene. R3HDM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by R3HDM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of R3HDM BINDING SITE, designated SEQ ID:17661, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85715] Another function of VGAM2530 is therefore inhibition of R3H Domain (binds single-stranded nucleic acids) Containing (R3HDM, Accession NM_015361). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with R3HDM. RBT1 (Accession NM_013368) is another VGAM2530 host target gene. RBT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBT1 BINDING SITE, designated SEQ ID:15013, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85716] Another function of VGAM2530 is therefore inhibition of RBT1 (Accession NM_013368). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBT1. RoXaN (Accession NM_025013) is another VGAM2530 host target gene. RoXaN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RoXaN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RoXaN BINDING SITE, designated SEQ ID:24604, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ

ID:5241.

[85717] Another function of VGAM2530 is therefore inhibition of RoXaN (Accession NM_025013). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RoXaN. U5-100K (Accession XM_006784) is another VGAM2530 host target gene. U5-100K BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by U5-100K, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of U5-100K BINDING SITE, designated SEQ ID:30012, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85718] Another function of VGAM2530 is therefore inhibition of U5-100K (Accession XM_006784). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U5-100K. ZAK (Accession NM_133646) is another VGAM2530 host target gene. ZAK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZAK, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZAK BINDING SITE, designated SEQ ID:28607, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85719] Another function of VGAM2530 is therefore inhibition of ZAK (Accession NM_133646). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAK. ZER6 (Accession XM_032742) is another VGAM2530 host target gene. ZER6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZER6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZER6 BINDING SITE, designated SEQ ID:31745, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85720] Another function of VGAM2530 is therefore inhibition of ZER6 (Accession XM_032742). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ZER6. LOC138389 (Accession XM_072534) is another VGAM2530 host target gene. LOC138389 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC138389, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138389 BINDING SITE, designated SEQ ID:37508, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85721] Another function of VGAM2530 is therefore inhibition of LOC138389 (Accession XM_072534). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138389. LOC145900 (Accession XM_085276) is another VGAM2530 host target gene. LOC145900 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145900, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145900 BINDING SITE, designated SEQ ID:38014, to

the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85722] Another function of VGAM2530 is therefore inhibition of LOC145900 (Accession XM_085276). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145900. LOC148137 (Accession NM_144692) is another VGAM2530 host target gene. LOC148137 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148137, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE, designated SEQ ID:29520, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85723] Another function of VGAM2530 is therefore inhibition of LOC148137 (Accession NM_144692). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148137. LOC148508 (Accession XM_097478) is another VGAM2530 host target gene. LOC148508 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC148508, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148508 BINDING SITE, designated SEQ ID:40885, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85724] Another function of VGAM2530 is therefore inhibition of LOC148508 (Accession XM_097478). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148508. LOC148534 (Accession XM_086222) is another VGAM2530 host target gene. LOC148534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148534 BINDING SITE, designated SEQ ID:38551, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85725] Another function of VGAM2530 is therefore inhibition of LOC148534 (Accession XM_086222). Accordingly, utilities

of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148534. LOC148930 (Accession XM_086369) is another VGAM2530 host target gene. LOC148930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148930 BINDING SITE, designated SEQ ID:38620, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85726] Another function of VGAM2530 is therefore inhibition of LOC148930 (Accession XM_086369). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148930. LOC149721 (Accession XM_086649) is another VGAM2530 host target gene. LOC149721 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC149721 BINDING SITE, designated SEQ ID:38814, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85727] Another function of VGAM2530 is therefore inhibition of LOC149721 (Accession XM_086649). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149721. LOC150157 (Accession XM_097823) is another VGAM2530 host target gene. LOC150157 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150157, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150157 BINDING SITE, designated SEQ ID:41143, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85728] Another function of VGAM2530 is therefore inhibition of LOC150157 (Accession XM_097823). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150157. LOC152972 (Accession XM_087572) is another VGAM2530 host target gene. LOC152972 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152972, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152972 BINDING SITE, designated SEQ ID:39346, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85729] Another function of VGAM2530 is therefore inhibition of LOC152972 (Accession XM_087572). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152972. LOC196890 (Accession XM_116951) is another VGAM2530 host target gene. LOC196890 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196890, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196890 BINDING SITE, designated SEQ ID:43155, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85730] Another function of VGAM2530 is therefore inhibition of

LOC196890 (Accession XM_116951). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196890. LOC200014 (Accession XM_114087) is another VGAM2530 host target gene. LOC200014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200014 BINDING SITE, designated SEQ ID:42696, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85731] Another function of VGAM2530 is therefore inhibition of LOC200014 (Accession XM_114087). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200014. LOC200853 (Accession XM_114308) is another VGAM2530 host target gene. LOC200853 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200853, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC200853 BINDING SITE, designated SEQ ID:42869, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85732] Another function of VGAM2530 is therefore inhibition of LOC200853 (Accession XM_114308). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200853. LOC253805 (Accession XM_172854) is another VGAM2530 host target gene. LOC253805 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253805, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253805 BINDING SITE, designated SEQ ID:46139, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85733] Another function of VGAM2530 is therefore inhibition of LOC253805 (Accession XM_172854). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805. LOC90593 (Accession XM_032815) is an-

other VGAM2530 host target gene. LOC90593 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90593, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90593 BINDING SITE, designated SEQ ID:31767, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85734] Another function of VGAM2530 is therefore inhibition of LOC90593 (Accession XM_032815). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90593. LOC91516 (Accession XM_038924) is another VGAM2530 host target gene. LOC91516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91516 BINDING SITE, designated SEQ ID:32957, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85735] Another function of VGAM2530 is therefore inhibition of LOC91516 (Accession XM_038924). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91516. LOC92539 (Accession XM_045632) is another VGAM2530 host target gene. LOC92539 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92539, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92539 BINDING SITE, designated SEQ ID:34506, to the nucleotide sequence of VGAM2530 RNA, herein designated VGAM RNA, also designated SEQ ID:5241.

[85736] Another function of VGAM2530 is therefore inhibition of LOC92539 (Accession XM_045632). Accordingly, utilities of VGAM2530 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92539. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2531 (VGAM2531) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[85737] VGAM2531 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2531 was detected is described hereinabove with reference to Figs. 1-8.

[85738] VGAM2531 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pepper Ringspot Virus. VGAM2531 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85739] VGAM2531 gene encodes a VGAM2531 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2531 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2531 precursor RNA is designated SEQ ID:2517, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2517 is located at position 2562 relative to the genome of Pepper Ringspot Virus.

[85740] VGAM2531 precursor RNA folds onto itself, forming VGAM2531 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85741] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2531 folded precursor RNA into VGAM2531 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2531 RNA is designated SEQ ID:5242, and is provided hereinbelow with reference to the sequence listing part.

[85742] VGAM2531 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2531 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85743] VGAM2531 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2531 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2531 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85744] The complementary binding of VGAM2531 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2531 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2531 host target RNA into VGAM2531 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85745] It is appreciated that VGAM2531 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2531 host target genes. The mRNA of each one of this plurality of VGAM2531 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2531 RNA, herein designated VGAM RNA, and which when bound by VGAM2531 RNA causes inhibition of translation of respective one or more VGAM2531 host target proteins.

[85746] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2531 gene, herein designated VGAM GENE, on one or more VGAM2531 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85747] It is yet further appreciated that a function of VGAM2531 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2531 include diagnosis, prevention and treatment of viral infection by Pepper Ringspot Virus. Specific functions, and accordingly utilities, of VGAM2531 correlate with, and may be deduced from, the identity of the host target genes which VGAM2531 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[85748] Nucleotide sequences of the VGAM2531 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2531 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2531 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2531 are further described hereinbelow with reference to Table 1.

[85749] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2531 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2531 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85750] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2531 gene, herein designated VGAM is inhibition of expression of VGAM2531 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2531 correlate with, and may be deduced from, the identity of the target genes which VGAM2531 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85751] Diacylglycerol O-acyltransferase Homolog 2 (mouse) (DGAT2, Accession NM_032564) is a VGAM2531 host target gene. DGAT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGAT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGAT2 BINDING SITE, designated SEQ ID:26288, to the nucleotide sequence of VGAM2531 RNA, herein designated VGAM RNA, also designated SEQ ID:5242.

[85752] A function of VGAM2531 is therefore inhibition of Diacylglycerol O-acyltransferase Homolog 2 (mouse) (DGAT2, Accession NM_032564). Accordingly, utilities of VGAM2531 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGAT2. Major Histocompatibility Complex, Class II, DQ Alpha 1 (HLA-DQA1, Accession XM_175260) is another VGAM2531 host target gene. HLA-DQA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HLA-DQA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of HLA-DQA1 BINDING SITE, designated SEQ ID:46725, to the nucleotide sequence of VGAM2531 RNA, herein designated VGAM RNA, also designated SEQ ID:5242.

[85753] Another function of VGAM2531 is therefore inhibition of Major Histocompatibility Complex, Class II, DQ Alpha 1 (HLA-DQA1, Accession XM_175260), a gene which is alpha 1 chain of HLA-DQ1 class II molecule (Ia antigen) which binds peptides and presents them to CD4+ T lymphocytes. Accordingly, utilities of VGAM2531 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLA-DQA1. The function of HLA-DQA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM132.FLJ00001 (Accession XM_088525) is another VGAM2531 host target gene. FLJ00001 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00001, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00001 BINDING SITE, designated SEQ ID:39788, to the nucleotide

sequence of VGAM2531 RNA, herein designated VGAM RNA, also designated SEQ ID:5242.

[85754] Another function of VGAM2531 is therefore inhibition of FLJ00001 (Accession XM_088525). Accordingly, utilities of VGAM2531 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00001. LOC255042 (Accession XM_170896) is another VGAM2531 host target gene. LOC255042 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255042 BINDING SITE, designated SEQ ID:45647, to the nucleotide sequence of VGAM2531 RNA, herein designated VGAM RNA, also designated SEQ ID:5242.

[85755] Another function of VGAM2531 is therefore inhibition of LOC255042 (Accession XM_170896). Accordingly, utilities of VGAM2531 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255042. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2532 (VGAM2532) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85756] VGAM2532 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2532 was detected is described hereinabove with reference to Figs. 1-8.

[85757] VGAM2532 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rio Bravo Virus. VGAM2532 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85758] VGAM2532 gene encodes a VGAM2532 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2532 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2532 precursor RNA is designated SEQ ID:2518, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2518 is located at position 643 relative to the genome of Rio Bravo Virus.

[85759] VGAM2532 precursor RNA folds onto itself, forming VGAM2532 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85760] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2532 folded precursor RNA into VGAM2532 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2532 RNA is designated SEQ ID:5243, and is provided hereinbelow with reference to the sequence listing part.

[85761] VGAM2532 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2532 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2532 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85762] VGAM2532 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2532 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2532 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85763] The complementary binding of VGAM2532 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2532 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2532 host target RNA into VGAM2532 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85764] It is appreciated that VGAM2532 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2532 host target genes. The mRNA of each one of this plurality of VGAM2532 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2532 RNA, herein designated VGAM RNA, and which when bound by VGAM2532 RNA causes inhibition of translation of respective one or more VGAM2532 host target proteins.

[85765] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2532 gene, herein designated VGAM GENE, on one or more VGAM2532 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85766] It is yet further appreciated that a function of VGAM2532 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2532 include diagnosis, prevention and treatment of viral infection by Rio Bravo Virus. Specific functions, and accordingly utilities, of VGAM2532 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2532 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85767] Nucleotide sequences of the VGAM2532 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2532 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2532 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2532 are further described hereinbelow with reference to Table 1.

[85768] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2532 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2532 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85769] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2532 gene, herein designated VGAM is inhibition of expression of VGAM2532 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2532 correlate with, and may be deduced from, the identity of the target genes which VGAM2532

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85770] BRAG (Accession NM_014863) is a VGAM2532 host target gene. BRAG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRAG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRAG BINDING SITE, designated SEQ ID:16939, to the nucleotide sequence of VGAM2532 RNA, herein designated VGAM RNA, also designated SEQ ID:5243.

[85771] A function of VGAM2532 is therefore inhibition of BRAG (Accession NM_014863). Accordingly, utilities of VGAM2532 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRAG. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2533 (VGAM2533) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85772] VGAM2533 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2533 was detected is described hereinabove with reference to Figs. 1-8.

[85773] VGAM2533 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rio Bravo Virus. VGAM2533 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85774] VGAM2533 gene encodes a VGAM2533 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2533 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2533 precursor RNA is designated SEQ ID:2519, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2519 is located at position 3063 relative to the genome of Rio Bravo Virus.

[85775] VGAM2533 precursor RNA folds onto itself, forming VGAM2533 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85776] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2533 folded precursor RNA into VGAM2533 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2533 RNA is designated SEQ ID:5244, and is provided hereinbelow with reference to the sequence listing part.

[85777] VGAM2533 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2533 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85778] VGAM2533 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2533 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2533 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85779] The complementary binding of VGAM2533 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2533 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2533 host target RNA into VGAM2533 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85780] It is appreciated that VGAM2533 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2533 host target genes. The mRNA of each one of this plurality of VGAM2533 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2533 RNA, herein designated VGAM RNA, and which when bound by VGAM2533 RNA causes inhibition of translation of respective one or more VGAM2533 host target proteins.

[85781] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2533 gene, herein designated VGAM GENE, on one or more VGAM2533 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85782] It is yet further appreciated that a function of VGAM2533 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of viral infection by Rio Bravo Virus. Specific functions, and accordingly utilities, of VGAM2533 correlate with, and may be deduced from, the identity of the host target genes which VGAM2533 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85783] Nucleotide sequences of the VGAM2533 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2533 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2533 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2533 are further described hereinbelow with reference to Table 1.

[85784] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2533 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2533 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85785] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2533 gene, herein designated VGAM is inhibition of expression of VGAM2533 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2533 correlate with, and may be deduced from, the identity of the target genes which VGAM2533 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85786] CRACC (Accession NM_021181) is a VGAM2533 host target gene. CRACC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRACC, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRACC BINDING SITE, designated SEQ ID:22153, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85787] A function of VGAM2533 is therefore inhibition of CRACC (Accession NM_021181), a gene which may participate in adhesion reactions between t lymphocytes and accessory cells. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRACC. The function of CRACC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM26.Inositol 1,4,5-triphosphate Receptor, Type 3 (ITPR3, Accession NM_002224) is another VGAM2533 host target gene. ITPR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITPR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPR3 BINDING SITE, designated SEQ ID:7997,

to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85788] Another function of VGAM2533 is therefore inhibition of Inositol 1,4,5-triphosphate Receptor, Type 3 (ITPR3, Accession NM_002224), a gene which may be responsible for calcium release from intracellular stores. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPR3. The function of ITPR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM310.Laminin, Gamma 1 (formerly LAMB2) (LAMC1, Accession NM_002293) is another VGAM2533 host target gene. LAMC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LAMC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAMC1 BINDING SITE, designated SEQ ID:8079, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85789] Another function of VGAM2533 is therefore inhibition of

Laminin, Gamma 1 (formerly LAMB2) (LAMC1, Accession NM_002293), a gene which may mediate the attachment, migration, and organization of cells into tissues. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMC1. The function of LAMC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM812.LFG (Accession XM_084780) is another VGAM2533 host target gene. LFG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LFG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LFG BINDING SITE, designated SEQ ID:37688, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85790] Another function of VGAM2533 is therefore inhibition of LFG (Accession XM_084780). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LFG. Protein Tyrosine Phosphatase, Receptor Type, N (PTPRN,

Accession NM_002846) is another VGAM2533 host target gene. PTPRN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPRN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRN BINDING SITE, designated SEQ ID:8734, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85791] Another function of VGAM2533 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, N (PTPRN, Accession NM_002846). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRN. Retinoblastoma Binding Protein 9 (RBBP9, Accession XM_046553) is another VGAM2533 host target gene. RBBP9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBBP9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBBP9 BINDING SITE, designated SEQ

ID:34741, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85792] Another function of VGAM2533 is therefore inhibition of Retinoblastoma Binding Protein 9 (RBBP9, Accession XM_046553). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP9. Transducin (beta)-like 1X-linked (TBL1X, Accession NM_005647) is another VGAM2533 host target gene. TBL1X BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBL1X, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBL1X BINDING SITE, designated SEQ ID:12182, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85793] Another function of VGAM2533 is therefore inhibition of Transducin (beta)-like 1X-linked (TBL1X, Accession NM_005647), a gene which activates latent HDAC3 activity. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with TBL1X. The function of TBL1X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.Telomeric Repeat Binding Factor (NIMA-interacting) 1 (TERF1, Accession NM_017489) is another VGAM2533 host target gene. TERF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TERF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated SEQ ID:18951, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85794] Another function of VGAM2533 is therefore inhibition of Telomeric Repeat Binding Factor (NIMA-interacting) 1 (TERF1, Accession NM_017489), a gene which negatively regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF1. The function of TERF1 and its association with various diseases and clini-

cal conditions, has been established by previous studies, as described hereinabove with reference to VGAM189.Trichorhinophalangeal Syndrome I (TRPS1, Accession NM_014112) is another VGAM2533 host target gene. TRPS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRPS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPS1 BINDING SITE, designated SEQ ID:15360, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85795] Another function of VGAM2533 is therefore inhibition of Trichorhinophalangeal Syndrome I (TRPS1, Accession NM_014112), a gene which may function as a transcriptional activator protein. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPS1. The function of TRPS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.Williams-Beuren Syndrome Chromosome Re-

gion 1 (WBSCR1, Accession NM_022170) is another VGAM2533 host target gene. WBSCR1 BINDING SITE1 and WBSCR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WBSCR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WBSCR1 BINDING SITE1 and WBSCR1 BINDING SITE2, designated SEQ ID:22724 and SEQ ID:25707 respectively, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85796] Another function of VGAM2533 is therefore inhibition of Williams-Beuren Syndrome Chromosome Region 1 (WBSCR1, Accession NM_022170), a gene which stimulates protein translation. Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR1. The function of WBSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM110.Cytoskeleton Associated Protein 2 (CKAP2, Accession NM_018204) is another VGAM2533

host target gene. CKAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CKAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CKAP2 BINDING SITE, designated SEQ ID:20089, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85797] Another function of VGAM2533 is therefore inhibition of Cytoskeleton Associated Protein 2 (CKAP2, Accession NM_018204). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CKAP2. Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989) is another VGAM2533 host target gene. DIO2 BINDING SITE1 and DIO2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DIO2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIO2 BINDING SITE1 and DIO2 BINDING SITE2, designated SEQ ID:15169 and SEQ ID:6458 respectively, to

the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85798] Another function of VGAM2533 is therefore inhibition of Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIO2. FLJ10702 (Accession NM_018184) is another VGAM2533 host target gene. FLJ10702 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10702, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10702 BINDING SITE, designated SEQ ID:20026, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85799] Another function of VGAM2533 is therefore inhibition of FLJ10702 (Accession NM_018184). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10702. FLJ11117 (Accession NM_018329) is another VGAM2533 host target gene. FLJ11117 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11117 BINDING SITE, designated SEQ ID:20326, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85800] Another function of VGAM2533 is therefore inhibition of FLJ11117 (Accession NM_018329). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11117. KIAA0295 (Accession XM_042833) is another VGAM2533 host target gene. KIAA0295 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0295, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0295 BINDING SITE, designated SEQ ID:33781, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85801] Another function of VGAM2533 is therefore inhibition of

KIAA0295 (Accession XM_042833). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0295. KIAA0836 (Accession XM_035390) is another VGAM2533 host target gene. KIAA0836 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0836, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0836 BINDING SITE, designated SEQ ID:32249, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85802] Another function of VGAM2533 is therefore inhibition of KIAA0836 (Accession XM_035390). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0836. Leucine Rich Repeat (in FLII) Interacting Protein 2 (LRRFIP2, Accession NM_017724) is another VGAM2533 host target gene. LRRFIP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LRRFIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRRFIP2 BINDING SITE, designated SEQ ID:19314, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85803] Another function of VGAM2533 is therefore inhibition of Leucine Rich Repeat (in FLII) Interacting Protein 2 (LRRFIP2, Accession NM_017724). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRRFIP2. PGS1 (Accession NM_024419) is another VGAM2533 host target gene. PGS1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PGS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PGS1 BINDING SITE, designated SEQ ID:23658, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85804] Another function of VGAM2533 is therefore inhibition of PGS1 (Accession NM_024419). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PGS1. Stathmin-like 3 (STMN3, Accession NM_015894) is another VGAM2533 host target gene. STMN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STMN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STMN3 BINDING SITE, designated SEQ ID:18040, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85805] Another function of VGAM2533 is therefore inhibition of Stathmin-like 3 (STMN3, Accession NM_015894). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STMN3. TACTILE (Accession NM_005816) is another VGAM2533 host target gene. TACTILE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACTILE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACTILE BINDING SITE, designated SEQ ID:12415, to the nucleotide

sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85806] Another function of VGAM2533 is therefore inhibition of TACTILE (Accession NM_005816). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACTILE. T-cell Leukemia/lymphoma 6 (TCL6, Accession NM_020553) is another VGAM2533 host target gene. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TCL6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:21777 and SEQ ID:21779 respectively, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85807] Another function of VGAM2533 is therefore inhibition of T-cell Leukemia/lymphoma 6 (TCL6, Accession NM_020553). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6. LOC152620

(Accession XM_011108) is another VGAM2533 host target gene. LOC152620 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152620, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152620 BINDING SITE, designated SEQ ID:30171, to the nucleotide sequence of VGAM2533 RNA, herein designated VGAM RNA, also designated SEQ ID:5244.

[85808] Another function of VGAM2533 is therefore inhibition of LOC152620 (Accession XM_011108). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152620. LOC158668 (Accession XM_045161) is another VGAM2533 host target gene. LOC158668 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158668, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158668 BINDING SITE, designated SEQ ID:34376, to the nucleotide sequence of VGAM2533 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5244.

[85809] Another function of VGAM2533 is therefore inhibition of LOC158668 (Accession XM_045161). Accordingly, utilities of VGAM2533 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158668. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2534 (VGAM2534) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85810] VGAM2534 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2534 was detected is described hereinabove with reference to Figs. 1-8.

[85811] VGAM2534 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rio Bravo Virus. VGAM2534 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85812] VGAM2534 gene encodes a VGAM2534 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2534 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2534 precursor RNA is designated SEQ ID:2520, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2520 is located at position 7314 relative to the genome of Rio Bravo Virus.

[85813] VGAM2534 precursor RNA folds onto itself, forming VGAM2534 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85814] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2534 folded precursor RNA into VGAM2534 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM2534 RNA is designated SEQ ID:5245, and is provided hereinbelow with reference to the sequence listing part.

[85815] VGAM2534 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2534 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85816] VGAM2534 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2534 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2534 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85817] The complementary binding of VGAM2534 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2534 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2534 host target RNA into VGAM2534 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85818] It is appreciated that VGAM2534 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2534 host target genes. The mRNA of

each one of this plurality of VGAM2534 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2534 RNA, herein designated VGAM RNA, and which when bound by VGAM2534 RNA causes inhibition of translation of respective one or more VGAM2534 host target proteins.

[85819] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2534 gene, herein designated VGAM GENE, on one or more VGAM2534 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[85820] It is yet further appreciated that a function of VGAM2534 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of viral infection by Rio Bravo Virus. Specific functions, and accordingly utilities, of VGAM2534 correlate with, and may be deduced from, the identity of the host target genes which VGAM2534 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85821] Nucleotide sequences of the VGAM2534 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2534 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2534 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2534 are further described hereinbelow with reference to Table 1.

[85822] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2534 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2534 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85823] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2534 gene, herein designated VGAM is inhibition of expression of VGAM2534 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2534 correlate with, and may be deduced from, the identity of the target genes which VGAM2534 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85824] UDP-Gal:betaGlcNAc Beta 1,3-galactosyltransferase, Polypeptide 3 (B3GALT3, Accession NM_003781) is a VGAM2534 host target gene. B3GALT3 BINDING SITE1 through B3GALT3 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by B3GALT3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B3GALT3 BINDING SITE1 through B3GALT3 BINDING SITE3, designated SEQ ID:9866, SEQ ID:27015 and SEQ ID:27018 respectively, to the nucleotide sequence of VGAM2534 RNA, herein designated VGAM RNA, also designated SEQ ID:5245.

[85825] A function of VGAM2534 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,3-galactosyltransferase, Polypeptide 3 (B3GALT3, Accession NM_003781). Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GALT3. Fibroblast Growth Factor 1 (acidic) (FGF1, Accession NM_033137) is another VGAM2534 host target gene. FGF1 BINDING SITE1 through FGF1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FGF1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF1 BINDING SITE1 through FGF1 BINDING SITE3, designated SEQ ID:26988, SEQ ID:26986 and SEQ ID:6469 respectively, to the nucleotide sequence of VGAM2534 RNA, herein designated VGAM RNA, also designated SEQ ID:5245.

[85826] Another function of VGAM2534 is therefore inhibition of Fibroblast Growth Factor 1 (acidic) (FGF1, Accession NM_033137), a gene which potent mitogen for a variety of cell types. Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF1. The function of FGF1 and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.AP1 Gamma Subunit Binding Protein 1 (AP1GBP1, Accession NM_080550) is another VGAM2534 host target gene. AP1GBP1 BINDING SITE1 through AP1GBP1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AP1GBP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE1 through AP1GBP1 BINDING SITE3, designated SEQ ID:27869, SEQ ID:27875 and SEQ ID:24616 respectively, to the nucleotide sequence of VGAM2534 RNA, herein designated VGAM RNA, also designated SEQ ID:5245.

[85827] Another function of VGAM2534 is therefore inhibition of AP1 Gamma Subunit Binding Protein 1 (AP1GBP1, Accession NM_080550). Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1. KIAA1260 (Accession XM_010461) is another VGAM2534 host target gene. KIAA1260 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by KIAA1260, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1260 BINDING SITE, designated SEQ ID:30155, to the nucleotide sequence of VGAM2534 RNA, herein designated VGAM RNA, also designated SEQ ID:5245.

[85828] Another function of VGAM2534 is therefore inhibition of KIAA1260 (Accession XM_010461). Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1260. Stromal Interaction Molecule 2 (STIM2, Accession NM_020860) is another VGAM2534 host target gene. STIM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STIM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STIM2 BINDING SITE, designated SEQ ID:21913, to the nucleotide sequence of VGAM2534 RNA, herein designated VGAM RNA, also designated SEQ ID:5245.

[85829] Another function of VGAM2534 is therefore inhibition of Stromal Interaction Molecule 2 (STIM2, Accession NM_020860). Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STIM2. LOC130752 (Accession XM_059468) is another VGAM2534 host target gene. LOC130752 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130752, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130752 BINDING SITE, designated SEQ ID:37005, to the nucleotide sequence of VGAM2534 RNA, herein designated VGAM RNA, also designated SEQ ID:5245.

[85830] Another function of VGAM2534 is therefore inhibition of LOC130752 (Accession XM_059468). Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130752. LOC157869 (Accession XM_088409) is another VGAM2534 host target gene. LOC157869 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157869, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157869 BINDING SITE, designated SEQ ID:39674, to the nucleotide sequence of VGAM2534 RNA, herein designated VGAM RNA, also designated SEQ ID:5245.

[85831] Another function of VGAM2534 is therefore inhibition of LOC157869 (Accession XM_088409). Accordingly, utilities of VGAM2534 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157869. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2535 (VGAM2535) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85832] VGAM2535 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2535 was detected is described hereinabove with reference to Figs. 1-8.

[85833] VGAM2535 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rio Bravo Virus.

VGAM2535 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85834] VGAM2535 gene encodes a VGAM2535 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2535 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2535 precursor RNA is designated SEQ ID:2521, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2521 is located at position 5612 relative to the genome of Rio Bravo Virus.

[85835] VGAM2535 precursor RNA folds onto itself, forming VGAM2535 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85836] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2535 folded precursor RNA into VGAM2535 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2535 RNA is designated SEQ ID:5246, and is provided hereinbelow with reference to the sequence listing part.

[85837] VGAM2535 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2535 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85838] VGAM2535 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2535 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2535 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85839] The complementary binding of VGAM2535 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2535 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2535 host target RNA into VGAM2535 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85840] It is appreciated that VGAM2535 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2535 host target genes. The mRNA of each one of this plurality of VGAM2535 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2535 RNA, herein designated VGAM RNA, and which when bound by VGAM2535 RNA causes inhibition of translation of respective one or more VGAM2535 host target proteins.

[85841] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2535 gene, herein designated VGAM GENE, on one or more VGAM2535 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85842] It is yet further appreciated that a function of VGAM2535 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of viral infection by Rio Bravo Virus. Specific functions, and accordingly utilities, of VGAM2535 correlate with, and may be deduced from, the identity of the host target genes which VGAM2535 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85843] Nucleotide sequences of the VGAM2535 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2535 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2535 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2535 are further described hereinbelow with reference to Table 1.

[85844] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2535 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2535 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85845] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2535 gene, herein designated VGAM is inhibition of expression of VGAM2535 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2535 correlate with, and may be deduced from, the identity of the target genes which VGAM2535 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85846] Caspase 10, Apoptosis-related Cysteine Protease (CASP10, Accession NM_032976) is a VGAM2535 host target gene. CASP10 BINDING SITE1 and CASP10 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CASP10, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASP10

BINDING SITE1 and CASP10 BINDING SITE2, designated SEQ ID:26833 and SEQ ID:26836 respectively, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85847] A function of VGAM2535 is therefore inhibition of Caspase 10, Apoptosis-related Cysteine Protease (CASP10, Accession NM_032976), a gene which is one aspartate-specific cysteine protease and important in death receptor signaling or other cellular processes. Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP10. The function of CASP10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.CPEB1 (Accession NM_030594) is another VGAM2535 host target gene. CPEB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPEB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPEB1 BINDING SITE, designated SEQ ID:24959, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA,

also designated SEQ ID:5246.

[85848] Another function of VGAM2535 is therefore inhibition of CPEB1 (Accession NM_030594). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPEB1. Family with Sequence Similarity 8, Member A1 (FAM8A1, Accession NM_016255) is another VGAM2535 host target gene. FAM8A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FAM8A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FAM8A1 BINDING SITE, designated SEQ ID:18384, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85849] Another function of VGAM2535 is therefore inhibition of Family with Sequence Similarity 8, Member A1 (FAM8A1, Accession NM_016255). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAM8A1. FLJ20280 (Accession NM_017741) is another VGAM2535 host target gene. FLJ20280 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20280, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20280 BINDING SITE, designated SEQ ID:19332, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85850] Another function of VGAM2535 is therefore inhibition of FLJ20280 (Accession NM_017741). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20280. KIAA0350 (Accession XM_028332) is another VGAM2535 host target gene. KIAA0350 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0350, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0350 BINDING SITE, designated SEQ ID:30668, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85851] Another function of VGAM2535 is therefore inhibition of

KIAA0350 (Accession XM_028332). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0350. KIAA0469 (Accession NM_014851) is another VGAM2535 host target gene. KIAA0469 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0469, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE, designated SEQ ID:16895, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85852] Another function of VGAM2535 is therefore inhibition of KIAA0469 (Accession NM_014851). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469. KIAA1117 (Accession XM_028219) is another VGAM2535 host target gene. KIAA1117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1117 BINDING SITE, designated SEQ ID:30633, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85853] Another function of VGAM2535 is therefore inhibition of KIAA1117 (Accession XM_028219). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1117. KIAA1128 (Accession XM_043596) is another VGAM2535 host target gene. KIAA1128 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1128, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1128 BINDING SITE, designated SEQ ID:33972, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85854] Another function of VGAM2535 is therefore inhibition of KIAA1128 (Accession XM_043596). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1128. Microtubule-actin Crosslinking Factor 1

(MACF1, Accession NM_012090) is another VGAM2535 host target gene. MACF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MACF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MACF1 BINDING SITE, designated SEQ ID:14378, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85855] Another function of VGAM2535 is therefore inhibition of Microtubule-actin Crosslinking Factor 1 (MACF1, Accession NM_012090). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MACF1. LOC157273 (Accession XM_098743) is another VGAM2535 host target gene. LOC157273 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157273, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157273 BINDING SITE, designated SEQ ID:41784, to the nucleotide sequence of

VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85856] Another function of VGAM2535 is therefore inhibition of LOC157273 (Accession XM_098743). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157273. LOC202020 (Accession XM_114419) is another VGAM2535 host target gene. LOC202020 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202020, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202020 BINDING SITE, designated SEQ ID:42955, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85857] Another function of VGAM2535 is therefore inhibition of LOC202020 (Accession XM_114419). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202020. LOC253250 (Accession XM_170646) is another VGAM2535 host target gene. LOC253250 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC253250, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253250 BINDING SITE, designated SEQ ID:45427, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85858] Another function of VGAM2535 is therefore inhibition of LOC253250 (Accession XM_170646). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253250. LOC257106 (Accession XM_170910) is another VGAM2535 host target gene. LOC257106 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257106 BINDING SITE, designated SEQ ID:45680, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85859] Another function of VGAM2535 is therefore inhibition of LOC257106 (Accession XM_170910). Accordingly, utilities

of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257106. LOC257463 (Accession XM_048605) is another VGAM2535 host target gene. LOC257463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257463 BINDING SITE, designated SEQ ID:35211, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85860] Another function of VGAM2535 is therefore inhibition of LOC257463 (Accession XM_048605). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257463. LOC57826 (Accession NM_021183) is another VGAM2535 host target gene. LOC57826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC57826 BINDING SITE, designated SEQ ID:22160, to the nucleotide sequence of VGAM2535 RNA, herein designated VGAM RNA, also designated SEQ ID:5246.

[85861] Another function of VGAM2535 is therefore inhibition of LOC57826 (Accession NM_021183). Accordingly, utilities of VGAM2535 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57826. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2536 (VGAM2536) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85862] VGAM2536 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2536 was detected is described hereinabove with reference to Figs. 1-8.

[85863] VGAM2536 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pestivirus Reindeer-1. VGAM2536 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[85864] VGAM2536 gene encodes a VGAM2536 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2536 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2536 precursor RNA is designated SEQ ID:2522, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2522 is located at position 4448 relative to the genome of Pestivirus Reindeer-1.

[85865] VGAM2536 precursor RNA folds onto itself, forming VGAM2536 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85866] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2536 folded precursor RNA into VGAM2536 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2536 RNA is designated SEQ ID:5247, and is provided hereinbelow with reference to the sequence listing part.

[85867] VGAM2536 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2536 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85868] VGAM2536 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2536 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2536 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85869] The complementary binding of VGAM2536 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2536 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2536 host target RNA into VGAM2536 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[85870] It is appreciated that VGAM2536 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2536 host target genes. The mRNA of each one of this plurality of VGAM2536 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2536 RNA, herein designated VGAM RNA, and which when bound by VGAM2536 RNA causes inhibition of translation of respective one or more VGAM2536 host target proteins.

[85871] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2536 gene, herein designated VGAM GENE, on one or more VGAM2536 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85872] It is yet further appreciated that a function of VGAM2536 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2536 include diagnosis, prevention and treatment of viral infection by Pestivirus Reindeer-1. Specific functions, and accordingly utilities, of VGAM2536 correlate with, and may be deduced from, the identity of the host target genes which VGAM2536 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85873] Nucleotide sequences of the VGAM2536 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2536 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2536 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2536 are further described hereinbelow with reference to Table 1.

[85874] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2536 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2536 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85875] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2536 gene, herein designated VGAM is inhibition of expression of VGAM2536 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2536 correlate with, and may be deduced from, the identity of the target genes which VGAM2536 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85876] UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1, Accession NM_020474) is a VGAM2536 host target gene. GALNT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALNT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNT1 BINDING SITE, designated SEQ ID:21725, to the nucleotide sequence of VGAM2536 RNA, herein designated VGAM RNA, also designated SEQ

ID:5247.

[85877] A function of VGAM2536 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1, Accession NM_020474), a gene which transfers an N-acetyl galactosamine (GalNAc) to a serine or threonine residue in the first step of O-linked oligosaccharide biosynthesis. Accordingly, utilities of VGAM2536 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT1. The function of GALNT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.FLJ12787 (Accession NM_032175) is another VGAM2536 host target gene. FLJ12787 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12787, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12787 BINDING SITE, designated SEQ ID:25890, to the nucleotide sequence of VGAM2536 RNA, herein designated VGAM RNA, also designated SEQ ID:5247.

[85878] Another function of VGAM2536 is therefore inhibition of FLJ12787 (Accession NM_032175). Accordingly, utilities of VGAM2536 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12787. SV2B (Accession NM_014848) is another VGAM2536 host target gene. SV2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SV2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SV2B BINDING SITE, designated SEQ ID:16880, to the nucleotide sequence of VGAM2536 RNA, herein designated VGAM RNA, also designated SEQ ID:5247.

[85879] Another function of VGAM2536 is therefore inhibition of SV2B (Accession NM_014848). Accordingly, utilities of VGAM2536 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SV2B. TA-PP2C (Accession NM_139283) is another VGAM2536 host target gene. TA-PP2C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TA-PP2C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TA-PP2C BINDING SITE, designated SEQ ID:29284, to the nucleotide sequence of VGAM2536 RNA, herein designated VGAM RNA, also designated SEQ ID:5247.

[85880] Another function of VGAM2536 is therefore inhibition of TA-PP2C (Accession NM_139283). Accordingly, utilities of VGAM2536 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TA-PP2C. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2537 (VGAM2537) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[85881] VGAM2537 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2537 was detected is described hereinabove with reference to Figs. 1-8.

[85882] VGAM2537 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pestivirus Reindeer-1. VGAM2537 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[85883] VGAM2537 gene encodes a VGAM2537 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2537 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2537 precursor RNA is designated SEQ ID:2523, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2523 is located at position 4253 relative to the genome of Pestivirus Reindeer-1.

[85884] VGAM2537 precursor RNA folds onto itself, forming VGAM2537 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[85885] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2537 folded precursor RNA into VGAM2537

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2537 RNA is designated SEQ ID:5248, and is provided hereinbelow with reference to the sequence listing part.

[85886] VGAM2537 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2537 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[85887] VGAM2537 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2537 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2537 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[85888] The complementary binding of VGAM2537 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2537 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2537 host target RNA into VGAM2537 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[85889] It is appreciated that VGAM2537 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2537 host target genes. The mRNA of each one of this plurality of VGAM2537 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2537 RNA, herein designated VGAM RNA, and which when bound by VGAM2537 RNA causes inhibition of translation of respective one or more VGAM2537 host target proteins.

[85890] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2537 gene, herein designated VGAM GENE, on one or more VGAM2537 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[85891] It is yet further appreciated that a function of VGAM2537 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of viral infection by Pestivirus Reindeer-1. Specific functions, and accordingly utilities, of VGAM2537 correlate with, and may be deduced from, the identity of the host target genes which VGAM2537 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[85892] Nucleotide sequences of the VGAM2537 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2537 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2537 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2537 are further described hereinbelow with reference to Table 1.

[85893] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2537 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2537 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[85894] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2537 gene, herein designated VGAM is inhibition of expression of VGAM2537 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2537 correlate with, and may be deduced from, the identity of the target genes which VGAM2537 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[85895] Agrin (AGRN, Accession XM_086178) is a VGAM2537 host target gene. AGRN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AGRN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AGRN BINDING SITE, designated SEQ ID:38535, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ

ID:5248.

[85896] A function of VGAM2537 is therefore inhibition of Agrin (AGRN, Accession XM_086178), a gene which a neuronal aggregating factor that induces the aggregation of acetylcholine receptors . Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGRN. The function of AGRN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1063.Ankyrin 1, Erythrocytic (ANK1, Accession XM_016774) is another VGAM2537 host target gene. ANK1 BINDING SITE1 through ANK1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ANK1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANK1 BINDING SITE1 through ANK1 BINDING SITE3, designated SEQ ID:30281, SEQ ID:5477 and SEQ ID:21730 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85897] Another function of VGAM2537 is therefore inhibition of

Ankyrin 1, Erythrocytic (ANK1, Accession XM_016774). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANK1. Androgen Receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) (AR, Accession NM_000044) is another VGAM2537 host target gene. AR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AR BINDING SITE, designated SEQ ID:5486, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85898] Another function of VGAM2537 is therefore inhibition of Androgen Receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) (AR, Accession NM_000044), a gene which are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with AR. The function of AR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1971.ATPase, Na+/K+ Transporting, Beta 2 Polypeptide (ATP1B2, Accession NM_001678) is another VGAM2537 host target gene. ATP1B2 BINDING SITE1 and ATP1B2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ATP1B2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1B2 BINDING SITE1 and ATP1B2 BINDING SITE2, designated SEQ ID:7390 and SEQ ID:7391 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85899] Another function of VGAM2537 is therefore inhibition of ATPase, Na+/K+ Transporting, Beta 2 Polypeptide (ATP1B2, Accession NM_001678), a gene which catalyzes the hydrolysis of ATP coupled with the exchange of Na +/K+ ions across the plasma membrane. Accordingly, utilities of VGAM2537 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with ATP1B2. The function of ATP1B2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898) is another VGAM2537 host target gene. BCL11B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL11B BINDING SITE, designated SEQ ID:23160, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85900] Another function of VGAM2537 is therefore inhibition of B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL11B. B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_138931) is another VGAM2537 host target gene. BCL6 BINDING SITE is HOST TARGET binding

site found in the 5` untranslated region of mRNA encoded by BCL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL6 BINDING SITE, designated SEQ ID:29056, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85901] Another function of VGAM2537 is therefore inhibition of B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_138931), a gene which is involved in the generation and maintenance of both T and B cells during immune responses. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL6. The function of BCL6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM481.Breakpoint Cluster Region (BCR, Accession NM_021574) is another VGAM2537 host target gene. BCR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BCR, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCR BINDING SITE, designated SEQ ID:22237, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85902] Another function of VGAM2537 is therefore inhibition of Breakpoint Cluster Region (BCR, Accession NM_021574), a gene which is a serine/threonine kinase that involves in the t(9;22) translocation (Philadelphia chromosome). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCR. The function of BCR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2151.BTG Family, Member 2 (BTG2, Accession NM_006763) is another VGAM2537 host target gene. BTG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTG2 BINDING SITE, designated SEQ ID:13626, to the nucleotide sequence of VGAM2537

RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85903] Another function of VGAM2537 is therefore inhibition of BTG Family, Member 2 (BTG2, Accession NM_006763). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTG2. Complement Component 5 Receptor 1 (C5a ligand) (C5R1, Accession NM_001736) is another VGAM2537 host target gene. C5R1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5R1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5R1 BINDING SITE, designated SEQ ID:7474, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85904] Another function of VGAM2537 is therefore inhibition of Complement Component 5 Receptor 1 (C5a ligand) (C5R1, Accession NM_001736), a gene which has a nonredundant function and is required for mucosal host cell defense in the lung. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with C5R1. The function of C5R1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM484.CD8 Antigen, Alpha Polypeptide (p32) (CD8A, Accession NM_001768) is another VGAM2537 host target gene. CD8A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD8A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD8A BINDING SITE, designated SEQ ID:7529, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85905] Another function of VGAM2537 is therefore inhibition of CD8 Antigen, Alpha Polypeptide (p32) (CD8A, Accession NM_001768), a gene which is thought to play a role in the process of t-cell mediated killing. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD8A. The function of CD8A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM609.Cyclin-dependent Kinase Inhibitor 1A (p21, Cip1) (CDKN1A, Accession NM_078467) is another VGAM2537 host target gene. CDKN1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDKN1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDKN1A BINDING SITE, designated SEQ ID:27780, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85906] Another function of VGAM2537 is therefore inhibition of Cyclin-dependent Kinase Inhibitor 1A (p21, Cip1) (CDKN1A, Accession NM_078467), a gene which inhibits cyclin-kinase activity and probably serves as the effector of p53 cell cycle control. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKN1A. The function of CDKN1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1912.Clock Homolog (mouse) (CLOCK, Accession NM_004898) is another VGAM2537 host target

gene. CLOCK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLOCK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLOCK BINDING SITE, designated SEQ ID:11333, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85907] Another function of VGAM2537 is therefore inhibition of Clock Homolog (mouse) (CLOCK, Accession NM_004898). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLOCK. Coronin, Actin Binding Protein, 2B (CORO2B, Accession XM_035403) is another VGAM2537 host target gene. CORO2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CORO2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CORO2B BINDING SITE, designated SEQ ID:32255, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM

RNA, also designated SEQ ID:5248.

[85908] Another function of VGAM2537 is therefore inhibition of Coronin, Actin Binding Protein, 2B (CORO2B, Accession XM_035403), a gene which may play a role in the reorganization of neuronal actin structure. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CORO2B. The function of CORO2B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM923.Corticotropin Releasing Hormone Receptor 2 (CRHR2, Accession NM_001883) is another VGAM2537 host target gene. CRHR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRHR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRHR2 BINDING SITE, designated SEQ ID:7611, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85909] Another function of VGAM2537 is therefore inhibition of Corticotropin Releasing Hormone Receptor 2 (CRHR2, Ac-

cession NM_001883), a gene which is a corticotropin releasing factor receptor type II. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRHR2. The function of CRHR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM737.C-src Tyrosine Kinase (CSK, Accession NM_004383) is another VGAM2537 host target gene. CSK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CSK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSK BINDING SITE, designated SEQ ID:10608, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85910] Another function of VGAM2537 is therefore inhibition of C-src Tyrosine Kinase (CSK, Accession NM_004383), a gene which down-regulates antigen receptor signaling in T lymphocytes and the c-src oncoprotein. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with CSK. The function of CSK has been established by previous studies. Partanen et al. (1991) cloned a novel cytoplasmic tyrosine kinase designated CSK. This tyrosine kinase was shown to downregulate the tyrosine kinase activity of the c-src oncoprotein (OMIM Ref. No. 190090) through tyrosine phosphorylation of the c-src carboxy terminus. Since cell transformation by SRC oncoproteins is caused by various mechanisms that interfere with this phosphorylation, the CSK gene might function as an antioncogene (Armstrong et al., 1992). The CSK gene is ubiquitously expressed in human tissues as 2 mRNA species of 2.6 and 3.4 kb, although in some tissues and cell lines, only the larger mRNA is detected Cloutier and Veillette (1996) used the yeast 2-hybrid system to identify proteins associated with CSK. They found that the Src homology-3 (SH3) domain of CSK associates with a proline-rich region of PEP (OMIM Ref. No. 600716), a protein-tyrosine phosphatase expressed in hemopoietic cells. Cloutier and Veillette (1996) showed that this association is highly specific and speculated that PEP may be an effector and/or regulator of CSK in T cells and other hemopoietic cells

[85911] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[85912] Armstrong, E.; Cannizzaro, L.; Bergman, M.; Huebner, K.; Alitalo, K. : The c-src tyrosine kinase (CSK) gene, a potential antioncogene, localizes to human chromosome region 15q23-q25. Cytogenet. Cell Genet. 60: 119-120, 1992. ; and

[85913] Cloutier, J.-F.; Veillette, A. : Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosine phosphatase PEP in T cells and other hemopoietic cells. EMBO J. 15: 4909.

[85914] Further studies establishing the function and utilities of CSK are found in John Hopkins OMIM database record ID 124095, and in sited publications numbered 3685-3687 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Drebrin 1 (DBN1, Accession NM_004395) is another VGAM2537 host target gene. DBN1 BINDING SITE1 and DBN1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DBN1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DBN1 BINDING SITE1

and DBN1 BINDING SITE2, designated SEQ ID:10639 and SEQ ID:28122 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85915] Another function of VGAM2537 is therefore inhibition of Drebrin 1 (DBN1, Accession NM_004395). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBN1. DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (DDX11, Accession NM_004399) is another VGAM2537 host target gene. DDX11 BINDING SITE1 and DDX11 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DDX11, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDX11 BINDING SITE1 and DDX11 BINDING SITE2, designated SEQ ID:10652 and SEQ ID:13561 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85916] Another function of VGAM2537 is therefore inhibition of DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 11

(CHL1-like helicase homolog, S. cerevisiae) (DDX11, Accession NM_004399), a gene which could be an ATP-dependent DNA-binding helicase and may intervene in cell cycle regulation. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX11. The function of DDX11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1533.Doublesex and Mab-3 Related Transcription Factor 2 (DMRT2, Accession NM_006557) is another VGAM2537 host target gene. DMRT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DMRT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMRT2 BINDING SITE, designated SEQ ID:13323, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85917] Another function of VGAM2537 is therefore inhibition of Doublesex and Mab-3 Related Transcription Factor 2 (DMRT2, Accession NM_006557), a gene which May be in-

volved in male sexual development. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMRT2. The function of DMRT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Dual Specificity Phosphatase 4 (DUSP4, Accession NM_057158) is another VGAM2537 host target gene. DUSP4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DUSP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DUSP4 BINDING SITE, designated SEQ ID:27667, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85918] Another function of VGAM2537 is therefore inhibition of Dual Specificity Phosphatase 4 (DUSP4, Accession NM_057158), a gene which regulates mitogenic signal transduction. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP4. The function of

DUSP4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM110.ELK1, Member of ETS Oncogene Family (ELK1, Accession NM_005229) is another VGAM2537 host target gene. ELK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELK1 BINDING SITE, designated SEQ ID:11732, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85919] Another function of VGAM2537 is therefore inhibition of ELK1, Member of ETS Oncogene Family (ELK1, Accession NM_005229), a gene which stimulates transcription. can form a ternary complex with the serum response factor and the ets and srf motifs of the fos serum response element. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELK1. The function of ELK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to VGAM178.Estrogen-related Receptor Gamma (ESRRG, Accession XM_039053) is another VGAM2537 host target gene. ESRRG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESRRG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESRRG BINDING SITE, designated SEQ ID:32998, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85920] Another function of VGAM2537 is therefore inhibition of Estrogen-related Receptor Gamma (ESRRG, Accession XM_039053), a gene which Estrogen-related receptor gamma. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESRRG. The function of ESRRG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM359.Fibroblast Growth Factor 12 (FGF12, Accession NM_021032) is another VGAM2537 host target gene. FGF12 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by FGF12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF12 BINDING SITE, designated SEQ ID:22019, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85921] Another function of VGAM2537 is therefore inhibition of Fibroblast Growth Factor 12 (FGF12, Accession NM_021032), a gene which probably involved in nervous system development and function. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF12. The function of FGF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1025.FXYD Domain Containing Ion Transport Regulator 6 (FXYD6, Accession NM_022003) is another VGAM2537 host target gene. FXYD6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FXYD6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FXYD6 BINDING SITE, designated SEQ ID:22550, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85922] Another function of VGAM2537 is therefore inhibition of FXYD Domain Containing Ion Transport Regulator 6 (FXYD6, Accession NM_022003). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FXYD6. Gamma-aminobutyric Acid (GABA) A Receptor, Epsilon (GABRE, Accession NM_021990) is another VGAM2537 host target gene. GABRE BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GABRE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABRE BINDING SITE, designated SEQ ID:22529, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85923] Another function of VGAM2537 is therefore inhibition of Gamma-aminobutyric Acid (GABA) A Receptor, Epsilon

(GABRE, Accession NM_021990), a gene which mediates neuronal inhibition by binding to the gaba/ benzodiazepine receptor and opening an integral chloride channel. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABRE. The function of GABRE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM259.Galactosamine (N-acetyl)-6-sulfate Sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA) (GALNS, Accession NM_000512) is another VGAM2537 host target gene. GALNS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALNS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNS BINDING SITE, designated SEQ ID:6124, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85924] Another function of VGAM2537 is therefore inhibition of Galactosamine (N-acetyl)-6-sulfate Sulfatase (Morquio

syndrome, mucopolysaccharidosis type IVA) (GALNS, Accession NM_000512). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNS. Glucagon-like Peptide 1 Receptor (GLP1R, Accession NM_002062) is another VGAM2537 host target gene. GLP1R BINDING SITE1 and GLP1R BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GLP1R, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GLP1R BINDING SITE1 and GLP1R BINDING SITE2, designated SEQ ID:7822 and SEQ ID:7823 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85925] Another function of VGAM2537 is therefore inhibition of Glucagon-like Peptide 1 Receptor (GLP1R, Accession NM_002062), a gene which is mediated by g proteins which activate adenylyl cyclase. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLP1R. The function of GLP1R and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1652.G Protein-coupled Receptor 45 (GPR45, Accession NM_007227) is another VGAM2537 host target gene. GPR45 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GPR45, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR45 BINDING SITE, designated SEQ ID:14094, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85926] Another function of VGAM2537 is therefore inhibition of G Protein-coupled Receptor 45 (GPR45, Accession NM_007227). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR45. Hepatoma-derived Growth Factor (high-mobility group protein 1-like) (HDGF, Accession NM_004494) is another VGAM2537 host target gene. HDGF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HDGF, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HDGF BINDING SITE, designated SEQ ID:10832, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85927] Another function of VGAM2537 is therefore inhibition of Hepatoma-derived Growth Factor (high-mobility group protein 1-like) (HDGF, Accession NM_004494), a gene which is a heparin-binding protein, with mitogenic activity for fibroblasts. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HDGF. The function of HDGF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Hippocalcin-like 1 (HPCAL1, Accession NM_002149) is another VGAM2537 host target gene. HPCAL1 BINDING SITE1 through HPCAL1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HPCAL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HPCAL1 BINDING

SITE1 through HPCAL1 BINDING SITE3, designated SEQ ID:7927, SEQ ID:28635 and SEQ ID:28634 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85928] Another function of VGAM2537 is therefore inhibition of Hippocalcin-like 1 (HPCAL1, Accession NM_002149). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPCAL1. Insulin-like Growth Factor Binding Protein 4 (IGFBP4, Accession NM_001552) is another VGAM2537 host target gene. IGFBP4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IGFBP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IGFBP4 BINDING SITE, designated SEQ ID:7275, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85929] Another function of VGAM2537 is therefore inhibition of Insulin-like Growth Factor Binding Protein 4 (IGFBP4, Accession NM_001552), a gene which prolongs the half-life of the igfs and inhibit or stimulate their growth promoting

effects on cell culture. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IGFBP4. The function of IGFBP4 has been established by previous studies. Six structurally distinct insulin-like growth factor binding proteins have been isolated and their cDNAs cloned: IGFBP1 (OMIM Ref. No. 146730), IGFBP2 (OMIM Ref. No. 146731), IGFBP3 (OMIM Ref. No. 146732), IGFBP4, IGFBP5 (OMIM Ref. No. 146734), and IGFBP6 (OMIM Ref. No. 146735). The proteins display strong sequence homologies, suggesting that they are encoded by a closely related family of genes. The IGFBPs contain 3 structurally distinct domains each comprising approximately one-third of the molecule. The N-terminal domain 1 and the C-terminal domain 3 of the 6 human IGFBPs show moderate to high levels of sequence identity including 12 and 6 invariant cysteine residues in domains 1 and 3, respectively (IGFBP6 contains 10 cysteine residues in domain 1), and are thought to be the IGF binding domains. Domain 2 is defined primarily by a lack of sequence identity among the 6 IGFBPs and by a lack of cysteine residues, though it does contain 2 cysteines in IGFBP4. Domain 3 is homologous to the thyroglobulin type I repeat unit. Kiefer et al. (1992)

characterized recombinant human insulin-like growth factor binding proteins 4, 5, and 6 by their expression in yeast as fusion proteins with ubiquitin (OMIM Ref. No. 191320). Results of the study suggested to the authors that the primary effect of the 3 proteins is the attenuation of IGF activity and suggested that they contribute to the control of IGF-mediated cell growth and metabolism. Based on peptide sequences of a purified insulin-like growth factor-binding protein (IGFBP), Shimasaki et al. (1990) cloned rat IGFBP4 using PCR. They used the rat cDNA to clone the human ortholog from a liver cDNA library. Human IGFBP4 encodes a 258-amino acid polypeptide, which includes a 21-amino acid signal sequence. The protein is very hydrophilic, which may facilitate its ability as a carrier protein for the IGFs in blood. Northern blot analysis of rat tissues revealed expression in all tissues examined, with highest expression in liver. Shimasaki et al. (1990) stated that IGFBP4 acts as an inhibitor of IGF-induced bone cell proliferation.

[85930] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[85931] Shimasaki, S.; Uchiyama, F.; Shimonaka, M.; Ling, N. :

Molecular cloning of the cDNAs encoding a novel insulin-like growth factor-binding protein from rat and human. Molec. Endocr. 4: 1451-1458, 1990. ; and

[85932] Kiefer, M. C.; Schmid, C.; Waldvogel, M.; Schlapfer, I.; Futo, E.; Masiarz, F. R.; Green, K.; Barr, P. J.; Zapf, J. : Characterization of recombinant human insulin-like growth factor bin.

[85933] Further studies establishing the function and utilities of IGFBP4 are found in John Hopkins OMIM database record ID 146733, and in sited publications numbered 3023-3027 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Interleukin 8 Receptor, Alpha (IL8RA, Accession NM_000634) is another VGAM2537 host target gene. IL8RA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL8RA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL8RA BINDING SITE, designated SEQ ID:6266, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85934] Another function of VGAM2537 is therefore inhibition of

Interleukin 8 Receptor, Alpha (IL8RA, Accession NM_000634), a gene which is the receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL8RA. The function of IL8RA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM300.Potassium Voltage-gated Channel, Isk-related Family, Member 1-like (KCNE1L, Accession NM_012282) is another VGAM2537 host target gene. KCNE1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNE1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNE1L BINDING SITE, designated SEQ ID:14614, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85935] Another function of VGAM2537 is therefore inhibition of Potassium Voltage-gated Channel, Isk-related Family, Member 1-like (KCNE1L, Accession NM_012282), a gene

which is a potassium voltage-gated channel. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNE1L. The function of KCNE1L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1864.Potassium Channel, Subfamily K, Member 4 (KCNK4, Accession NM_016611) is another VGAM2537 host target gene. KCNK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNK4 BINDING SITE, designated SEQ ID:18716, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85936] Another function of VGAM2537 is therefore inhibition of Potassium Channel, Subfamily K, Member 4 (KCNK4, Accession NM_016611). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK4. L1 Cell Adhesion Molecule (hydrocephalus, stenosis of aqueduct of

Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) Syndrome, Spastic Paraplegia 1) (L1CAM, Accession NM_024003) is another VGAM2537 host target gene. L1CAM BINDING SITE1 and L1CAM BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by L1CAM, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of L1CAM BINDING SITE1 and L1CAM BINDING SITE2, designated SEQ ID:23429 and SEQ ID:6001 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85937] Another function of VGAM2537 is therefore inhibition of L1 Cell Adhesion Molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) Syndrome, Spastic Paraplegia 1) (L1CAM, Accession NM_024003). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with L1CAM. MAX Binding Protein (MNT, Accession NM_020310) is another VGAM2537 host target gene. MNT BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by MNT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MNT BINDING SITE, designated SEQ ID:21560, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85938] Another function of VGAM2537 is therefore inhibition of MAX Binding Protein (MNT, Accession NM_020310). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MNT. Myotubularin Related Protein 3 (MTMR3, Accession NM_021090) is another VGAM2537 host target gene. MTMR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTMR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTMR3 BINDING SITE, designated SEQ ID:22072, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85939] Another function of VGAM2537 is therefore inhibition of

Myotubularin Related Protein 3 (MTMR3, Accession NM_021090), a gene which could be a tyrosine-phosphatase. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTMR3. The function of MTMR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1718.Nescient Helix Loop Helix 1 (NHLH1, Accession NM_005598) is another VGAM2537 host target gene. NHLH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NHLH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NHLH1 BINDING SITE, designated SEQ ID:12125, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85940] Another function of VGAM2537 is therefore inhibition of Nescient Helix Loop Helix 1 (NHLH1, Accession NM_005598), a gene which may have a role in development of the nervous system. Accordingly, utilities of

VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NHLH1. The function of NHLH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1923.Platelet-activating Factor Acetylhydrolase, Isoform Ib, Alpha Subunit 45kDa (PAFAH1B1, Accession NM_000430) is another VGAM2537 host target gene. PAFAH1B1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PAFAH1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAFAH1B1 BINDING SITE, designated SEQ ID:6010, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85941] Another function of VGAM2537 is therefore inhibition of Platelet-activating Factor Acetylhydrolase, Isoform Ib, Alpha Subunit 45kDa (PAFAH1B1, Accession NM_000430). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAFAH1B1. Paired Box Gene 5 (B-cell

lineage specific activator protein) (PAX5, Accession NM_016734) is another VGAM2537 host target gene. PAX5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAX5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAX5 BINDING SITE, designated SEQ ID:18790, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85942] Another function of VGAM2537 is therefore inhibition of Paired Box Gene 5 (B-cell lineage specific activator protein) (PAX5, Accession NM_016734), a gene which plays a role in B-cell differentiation, neural development and spermatogenesis. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAX5. The function of PAX5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.Phosphodiesterase 4A, CAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila) (PDE4A, Accession NM_006202) is another VGAM2537

host target gene. PDE4A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4A BINDING SITE, designated SEQ ID:12874, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85943] Another function of VGAM2537 is therefore inhibition of Phosphodiesterase 4A, CAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila) (PDE4A, Accession NM_006202), a gene which is a CAMP-specific phosphodiesterase . Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4A. The function of PDE4A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1214.Peroxisomal Biogenesis Factor 14 (PEX14, Accession XM_033059) is another VGAM2537 host target gene. PEX14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

PEX14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEX14 BINDING SITE, designated SEQ ID:31827, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85944] Another function of VGAM2537 is therefore inhibition of Peroxisomal Biogenesis Factor 14 (PEX14, Accession XM_033059), a gene which is a component of the peroxisomal translocation machinery with pex13 and pex17. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEX14. The function of PEX14 has been established by previous studies. Working with Saccharomyces cerevisiae, Albertini et al. (1997) described peroxin-14 (PEX14), the first membrane-bound peroxisomal protein that binds to the peroxisomal type-2 targeting signal (PTS2) receptor, PEX7 (OMIM Ref. No. 601757). Thus, the PEX14 protein may represent the functional docking site for PTS2-dependent protein import to the peroxisome. In addition to the interaction with the PTS2 receptor, PEX14 protein was found to interact with PEX5

protein (OMIM Ref. No. 600414), the PTS1 receptor. This observation suggested the overlapping of 2 import pathways, with PEX14 being the point of convergence. Moreover, PEX14 also interacted with 2 other membrane-bound peroxins, including the SH3 domain protein PEX13 (OMIM Ref. No. 601789), the putative docking protein for PTS1-dependent protein import. Albertini et al. (1997) proposed that these 3 peroxins are components of a common translocation machinery. Ligand blot analysis by Fransen et al. (1998) determined that PEX14 binds to both the PTS1 receptor (PEX5) and weakly with the SH3 domain of PEX13. Biochemical analysis indicated that PEX14 is required for the import of PTS1-containing proteins into peroxisomes.

[85945] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[85946] Albertini, M.; Rehling, P.; Erdmann, R.; Girzalsky, W.; Kiel, J. A. K. W.; Veenhuis, M.; Kunau, W.-H. : Pex14p, a peroxisomal membrane protein binding both receptors of the two PTS-dependent import pathways. Cell 89: 83-92, 1997. ; and

[85947] Fransen, M.; Terlecky, S. R.; Subramani, S. : Identification

of a human PTS1 receptor docking protein directly required for peroxisomal protein import. Proc. Nat. Acad. Sci. 95: 8087-80.

[85948] Further studies establishing the function and utilities of PEX14 are found in John Hopkins OMIM database record ID 601791, and in sited publications numbered 5791 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Polymeric Immunoglobulin Receptor (PIGR, Accession XM_052013) is another VGAM2537 host target gene. PIGR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIGR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIGR BINDING SITE, designated SEQ ID:35938, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85949] Another function of VGAM2537 is therefore inhibition of Polymeric Immunoglobulin Receptor (PIGR, Accession XM_052013). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGR. Phosphoinositide-

3-kinase, Catalytic, Delta Polypeptide (PIK3CD, Accession NM_005026) is another VGAM2537 host target gene. PIK3CD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIK3CD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIK3CD BINDING SITE, designated SEQ ID:11463, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85950] Another function of VGAM2537 is therefore inhibition of Phosphoinositide-3-kinase, Catalytic, Delta Polypeptide (PIK3CD, Accession NM_005026), a gene which regulating cell growth. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3CD. The function of PIK3CD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2434.Procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD, Accession NM_000302) is another

VGAM2537 host target gene. PLOD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLOD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLOD BINDING SITE, designated SEQ ID:5844, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85951] Another function of VGAM2537 is therefore inhibition of Procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD, Accession NM_000302). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLOD. Peanut-like 2 (Drosophila) (PNUTL2, Accession NM_080417) is another VGAM2537 host target gene. PNUTL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PNUTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PNUTL2 BINDING SITE, designated SEQ ID:27837, to the nucleotide

sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85952] Another function of VGAM2537 is therefore inhibition of Peanut-like 2 (Drosophila) (PNUTL2, Accession NM_080417), a gene which is involved in cytokinesis. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNUTL2. The function of PNUTL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.Polymerase (DNA directed), Eta (POLH, Accession NM_006502) is another VGAM2537 host target gene. POLH BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by POLH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POLH BINDING SITE, designated SEQ ID:13250, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85953] Another function of VGAM2537 is therefore inhibition of Polymerase (DNA directed), Eta (POLH, Accession

NM_006502). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLH. Prokineticin 1 (PROK1, Accession NM_032414) is another VGAM2537 host target gene. PROK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PROK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PROK1 BINDING SITE, designated SEQ ID:26200, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85954] Another function of VGAM2537 is therefore inhibition of Prokineticin 1 (PROK1, Accession NM_032414), a gene which induces proliferation, migration and fenestration in capillary endothelial cells derived from endocrine glands. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROK1. The function of PROK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1000.RAB,

Member of RAS Oncogene Family-like 2A (RABL2A, Accession NM_013412) is another VGAM2537 host target gene. RABL2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RABL2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RABL2A BINDING SITE, designated SEQ ID:15079, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85955] Another function of VGAM2537 is therefore inhibition of RAB, Member of RAS Oncogene Family-like 2A (RABL2A, Accession NM_013412). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2A. RAB, Member of RAS Oncogene Family-like 2B (RABL2B, Accession NM_007081) is another VGAM2537 host target gene. RABL2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RABL2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of RABL2B BINDING SITE, designated SEQ ID:13946, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85956] Another function of VGAM2537 is therefore inhibition of RAB, Member of RAS Oncogene Family-like 2B (RABL2B, Accession NM_007081). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2B. RNA (guanine-7-) Methyltransferase (RNMT, Accession NM_003799) is another VGAM2537 host target gene. RNMT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNMT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNMT BINDING SITE, designated SEQ ID:9884, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85957] Another function of VGAM2537 is therefore inhibition of RNA (guanine-7-) Methyltransferase (RNMT, Accession NM_003799), a gene which catalyzes the methylation of GpppN- at the guanine N7 position. Accordingly, utilities

of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNMT. The function of RNMT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.Secretogranin III (SCG3, Accession NM_013243) is another VGAM2537 host target gene. SCG3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SCG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCG3 BINDING SITE, designated SEQ ID:14901, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85958] Another function of VGAM2537 is therefore inhibition of Secretogranin III (SCG3, Accession NM_013243). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCG3. Syndecan 4 (amphiglycan, ryudocan) (SDC4, Accession NM_002999) is another VGAM2537 host target gene. SDC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by SDC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDC4 BINDING SITE, designated SEQ ID:8890, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85959] Another function of VGAM2537 is therefore inhibition of Syndecan 4 (amphiglycan, ryudocan) (SDC4, Accession NM_002999), a gene which is a cell surface proteoglycan. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDC4. The function of SDC4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.Selectin P Ligand (SELPLG, Accession XM_006867) is another VGAM2537 host target gene. SELPLG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SELPLG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SELPLG BINDING SITE, des-

ignated SEQ ID:30017, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85960] Another function of VGAM2537 is therefore inhibition of Selectin P Ligand (SELPLG, Accession XM_006867), a gene which binds to p-, e- and l-selectins, which mediates the tethering and rolling of neutrophils and t-lymphocytes on endothelial cells. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SELPLG. The function of SELPLG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Splicing Factor, Arginine/serine-rich 2, Interacting Protein (SFRS2IP, Accession NM_004719) is another VGAM2537 host target gene. SFRS2IP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFRS2IP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS2IP BINDING SITE, designated SEQ ID:11087, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM

RNA, also designated SEQ ID:5248.

[85961] Another function of VGAM2537 is therefore inhibition of Splicing Factor, Arginine/serine-rich 2, Interacting Protein (SFRS2IP, Accession NM_004719), a gene which plays an essential role in pre-mRNA splicing. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS2IP. The function of SFRS2IP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM700.SH3-domain GRB2-like 1 (SH3GL1, Accession NM_003025) is another VGAM2537 host target gene. SH3GL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3GL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3GL1 BINDING SITE, designated SEQ ID:8962, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85962] Another function of VGAM2537 is therefore inhibition of SH3-domain GRB2-like 1 (SH3GL1, Accession

NM_003025). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3GL1. SHC (Src homology 2 domain containing) Transforming Protein 1 (SHC1, Accession NM_003029) is another VGAM2537 host target gene. SHC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SHC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHC1 BINDING SITE, designated SEQ ID:8970, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85963] Another function of VGAM2537 is therefore inhibition of SHC (Src homology 2 domain containing) Transforming Protein 1 (SHC1, Accession NM_003029), a gene which couples activated growth factor receptors to a signaling pathway. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHC1. The function of SHC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM53.Sialic Acid

Binding Ig-like Lectin 6 (SIGLEC6, Accession XM_009378) is another VGAM2537 host target gene. SIGLEC6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SIGLEC6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIGLEC6 BINDING SITE, designated SEQ ID:30108, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85964] Another function of VGAM2537 is therefore inhibition of Sialic Acid Binding Ig-like Lectin 6 (SIGLEC6, Accession XM_009378), a gene which is a cell adhesion molecule for postnatal neural development. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC6. The function of SIGLEC6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1566.Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 5 (SLC9A5, Accession XM_007868) is another VGAM2537 host target gene. SLC9A5 BINDING SITE1 and SLC9A5 BINDING SITE2 are

HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC9A5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC9A5 BINDING SITE1 and SLC9A5 BINDING SITE2, designated SEQ ID:30064 and SEQ ID:10935 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85965] Another function of VGAM2537 is therefore inhibition of Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 5 (SLC9A5, Accession XM_007868). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC9A5. Syntrophin, Beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1, Accession NM_021021) is another VGAM2537 host target gene. SNTB1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SNTB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNTB1 BINDING SITE, designated SEQ

ID:22011, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85966] Another function of VGAM2537 is therefore inhibition of Syntrophin, Beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1, Accession NM_021021). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNTB1. SRY (sex determining region Y)-box 13 (SOX13, Accession NM_005686) is another VGAM2537 host target gene. SOX13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX13 BINDING SITE, designated SEQ ID:12242, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85967] Another function of VGAM2537 is therefore inhibition of SRY (sex determining region Y)-box 13 (SOX13, Accession NM_005686). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with SOX13. TAF4 RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 135kDa (TAF4, Accession NM_003185) is another VGAM2537 host target gene. TAF4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAF4 BINDING SITE, designated SEQ ID:9162, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85968] Another function of VGAM2537 is therefore inhibition of TAF4 RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 135kDa (TAF4, Accession NM_003185), a gene which plays a central role in mediating promoter responses to various activators and repressors. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAF4. The function of TAF4 has been established by previous studies. Transcription factor TFIID is a multiprotein complex composed of the TATA box-binding protein (TBP; 600075) and multiple TBP-

associated factors (TAFs; OMIM Ref. No. 313650). Tanese et al. (1996) cloned cDNAs encoding 2 subunits of the human TFIID complex: TAFII130 (also symbolized TAF2C1) and TAFII100 (TAF2D; 601787). The longest partial cDNA representing human TAFII130 encodes the predicted C-terminal 947 amino acids of the protein and 1.4 kb of 3-prime untranslated sequence; this cDNA appeared to be missing approximately 100 N-terminal amino acids of TAFII130. Tanese et al. (1996) showed that recombinant TAFII100 and TAFII130 associated with endogenous TAFs and TBP to form a TFIID complex in transfected 293 cells. Their experiments also suggested a role for TAFII130 as a direct coactivator target for Sp1 (OMIM Ref. No. 189906). See also TAF2C2 (OMIM Ref. No. 601689). By biochemical purification and genomic screening, Mengus et al. (1997) obtained a full-length cDNA encoding TAF2C1. Sequence analysis predicted that the 1,083-amino acid protein contains a C-terminal domain and a central region highly homologous to those of TAF2C2. TAF2C1 expression was found to enhance transactivation by the class II nuclear receptors RAR (see OMIM Ref. No. 180240), THRA (see OMIM Ref. No. 190120), and VDR (OMIM Ref. No. 601769) through activation function-2 in the C-terminal ligand-

binding domain.

[85969] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[85970] Mengus, G.; May, M.; Carre, L.; Chambon, P.; Davidson, I. : Human TAF(II)135 potentiates transcriptional activation by the AF-2s of the retinoic acid, vitamin D3, and thyroid hormone receptors in mammalian cells. Genes Dev. 11: 1381-1395, 1997. ; and

[85971] Tanese, N.; Saluja, D.; Vassallo, M. F.; Chen, J.-L.; Admon, A. : Molecular cloning and analysis of two subunits of the human TFIID complex: hTAFII130 and hTAFII100. Proc. Nat. Acad. S.

[85972] Further studies establishing the function and utilities of TAF4 are found in John Hopkins OMIM database record ID 601796, and in sited publications numbered 5225, 6238-623 and 1278 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-ence.TAP Binding Protein (tapasin) (TAPBP, Accession NM_003190) is another VGAM2537 host target gene. TAPBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAPBP, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAPBP BINDING SITE, designated SEQ ID:9179, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85973] Another function of VGAM2537 is therefore inhibition of TAP Binding Protein (tapasin) (TAPBP, Accession NM_003190), a gene which is involved in MHC class I-restricted antigen processing. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP. The function of TAPBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM122.Transcription Factor 1, Hepatic; LF-B1, Hepatic Nuclear Factor (HNF1), Albumin Proximal Factor (TCF1, Accession NM_000545) is another VGAM2537 host target gene. TCF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF1 BINDING SITE, designated SEQ

ID:6146, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85974] Another function of VGAM2537 is therefore inhibition of Transcription Factor 1, Hepatic; LF-B1, Hepatic Nuclear Factor (HNF1), Albumin Proximal Factor (TCF1, Accession NM_000545), a gene which is required for the expression of several liver specific genes. binds to the inverted palindrome 5'-gttaatnattaac-3'. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF1. The function of TCF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1189.Transcription Factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2, Accession NM_030756) is another VGAM2537 host target gene. TCF7L2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TCF7L2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF7L2 BINDING SITE, designated SEQ ID:25040, to the nucleotide

sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85975] Another function of VGAM2537 is therefore inhibition of Transcription Factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2, Accession NM_030756), a gene which is a transcriptional activator; interacts with ITF1 (TCF3); and contains basic helix-loop-helix domain. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF7L2. The function of TCF7L2 has been established by previous studies. The high mobility group (HMG) box is a DNA-binding domain. TCF7 (OMIM Ref. No. 189908), also called TCF1, and LEF1 (OMIM Ref. No. 153245), also called TCF1-alpha, are human lymphoid transcription factors that contain a virtually identical HMG box. By PCR of human genomic DNA using degenerate oligonucleotides based on the HMG boxes of TCF7 and LEF1, Castrop et al. (1992) identified the TCF7L1 (OMIM Ref. No. 604652) and TCF7L2 genes, which they called TCF3 and TCF4, respectively. TCF7L1 and TCF7L2 were not expressed in cells of the lymphoid lineage. The deduced amino acid sequences of the HMG boxes of TCF7L1, TCF7L2, and TCF7 show striking homology. The authors suggested the existence

of a subfamily of TCF7-like HMG box-containing transcription factors. Animal model experiments lend further support to the function of TCF7L2. To study the physiologic role of Tcf4 (which is encoded by the Tcf7l2 gene), Korinek et al. (1998) disrupted Tcf7l2 by homologous recombination. The homozygous null mice died shortly after birth. A single histopathologic abnormality was observed. An apparently normal transition of intestinal endoderm into epithelium occurred at approximately embryonic day (E) 14.5. However, no proliferative compartments were maintained in the prospective crypt regions between the villi. As a consequence, the neonatal epithelium was composed entirely of differentiated, nondividing villus cells. Korinek et al. (1998) concluded that the genetic program controlled by Tcf7l2 maintains the crypt stem cells of the small intestine. The constitutive activity of Tcf4 in APC-deficient epithelial cells may contribute to their malignant transformation by maintaining stem cell characteristics.

[85976] It is appreciated that the abovementioned animal model for TCF7L2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[85977] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[85978] Castrop, J.; van Norren, K.; Clevers, H. : A gene family of HMG-box transcription factors with homology to TCF-1. Nucleic Acids Res. 20: 611 only, 1992. ; and

[85979] Korinek, V.; Barker, N.; Moerer, P.; van Donselaar, E.; Huls, G.; Peters, P. J.; Clevers, H. : Depletion of epithelial stem-cell compartments in the small intestine of mice lacking Tcf-4.

[85980] Further studies establishing the function and utilities of TCF7L2 are found in John Hopkins OMIM database record ID 602228, and in sited publications numbered 5893-589 and 2303-2305 listed in the bibliography section herein-below, which are also hereby incorporated by refer-ence.TEA Domain Family Member 3 (TEAD3, Accession NM_003214) is another VGAM2537 host target gene. TEAD3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TEAD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEAD3 BINDING SITE, designated SEQ ID:9211, to the nucleotide sequence of VGAM2537 RNA,

herein designated VGAM RNA, also designated SEQ ID:5248.

[85981] Another function of VGAM2537 is therefore inhibition of TEA Domain Family Member 3 (TEAD3, Accession NM_003214), a gene which binds to multiple functional elements of the human chorionic somatomammotropin-b gene enhancer. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEAD3. The function of TEAD3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM299.Telomeric Repeat Binding Factor 2 (TERF2, Accession NM_005652) is another VGAM2537 host target gene. TERF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TERF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TERF2 BINDING SITE, designated SEQ ID:12190, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85982] Another function of VGAM2537 is therefore inhibition of Telomeric Repeat Binding Factor 2 (TERF2, Accession NM_005652), a gene which plays a key role in the protective activity of telomeres. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF2. The function of TERF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1689.TIA1 Cytotoxic Granule-associated RNA Binding Protein-like 1 (TIAL1, Accession NM_022333) is another VGAM2537 host target gene. TIAL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIAL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIAL1 BINDING SITE, designated SEQ ID:22741, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85983] Another function of VGAM2537 is therefore inhibition of TIA1 Cytotoxic Granule-associated RNA Binding Protein-like 1 (TIAL1, Accession NM_022333), a gene which pos-

sesses nucleolytic activity against cytotoxic lymphocyte target cells. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIAL1. The function of TIAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM350.Tumor Necrosis Factor (ligand) Superfamily, Member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF4, Accession NM_003326) is another VGAM2537 host target gene. TNFSF4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFSF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF4 BINDING SITE, designated SEQ ID:9330, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85984] Another function of VGAM2537 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF4, Accession NM_003326), a gene which co-

stimulates t cell proliferation and cytokine production. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF4. The function of TNFSF4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM463.Tumor Necrosis Factor (ligand) Superfamily, Member 5 (hyper-IgM syndrome) (TNFSF5, Accession NM_000074) is another VGAM2537 host target gene. TNFSF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF5 BINDING SITE, designated SEQ ID:5518, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85985] Another function of VGAM2537 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 5 (hyper-IgM syndrome) (TNFSF5, Accession NM_000074). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with TNFSF5. Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Epsilon Polypeptide (YWHAE, Accession NM_006761) is another VGAM2537 host target gene. YWHAE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YWHAE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YWHAE BINDING SITE, designated SEQ ID:13613, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85986] Another function of VGAM2537 is therefore inhibition of Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Epsilon Polypeptide (YWHAE, Accession NM_006761), a gene which binds to cdc25 and may facilitate cdc25 interaction with Raf-1 in vivo. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YWHAE. The function of YWHAE and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM656.Zinc Finger Protein 278 (ZNF278, Accession NM_014323) is another VGAM2537 host target gene. ZNF278 BINDING SITE1 through ZNF278 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ZNF278, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF278 BINDING SITE1 through ZNF278 BINDING SITE4, designated SEQ ID:15625, SEQ ID:25774, SEQ ID:25777 and SEQ ID:25784 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85987] Another function of VGAM2537 is therefore inhibition of Zinc Finger Protein 278 (ZNF278, Accession NM_014323), a gene which represses basal transcription as well as RNF4-mediated activation. Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF278. The function of ZNF278 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM414.AP1 Gamma Subunit Binding Pro-

tein 1 (AP1GBP1, Accession NM_080550) is another VGAM2537 host target gene. AP1GBP1 BINDING SITE1 and AP1GBP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AP1GBP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE1 and AP1GBP1 BINDING SITE2, designated SEQ ID:27872 and SEQ ID:13362 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85988] Another function of VGAM2537 is therefore inhibition of AP1 Gamma Subunit Binding Protein 1 (AP1GBP1, Accession NM_080550). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1. Chromosome 14 Open Reading Frame 4 (C14orf4, Accession XM_041104) is another VGAM2537 host target gene. C14orf4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C14orf4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of C14orf4 BINDING SITE, designated SEQ ID:33444, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85989] Another function of VGAM2537 is therefore inhibition of Chromosome 14 Open Reading Frame 4 (C14orf4, Accession XM_041104). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf4. Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575) is another VGAM2537 host target gene. C17orf31 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C17orf31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C17orf31 BINDING SITE, designated SEQ ID:19000, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85990] Another function of VGAM2537 is therefore inhibition of Chromosome 17 Open Reading Frame 31 (C17orf31, Ac-

cession NM_017575). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf31. Chromosome 1 Open Reading Frame 25 (C1orf25, Accession XM_051868) is another VGAM2537 host target gene. C1orf25 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C1orf25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf25 BINDING SITE, designated SEQ ID:35910, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85991] Another function of VGAM2537 is therefore inhibition of Chromosome 1 Open Reading Frame 25 (C1orf25, Accession XM_051868). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf25. CDC14 Cell Division Cycle 14 Homolog B (S. cerevisiae) (CDC14B, Accession NM_033332) is another VGAM2537 host target gene. CDC14B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

CDC14B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDC14B BINDING SITE, designated SEQ ID:27167, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85992] Another function of VGAM2537 is therefore inhibition of CDC14 Cell Division Cycle 14 Homolog B (S. cerevisiae) (CDC14B, Accession NM_033332). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14B. Calsyntenin 3 (CLSTN3, Accession NM_014718) is another VGAM2537 host target gene. CLSTN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLSTN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLSTN3 BINDING SITE, designated SEQ ID:16272, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85993] Another function of VGAM2537 is therefore inhibition of

Calsyntenin 3 (CLSTN3, Accession NM_014718). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLSTN3. COP9 Constitutive Photomorphogenic Homolog Subunit 7B (Arabidopsis) (COPS7B, Accession NM_022730) is another VGAM2537 host target gene. COPS7B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COPS7B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COPS7B BINDING SITE, designated SEQ ID:22933, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85994] Another function of VGAM2537 is therefore inhibition of COP9 Constitutive Photomorphogenic Homolog Subunit 7B (Arabidopsis) (COPS7B, Accession NM_022730). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COPS7B. DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 12 (CHL1-like helicase homolog, S. cerevisiae) (DDX12, Accession XM_006936) is another

VGAM2537 host target gene. DDX12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDX12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDX12 BINDING SITE, designated SEQ ID:30022, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85995] Another function of VGAM2537 is therefore inhibition of DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 12 (CHL1-like helicase homolog, S. cerevisiae) (DDX12, Accession XM_006936). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX12. DEFCAP (Accession NM_014922) is another VGAM2537 host target gene. DEFCAP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DEFCAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DEFCAP BINDING SITE, designated SEQ ID:17201, to the nucleotide sequence of VGAM2537 RNA,

herein designated VGAM RNA, also designated SEQ ID:5248.

[85996] Another function of VGAM2537 is therefore inhibition of DEFCAP (Accession NM_014922). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DEFCAP. Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989) is another VGAM2537 host target gene. DIO2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DIO2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIO2 BINDING SITE, designated SEQ ID:15167, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85997] Another function of VGAM2537 is therefore inhibition of Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIO2. DKFZp434J0617 (Accession NM_032246) is another VGAM2537 host target gene. DKFZp434J0617 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by DKFZp434J0617, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434J0617 BINDING SITE, designated SEQ ID:25982, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85998] Another function of VGAM2537 is therefore inhibition of DKFZp434J0617 (Accession NM_032246). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434J0617. DKFZP434N014 (Accession XM_027012) is another VGAM2537 host target gene. DKFZP434N014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434N014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434N014 BINDING SITE, designated SEQ ID:30389, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[85999] Another function of VGAM2537 is therefore inhibition of DKFZP434N014 (Accession XM_027012). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434N014. DKFZp434P0531 (Accession XM_166410) is another VGAM2537 host target gene. DKFZp434P0531 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434P0531, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434P0531 BINDING SITE, designated SEQ ID:44281, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86000] Another function of VGAM2537 is therefore inhibition of DKFZp434P0531 (Accession XM_166410). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434P0531. DKFZP586N0721 (Accession NM_015400) is another VGAM2537 host target gene. DKFZP586N0721 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

DKFZP586N0721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586N0721 BINDING SITE, designated SEQ ID:17708, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86001] Another function of VGAM2537 is therefore inhibition of DKFZP586N0721 (Accession NM_015400). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586N0721. DKFZp761G2113 (Accession XM_046017) is another VGAM2537 host target gene. DKFZp761G2113 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761G2113, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761G2113 BINDING SITE, designated SEQ ID:34641, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86002] Another function of VGAM2537 is therefore inhibition of

DKFZp761G2113 (Accession XM_046017). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761G2113. EZF-2 (Accession NM_018337) is another VGAM2537 host target gene. EZF-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EZF-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EZF-2 BINDING SITE, designated SEQ ID:20340, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86003] Another function of VGAM2537 is therefore inhibition of EZF-2 (Accession NM_018337). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EZF-2. F-box Only Protein 27 (FBXO27, Accession XM_059045) is another VGAM2537 host target gene. FBXO27 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXO27, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of FBXO27 BINDING SITE, designated SEQ ID:36834, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86004] Another function of VGAM2537 is therefore inhibition of F-box Only Protein 27 (FBXO27, Accession XM_059045). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO27. FHX (Accession NM_018416) is another VGAM2537 host target gene. FHX BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FHX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FHX BINDING SITE, designated SEQ ID:20457, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86005] Another function of VGAM2537 is therefore inhibition of FHX (Accession NM_018416). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHX. FLJ10074 (Accession NM_017988) is another VGAM2537

host target gene. FLJ10074 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10074, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10074 BINDING SITE, designated SEQ ID:19720, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86006] Another function of VGAM2537 is therefore inhibition of FLJ10074 (Accession NM_017988). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10074. FLJ10704 (Accession NM_018185) is another VGAM2537 host target gene. FLJ10704 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10704 BINDING SITE, designated SEQ ID:20032, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86007] Another function of VGAM2537 is therefore inhibition of FLJ10704 (Accession NM_018185). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10704. FLJ11286 (Accession NM_018381) is another VGAM2537 host target gene. FLJ11286 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11286 BINDING SITE, designated SEQ ID:20415, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86008] Another function of VGAM2537 is therefore inhibition of FLJ11286 (Accession NM_018381). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11286. FLJ11939 (Accession NM_024679) is another VGAM2537 host target gene. FLJ11939 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11939, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11939 BINDING SITE, designated SEQ ID:23991, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86009] Another function of VGAM2537 is therefore inhibition of FLJ11939 (Accession NM_024679). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11939. FLJ12541 (Accession NM_022369) is another VGAM2537 host target gene. FLJ12541 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12541, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12541 BINDING SITE, designated SEQ ID:22757, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86010] Another function of VGAM2537 is therefore inhibition of FLJ12541 (Accession NM_022369). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ12541. FLJ12816 (Accession NM_022060) is another VGAM2537 host target gene. FLJ12816 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12816, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12816 BINDING SITE, designated SEQ ID:22603, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86011] Another function of VGAM2537 is therefore inhibition of FLJ12816 (Accession NM_022060). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12816. FLJ12921 (Accession NM_024875) is another VGAM2537 host target gene. FLJ12921 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12921, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12921 BINDING SITE, designated SEQ ID:24309, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM

RNA, also designated SEQ ID:5248.

[86012] Another function of VGAM2537 is therefore inhibition of FLJ12921 (Accession NM_024875). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12921. FLJ14721 (Accession NM_032829) is another VGAM2537 host target gene. FLJ14721 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14721 BINDING SITE, designated SEQ ID:26604, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86013] Another function of VGAM2537 is therefore inhibition of FLJ14721 (Accession NM_032829). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14721. FLJ14950 (Accession NM_032865) is another VGAM2537 host target gene. FLJ14950 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14950, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14950 BINDING SITE, designated SEQ ID:26671, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86014] Another function of VGAM2537 is therefore inhibition of FLJ14950 (Accession NM_032865). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14950. FLJ22596 (Accession NM_025086) is another VGAM2537 host target gene. FLJ22596 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22596, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22596 BINDING SITE, designated SEQ ID:24703, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86015] Another function of VGAM2537 is therefore inhibition of FLJ22596 (Accession NM_025086). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ22596. FLJ23537 (Accession NM_024889) is another VGAM2537 host target gene. FLJ23537 BINDING SITE1 through FLJ23537 BINDING SITE16 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ23537, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23537 BINDING SITE1 through FLJ23537 BINDING SITE16, designated SEQ ID:24362, SEQ ID:24359, SEQ ID:24360, SEQ ID:24361, SEQ ID:24347, SEQ ID:24348, SEQ ID:24349, SEQ ID:24350, SEQ ID:24351, SEQ ID:24352, SEQ ID:24353, SEQ ID:24354, SEQ ID:24355, SEQ ID:24356, SEQ ID:24357 and SEQ ID:24358 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86016] Another function of VGAM2537 is therefore inhibition of FLJ23537 (Accession NM_024889). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23537. FLJ32658 (Accession NM_144688) is another VGAM2537 host target gene. FLJ32658 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ32658, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32658 BINDING SITE, designated SEQ ID:29508, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86017] Another function of VGAM2537 is therefore inhibition of FLJ32658 (Accession NM_144688). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32658. Guanine Nucleotide Binding Protein (G protein), Gamma 3 (GNG3, Accession NM_012202) is another VGAM2537 host target gene. GNG3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GNG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNG3 BINDING SITE, designated SEQ ID:14508, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86018] Another function of VGAM2537 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Gamma 3 (GNG3, Accession NM_012202). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG3. Glycoprotein A33 (transmembrane) (GPA33, Accession NM_005814) is another VGAM2537 host target gene. GPA33 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPA33, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPA33 BINDING SITE, designated SEQ ID:12403, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86019] Another function of VGAM2537 is therefore inhibition of Glycoprotein A33 (transmembrane) (GPA33, Accession NM_005814). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPA33. GR6 (Accession NM_007354) is another VGAM2537 host target gene. GR6 BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by GR6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GR6 BINDING SITE, designated SEQ ID:14281, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86020] Another function of VGAM2537 is therefore inhibition of GR6 (Accession NM_007354). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GR6. GTPBG3 (Accession NM_032620) is another VGAM2537 host target gene. GTPBG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTPBG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTPBG3 BINDING SITE, designated SEQ ID:26333, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86021] Another function of VGAM2537 is therefore inhibition of GTPBG3 (Accession NM_032620). Accordingly, utilities of

VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBG3. Hypermethylated In Cancer 2 (HIC2, Accession XM_036937) is another VGAM2537 host target gene. HIC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIC2 BINDING SITE, designated SEQ ID:32526, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86022] Another function of VGAM2537 is therefore inhibition of Hypermethylated In Cancer 2 (HIC2, Accession XM_036937). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC2. HMT1 HnRNP Methyltransferase-like 3 (S. cerevisiae) (HRMT1L3, Accession NM_019854) is another VGAM2537 host target gene. HRMT1L3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRMT1L3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of HRMT1L3 BINDING SITE, designated SEQ ID:21258, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86023] Another function of VGAM2537 is therefore inhibition of HMT1 HnRNP Methyltransferase-like 3 (S. cerevisiae) (HRMT1L3, Accession NM_019854). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRMT1L3. HTMP10 (Accession NM_033207) is another VGAM2537 host target gene. HTMP10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HTMP10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTMP10 BINDING SITE, designated SEQ ID:27048, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86024] Another function of VGAM2537 is therefore inhibition of HTMP10 (Accession NM_033207). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with HTMP10. IMP-2 (Accession NM_006548) is another VGAM2537 host target gene. IMP-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IMP-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IMP-2 BINDING SITE, designated SEQ ID:13304, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86025] Another function of VGAM2537 is therefore inhibition of IMP-2 (Accession NM_006548). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMP-2. KALI (Accession NM_052931) is another VGAM2537 host target gene. KALI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KALI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KALI BINDING SITE, designated SEQ ID:27488, to the nucleotide sequence of VGAM2537 RNA,

herein designated VGAM RNA, also designated SEQ ID:5248.

[86026] Another function of VGAM2537 is therefore inhibition of KALI (Accession NM_052931). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KALI. KIAA0121 (Accession XM_052386) is another VGAM2537 host target gene. KIAA0121 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0121 BINDING SITE, designated SEQ ID:35968, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86027] Another function of VGAM2537 is therefore inhibition of KIAA0121 (Accession XM_052386). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0121. KIAA0205 (Accession NM_014873) is another VGAM2537 host target gene. KIAA0205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0205 BINDING SITE, designated SEQ ID:17006, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86028] Another function of VGAM2537 is therefore inhibition of KIAA0205 (Accession NM_014873). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0205. KIAA0227 (Accession XM_027236) is another VGAM2537 host target gene. KIAA0227 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0227, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0227 BINDING SITE, designated SEQ ID:30452, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86029] Another function of VGAM2537 is therefore inhibition of KIAA0227 (Accession XM_027236). Accordingly, utilities

of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0227. KIAA0350 (Accession XM_028332) is another VGAM2537 host target gene. KIAA0350 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0350, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0350 BINDING SITE, designated SEQ ID:30666, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86030] Another function of VGAM2537 is therefore inhibition of KIAA0350 (Accession XM_028332). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0350. KIAA0451 (Accession NM_014826) is another VGAM2537 host target gene. KIAA0451 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0451, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0451 BINDING SITE, designated SEQ ID:16804, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86031] Another function of VGAM2537 is therefore inhibition of KIAA0451 (Accession NM_014826). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0451. KIAA0461 (Accession XM_047883) is another VGAM2537 host target gene. KIAA0461 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0461, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0461 BINDING SITE, designated SEQ ID:35074, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86032] Another function of VGAM2537 is therefore inhibition of KIAA0461 (Accession XM_047883). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0461. KIAA0731 (Accession XM_039975) is another VGAM2537 host target gene. KIAA0731 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0731, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0731 BINDING SITE, designated SEQ ID:33240, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86033] Another function of VGAM2537 is therefore inhibition of KIAA0731 (Accession XM_039975). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0731. KIAA0872 (Accession NM_014940) is another VGAM2537 host target gene. KIAA0872 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0872, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0872 BINDING SITE, designated SEQ ID:17244, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86034] Another function of VGAM2537 is therefore inhibition of

KIAA0872 (Accession NM_014940). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0872. KIAA1030 (Accession XM_167789) is another VGAM2537 host target gene. KIAA1030 BINDING SITE1 and KIAA1030 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1030, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1030 BINDING SITE1 and KIAA1030 BINDING SITE2, designated SEQ ID:44820 and SEQ ID:44821 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86035] Another function of VGAM2537 is therefore inhibition of KIAA1030 (Accession XM_167789). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1030. KIAA1205 (Accession XM_046305) is another VGAM2537 host target gene. KIAA1205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1205, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1205 BINDING SITE, designated SEQ ID:34706, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86036] Another function of VGAM2537 is therefore inhibition of KIAA1205 (Accession XM_046305). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1205. KIAA1465 (Accession XM_027396) is another VGAM2537 host target gene. KIAA1465 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1465 BINDING SITE, designated SEQ ID:30501, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86037] Another function of VGAM2537 is therefore inhibition of KIAA1465 (Accession XM_027396). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1465. KIAA1538 (Accession XM_049474) is another VGAM2537 host target gene. KIAA1538 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1538 BINDING SITE, designated SEQ ID:35423, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86038] Another function of VGAM2537 is therefore inhibition of KIAA1538 (Accession XM_049474). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1538. KIAA1750 (Accession XM_043067) is another VGAM2537 host target gene. KIAA1750 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1750, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1750 BINDING SITE, designated SEQ ID:33875, to the

nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86039] Another function of VGAM2537 is therefore inhibition of KIAA1750 (Accession XM_043067). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1750. KIAA1817 (Accession XM_042978) is another VGAM2537 host target gene. KIAA1817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1817 BINDING SITE, designated SEQ ID:33862, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86040] Another function of VGAM2537 is therefore inhibition of KIAA1817 (Accession XM_042978). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1817. KIAA1819 (Accession XM_045716) is another VGAM2537 host target gene. KIAA1819 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA1819, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1819 BINDING SITE, designated SEQ ID:34533, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86041] Another function of VGAM2537 is therefore inhibition of KIAA1819 (Accession XM_045716). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1819. KIAA1853 (Accession XM_045184) is another VGAM2537 host target gene. KIAA1853 BINDING SITE1 and KIAA1853 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1853, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1853 BINDING SITE1 and KIAA1853 BINDING SITE2, designated SEQ ID:34387 and SEQ ID:34386 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86042] Another function of VGAM2537 is therefore inhibition of KIAA1853 (Accession XM_045184). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1853. KIAA1855 (Accession XM_166453) is another VGAM2537 host target gene. KIAA1855 BINDING SITE1 and KIAA1855 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1855, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1855 BINDING SITE1 and KIAA1855 BINDING SITE2, designated SEQ ID:44355 and SEQ ID:25863 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86043] Another function of VGAM2537 is therefore inhibition of KIAA1855 (Accession XM_166453). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1855. KIAA1938 (Accession XM_166407) is another VGAM2537 host target gene. KIAA1938 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1938, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1938 BINDING SITE, designated SEQ ID:44276, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86044] Another function of VGAM2537 is therefore inhibition of KIAA1938 (Accession XM_166407). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1938. Mab-21-like 2 (C. elegans) (MAB21L2, Accession NM_006439) is another VGAM2537 host target gene. MAB21L2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAB21L2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAB21L2 BINDING SITE, designated SEQ ID:13150, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86045] Another function of VGAM2537 is therefore inhibition of

Mab-21-like 2 (C. elegans) (MAB21L2, Accession NM_006439). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAB21L2. METL (Accession NM_018396) is another VGAM2537 host target gene. METL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by METL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of METL BINDING SITE, designated SEQ ID:20433, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86046] Another function of VGAM2537 is therefore inhibition of METL (Accession NM_018396). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with METL. MGC2714 (Accession NM_032299) is another VGAM2537 host target gene. MGC2714 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC2714, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of MGC2714 BINDING SITE, designated SEQ ID:26079, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86047] Another function of VGAM2537 is therefore inhibition of MGC2714 (Accession NM_032299). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2714. MGC4737 (Accession NM_031466) is another VGAM2537 host target gene. MGC4737 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4737, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4737 BINDING SITE, designated SEQ ID:25506, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86048] Another function of VGAM2537 is therefore inhibition of MGC4737 (Accession NM_031466). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4737. MGC4796 (Accession XM_029031) is another

VGAM2537 host target gene. MGC4796 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4796, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4796 BINDING SITE, designated SEQ ID:30830, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86049] Another function of VGAM2537 is therefore inhibition of MGC4796 (Accession XM_029031). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4796. moblak (Accession NM_130807) is another VGAM2537 host target gene. moblak BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by moblak, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of moblak BINDING SITE, designated SEQ ID:28307, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86050] Another function of VGAM2537 is therefore inhibition of moblak (Accession NM_130807). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with moblak. N4BP3 (Accession XM_038920) is another VGAM2537 host target gene. N4BP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by N4BP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of N4BP3 BINDING SITE, designated SEQ ID:32935, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86051] Another function of VGAM2537 is therefore inhibition of N4BP3 (Accession XM_038920). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with N4BP3. NDST4 (Accession NM_022569) is another VGAM2537 host target gene. NDST4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NDST4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDST4 BINDING SITE, designated SEQ ID:22891, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86052] Another function of VGAM2537 is therefore inhibition of NDST4 (Accession NM_022569). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDST4. Neurexophilin 3 (NXPH3, Accession XM_037847) is another VGAM2537 host target gene. NXPH3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NXPH3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXPH3 BINDING SITE, designated SEQ ID:32718, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86053] Another function of VGAM2537 is therefore inhibition of Neurexophilin 3 (NXPH3, Accession XM_037847). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with NXPH3. P450RAI-2 (Accession NM_019885) is another VGAM2537 host target gene. P450RAI-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P450RAI-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P450RAI-2 BINDING SITE, designated SEQ ID:21268, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86054] Another function of VGAM2537 is therefore inhibition of P450RAI-2 (Accession NM_019885). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P450RAI-2. Protein Phosphatase 1, Regulatory Subunit 10 (PPP1R10, Accession NM_002714) is another VGAM2537 host target gene. PPP1R10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R10 BINDING SITE, designated SEQ ID:8575, to the nucleotide sequence of

VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86055] Another function of VGAM2537 is therefore inhibition of Protein Phosphatase 1, Regulatory Subunit 10 (PPP1R10, Accession NM_002714). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R10. PRKRI (Accession NM_006260) is another VGAM2537 host target gene. PRKRI BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRKRI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKRI BINDING SITE, designated SEQ ID:12944, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86056] Another function of VGAM2537 is therefore inhibition of PRKRI (Accession NM_006260). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKRI. Polymerase I and Transcript Release Factor (PTRF, Accession XM_032852) is another VGAM2537 host target gene.

PTRF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTRF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTRF BINDING SITE, designated SEQ ID:31782, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86057] Another function of VGAM2537 is therefore inhibition of Polymerase I and Transcript Release Factor (PTRF, Accession XM_032852). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTRF. RAB35, Member RAS Oncogene Family (RAB35, Accession NM_006861) is another VGAM2537 host target gene. RAB35 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB35, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB35 BINDING SITE, designated SEQ ID:13732, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86058] Another function of VGAM2537 is therefore inhibition of RAB35, Member RAS Oncogene Family (RAB35, Accession NM_006861). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB35. RAB3A Interacting Protein (rabin3)-like 1 (RAB3IL1, Accession NM_013401) is another VGAM2537 host target gene. RAB3IL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB3IL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB3IL1 BINDING SITE, designated SEQ ID:15062, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86059] Another function of VGAM2537 is therefore inhibition of RAB3A Interacting Protein (rabin3)-like 1 (RAB3IL1, Accession NM_013401). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB3IL1. RAI (Accession NM_006663) is another VGAM2537 host target gene. RAI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAI, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI BINDING SITE, designated SEQ ID:13470, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86060] Another function of VGAM2537 is therefore inhibition of RAI (Accession NM_006663). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI. REV1-like (yeast) (REV1L, Accession NM_016316) is another VGAM2537 host target gene. REV1L BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by REV1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of REV1L BINDING SITE, designated SEQ ID:18435, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86061] Another function of VGAM2537 is therefore inhibition of REV1-like (yeast) (REV1L, Accession NM_016316). Accordingly, utilities of VGAM2537 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with REV1L. Sema Domain, Transmembrane Domain (TM), and Cytoplasmic Domain, (semaphorin) 6B (SEMA6B, Accession NM_032108) is another VGAM2537 host target gene. SEMA6B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEMA6B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA6B BINDING SITE, designated SEQ ID:25799, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86062] Another function of VGAM2537 is therefore inhibition of Sema Domain, Transmembrane Domain (TM), and Cytoplasmic Domain, (semaphorin) 6B (SEMA6B, Accession NM_032108). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA6B. Smith-Magenis Syndrome Chromosome Region, Candidate 5 (SMCR5, Accession NM_144774) is another VGAM2537 host target gene. SMCR5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

SMCR5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMCR5 BINDING SITE, designated SEQ ID:29562, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86063] Another function of VGAM2537 is therefore inhibition of Smith-Magenis Syndrome Chromosome Region, Candidate 5 (SMCR5, Accession NM_144774). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCR5. SP192 (Accession NM_021639) is another VGAM2537 host target gene. SP192 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SP192, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SP192 BINDING SITE, designated SEQ ID:22296, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86064] Another function of VGAM2537 is therefore inhibition of

SP192 (Accession NM_021639). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP192. SSH2 (Accession XM_030846) is another VGAM2537 host target gene. SSH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSH2 BINDING SITE, designated SEQ ID:31180, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86065] Another function of VGAM2537 is therefore inhibition of SSH2 (Accession XM_030846). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSH2. Striatin, Calmodulin Binding Protein 3 (STRN3, Accession NM_014574) is another VGAM2537 host target gene. STRN3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by STRN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of STRN3 BINDING SITE, designated SEQ ID:15935, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86066] Another function of VGAM2537 is therefore inhibition of Striatin, Calmodulin Binding Protein 3 (STRN3, Accession NM_014574). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STRN3. Syntaxin 1B2 (STX1B2, Accession NM_052874) is another VGAM2537 host target gene. STX1B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STX1B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STX1B2 BINDING SITE, designated SEQ ID:27454, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86067] Another function of VGAM2537 is therefore inhibition of Syntaxin 1B2 (STX1B2, Accession NM_052874). Accordingly, utilities of VGAM2537 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with STX1B2. TRIP-Br2 (Accession NM_014755) is another VGAM2537 host target gene. TRIP-Br2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP-Br2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:16486, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86068] Another function of VGAM2537 is therefore inhibition of TRIP-Br2 (Accession NM_014755). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP-Br2. TUSP (Accession NM_020245) is another VGAM2537 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21524, to the nucleotide sequence of VGAM2537

RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86069] Another function of VGAM2537 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. Zinc Finger, DHHC Domain Containing 8 (ZDHHC8, Accession XM_033828) is another VGAM2537 host target gene. ZDHHC8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZDHHC8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZDHHC8 BINDING SITE, designated SEQ ID:31961, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86070] Another function of VGAM2537 is therefore inhibition of Zinc Finger, DHHC Domain Containing 8 (ZDHHC8, Accession XM_033828). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZDHHC8. ZIN (Accession NM_013403) is another VGAM2537 host target

gene. ZIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZIN BINDING SITE, designated SEQ ID:15071, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86071] Another function of VGAM2537 is therefore inhibition of ZIN (Accession NM_013403). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZIN. LOC116411 (Accession XM_058095) is another VGAM2537 host target gene. LOC116411 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC116411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC116411 BINDING SITE, designated SEQ ID:36565, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86072] Another function of VGAM2537 is therefore inhibition of

LOC116411 (Accession XM_058095). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116411. LOC120376 (Accession XM_071712) is another VGAM2537 host target gene. LOC120376 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC120376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120376 BINDING SITE, designated SEQ ID:37413, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86073] Another function of VGAM2537 is therefore inhibition of LOC120376 (Accession XM_071712). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120376. LOC123096 (Accession XM_058679) is another VGAM2537 host target gene. LOC123096 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC123096, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC123096 BINDING SITE, designated SEQ ID:36720, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86074] Another function of VGAM2537 is therefore inhibition of LOC123096 (Accession XM_058679). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC123096. LOC124446 (Accession XM_058805) is another VGAM2537 host target gene. LOC124446 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC124446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124446 BINDING SITE, designated SEQ ID:36750, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86075] Another function of VGAM2537 is therefore inhibition of LOC124446 (Accession XM_058805). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124446. LOC133308 (Accession XM_059638) is an-

other VGAM2537 host target gene. LOC133308 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC133308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133308 BINDING SITE, designated SEQ ID:37034, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86076] Another function of VGAM2537 is therefore inhibition of LOC133308 (Accession XM_059638). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133308. LOC142972 (Accession XM_036593) is another VGAM2537 host target gene. LOC142972 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142972, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142972 BINDING SITE, designated SEQ ID:32477, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86077] Another function of VGAM2537 is therefore inhibition of LOC142972 (Accession XM_036593). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142972. LOC143524 (Accession XM_084559) is another VGAM2537 host target gene. LOC143524 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143524, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143524 BINDING SITE, designated SEQ ID:37628, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86078] Another function of VGAM2537 is therefore inhibition of LOC143524 (Accession XM_084559). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143524. LOC143920 (Accession XM_084658) is another VGAM2537 host target gene. LOC143920 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143920, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143920 BINDING SITE, designated SEQ ID:37639, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86079] Another function of VGAM2537 is therefore inhibition of LOC143920 (Accession XM_084658). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143920. LOC144373 (Accession XM_084841) is another VGAM2537 host target gene. LOC144373 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144373, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144373 BINDING SITE, designated SEQ ID:37727, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86080] Another function of VGAM2537 is therefore inhibition of LOC144373 (Accession XM_084841). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144373. LOC144501 (Accession XM_096612) is another VGAM2537 host target gene. LOC144501 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144501, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144501 BINDING SITE, designated SEQ ID:40424, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86081] Another function of VGAM2537 is therefore inhibition of LOC144501 (Accession XM_096612). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144501. LOC144559 (Accession XM_084896) is another VGAM2537 host target gene. LOC144559 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144559, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144559 BINDING SITE, designated SEQ ID:37764, to the nucleotide sequence of VGAM2537 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5248.

[86082] Another function of VGAM2537 is therefore inhibition of LOC144559 (Accession XM_084896). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144559. LOC145255 (Accession XM_096748) is another VGAM2537 host target gene. LOC145255 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145255 BINDING SITE, designated SEQ ID:40528, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86083] Another function of VGAM2537 is therefore inhibition of LOC145255 (Accession XM_096748). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145255. LOC145719 (Accession XM_096848) is another VGAM2537 host target gene. LOC145719 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145719, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145719 BINDING SITE, designated SEQ ID:40575, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86084] Another function of VGAM2537 is therefore inhibition of LOC145719 (Accession XM_096848). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145719. LOC147057 (Accession XM_097166) is another VGAM2537 host target gene. LOC147057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147057 BINDING SITE, designated SEQ ID:40783, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86085] Another function of VGAM2537 is therefore inhibition of LOC147057 (Accession XM_097166). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147057. LOC149478 (Accession XM_086536) is another VGAM2537 host target gene. LOC149478 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149478, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149478 BINDING SITE, designated SEQ ID:38750, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86086] Another function of VGAM2537 is therefore inhibition of LOC149478 (Accession XM_086536). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478. LOC150135 (Accession XM_086785) is another VGAM2537 host target gene. LOC150135 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150135, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150135 BINDING SITE, designated SEQ ID:38845, to

the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86087] Another function of VGAM2537 is therefore inhibition of LOC150135 (Accession XM_086785). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150135. LOC150498 (Accession XM_086931) is another VGAM2537 host target gene. LOC150498 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150498, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150498 BINDING SITE, designated SEQ ID:38984, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86088] Another function of VGAM2537 is therefore inhibition of LOC150498 (Accession XM_086931). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150498. LOC152220 (Accession XM_098176) is another VGAM2537 host target gene. LOC152220 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC152220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152220 BINDING SITE, designated SEQ ID:41441, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86089] Another function of VGAM2537 is therefore inhibition of LOC152220 (Accession XM_098176). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152220. LOC155006 (Accession XM_088117) is another VGAM2537 host target gene. LOC155006 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155006, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155006 BINDING SITE, designated SEQ ID:39524, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86090] Another function of VGAM2537 is therefore inhibition of LOC155006 (Accession XM_088117). Accordingly, utilities

of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155006. LOC157848 (Accession XM_088405) is another VGAM2537 host target gene. LOC157848 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157848, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157848 BINDING SITE, designated SEQ ID:39673, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86091] Another function of VGAM2537 is therefore inhibition of LOC157848 (Accession XM_088405). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157848. LOC167147 (Accession XM_094310) is another VGAM2537 host target gene. LOC167147 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC167147, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC167147 BINDING SITE, designated SEQ ID:40226, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86092] Another function of VGAM2537 is therefore inhibition of LOC167147 (Accession XM_094310). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC167147. LOC199786 (Accession XM_114021) is another VGAM2537 host target gene. LOC199786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199786 BINDING SITE, designated SEQ ID:42619, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86093] Another function of VGAM2537 is therefore inhibition of LOC199786 (Accession XM_114021). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199786. LOC201500 (Accession XM_117101) is another VGAM2537 host target gene. LOC201500 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201500, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201500 BINDING SITE, designated SEQ ID:43223, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86094] Another function of VGAM2537 is therefore inhibition of LOC201500 (Accession XM_117101). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201500. LOC202460 (Accession XM_114493) is another VGAM2537 host target gene. LOC202460 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202460, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202460 BINDING SITE, designated SEQ ID:42982, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86095] Another function of VGAM2537 is therefore inhibition of

LOC202460 (Accession XM_114493). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202460. LOC203248 (Accession XM_114659) is another VGAM2537 host target gene. LOC203248 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203248, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203248 BINDING SITE, designated SEQ ID:43018, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86096] Another function of VGAM2537 is therefore inhibition of LOC203248 (Accession XM_114659). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203248. LOC203504 (Accession XM_117550) is another VGAM2537 host target gene. LOC203504 BINDING SITE1 and LOC203504 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC203504, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203504 BINDING SITE1 and LOC203504 BINDING SITE2, designated SEQ ID:43568 and SEQ ID:43569 respectively, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86097] Another function of VGAM2537 is therefore inhibition of LOC203504 (Accession XM_117550). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203504. LOC221833 (Accession XM_166519) is another VGAM2537 host target gene. LOC221833 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221833, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221833 BINDING SITE, designated SEQ ID:44455, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86098] Another function of VGAM2537 is therefore inhibition of LOC221833 (Accession XM_166519). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC221833. LOC221922 (Accession XM_166555) is another VGAM2537 host target gene. LOC221922 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221922, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221922 BINDING SITE, designated SEQ ID:44532, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86099] Another function of VGAM2537 is therefore inhibition of LOC221922 (Accession XM_166555). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221922. LOC221935 (Accession XM_166537) is another VGAM2537 host target gene. LOC221935 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221935, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221935 BINDING SITE, designated SEQ ID:44500, to

the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86100] Another function of VGAM2537 is therefore inhibition of LOC221935 (Accession XM_166537). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221935. LOC222070 (Accession XM_168433) is another VGAM2537 host target gene. LOC222070 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222070, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222070 BINDING SITE, designated SEQ ID:45179, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86101] Another function of VGAM2537 is therefore inhibition of LOC222070 (Accession XM_168433). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222070. LOC253143 (Accession XM_173062) is another VGAM2537 host target gene. LOC253143 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC253143, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253143 BINDING SITE, designated SEQ ID:46315, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86102] Another function of VGAM2537 is therefore inhibition of LOC253143 (Accession XM_173062). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253143. LOC254387 (Accession XM_170731) is another VGAM2537 host target gene. LOC254387 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254387 BINDING SITE, designated SEQ ID:45488, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86103] Another function of VGAM2537 is therefore inhibition of LOC254387 (Accession XM_170731). Accordingly, utilities

of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254387. LOC255515 (Accession XM_171185) is another VGAM2537 host target gene. LOC255515 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255515 BINDING SITE, designated SEQ ID:45960, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86104] Another function of VGAM2537 is therefore inhibition of LOC255515 (Accession XM_171185). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255515. LOC257463 (Accession XM_048605) is another VGAM2537 host target gene. LOC257463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC257463 BINDING SITE, designated SEQ ID:35209, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86105] Another function of VGAM2537 is therefore inhibition of LOC257463 (Accession XM_048605). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257463. LOC56961 (Accession XM_031857) is another VGAM2537 host target gene. LOC56961 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC56961, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56961 BINDING SITE, designated SEQ ID:31506, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86106] Another function of VGAM2537 is therefore inhibition of LOC56961 (Accession XM_031857). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56961. LOC57105 (Accession NM_020377) is another VGAM2537 host target gene. LOC57105 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57105, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57105 BINDING SITE, designated SEQ ID:21638, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86107] Another function of VGAM2537 is therefore inhibition of LOC57105 (Accession NM_020377). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57105. LOC90643 (Accession XM_033145) is another VGAM2537 host target gene. LOC90643 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90643, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90643 BINDING SITE, designated SEQ ID:31853, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86108] Another function of VGAM2537 is therefore inhibition of

LOC90643 (Accession XM_033145). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90643. LOC90906 (Accession XM_034809) is another VGAM2537 host target gene. LOC90906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90906 BINDING SITE, designated SEQ ID:32149, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86109] Another function of VGAM2537 is therefore inhibition of LOC90906 (Accession XM_034809). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90906. LOC91308 (Accession XM_037600) is another VGAM2537 host target gene. LOC91308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC91308 BINDING SITE, designated SEQ ID:32656, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86110] Another function of VGAM2537 is therefore inhibition of LOC91308 (Accession XM_037600). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91308. LOC91397 (Accession XM_038219) is another VGAM2537 host target gene. LOC91397 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91397 BINDING SITE, designated SEQ ID:32781, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86111] Another function of VGAM2537 is therefore inhibition of LOC91397 (Accession XM_038219). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91397. LOC91974 (Accession XM_041974) is another

VGAM2537 host target gene. LOC91974 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91974, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91974 BINDING SITE, designated SEQ ID:33652, to the nucleotide sequence of VGAM2537 RNA, herein designated VGAM RNA, also designated SEQ ID:5248.

[86112] Another function of VGAM2537 is therefore inhibition of LOC91974 (Accession XM_041974). Accordingly, utilities of VGAM2537 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91974. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2538 (VGAM2538) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86113] VGAM2538 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2538 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[86114] VGAM2538 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pestivirus Reindeer-1. VGAM2538 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86115] VGAM2538 gene encodes a VGAM2538 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2538 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2538 precursor RNA is designated SEQ ID:2524, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2524 is located at position 2796 relative to the genome of Pestivirus Reindeer-1.

[86116] VGAM2538 precursor RNA folds onto itself, forming VGAM2538 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86117] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2538 folded precursor RNA into VGAM2538 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2538 RNA is designated SEQ ID:5249, and is provided hereinbelow with reference to the sequence listing part.

[86118] VGAM2538 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2538 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86119] VGAM2538 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2538 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2538 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2538 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86120] The complementary binding of VGAM2538 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2538 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2538 host target RNA into VGAM2538 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86121] It is appreciated that VGAM2538 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2538 host target genes. The mRNA of each one of this plurality of VGAM2538 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2538 RNA, herein designated VGAM RNA, and which when bound by VGAM2538 RNA causes inhibition of translation of respective one or more VGAM2538 host target proteins.

[86122] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2538 gene, herein designated VGAM GENE, on one or more VGAM2538 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86123] It is yet further appreciated that a function of VGAM2538 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of viral infection by Pestivirus Reindeer-1. Specific functions, and accordingly utilities, of VGAM2538 correlate with, and may be deduced from, the identity of the host target genes which VGAM2538 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86124] Nucleotide sequences of the VGAM2538 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2538 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2538 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2538 are further described hereinbelow with reference to Table 1.

[86125] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2538 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2538 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86126] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2538 gene, herein designated VGAM is inhibition of expression of VGAM2538 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2538 correlate with, and may be deduced from, the identity of the target genes which VGAM2538 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86127] Aquaporin 6, Kidney Specific (AQP6, Accession NM_053286) is a VGAM2538 host target gene. AQP6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AQP6, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:27615, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86128] A function of VGAM2538 is therefore inhibition of Aquaporin 6, Kidney Specific (AQP6, Accession NM_053286), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid-base metabolism. Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6. The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM340.Coagulation Factor VII (serum prothrombin conversion accelerator) (F7, Accession NM_000131) is another VGAM2538 host target gene. F7 BINDING SITE1 and F7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by F7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

F7 BINDING SITE1 and F7 BINDING SITE2, designated SEQ ID:5611 and SEQ ID:21240 respectively, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86129] Another function of VGAM2538 is therefore inhibition of Coagulation Factor VII (serum prothrombin conversion accelerator) (F7, Accession NM_000131). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F7. Translin (TSN, Accession NM_004622) is another VGAM2538 host target gene. TSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSN BINDING SITE, designated SEQ ID:10983, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86130] Another function of VGAM2538 is therefore inhibition of Translin (TSN, Accession NM_004622), a gene which is a DNA binding protein and involved in DNA repair, replication, or recombination. Accordingly, utilities of VGAM2538

include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSN. The function of TSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM98.ARGBP2 (Accession NM_003603) is another VGAM2538 host target gene. ARGBP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARGBP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARGBP2 BINDING SITE, designated SEQ ID:9659, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86131] Another function of VGAM2538 is therefore inhibition of ARGBP2 (Accession NM_003603). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARGBP2. FLJ11800 (Accession NM_024974) is another VGAM2538 host target gene. FLJ11800 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11800, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11800 BINDING SITE, designated SEQ ID:24530, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86132] Another function of VGAM2538 is therefore inhibition of FLJ11800 (Accession NM_024974). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11800. FLJ12649 (Accession NM_024597) is another VGAM2538 host target gene. FLJ12649 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12649 BINDING SITE, designated SEQ ID:23833, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86133] Another function of VGAM2538 is therefore inhibition of FLJ12649 (Accession NM_024597). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12649. GREB1 (Accession XM_051545) is another VGAM2538 host target gene. GREB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GREB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE, designated SEQ ID:35851, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86134] Another function of VGAM2538 is therefore inhibition of GREB1 (Accession XM_051545). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GREB1. MGC3329 (Accession NM_024086) is another VGAM2538 host target gene. MGC3329 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3329, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3329 BINDING SITE, designated SEQ ID:23528, to the nucleotide sequence of

VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86135] Another function of VGAM2538 is therefore inhibition of MGC3329 (Accession NM_024086). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3329. S164 (Accession XM_027330) is another VGAM2538 host target gene. S164 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by S164, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of S164 BINDING SITE, designated SEQ ID:30482, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86136] Another function of VGAM2538 is therefore inhibition of S164 (Accession XM_027330). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with S164. TNF Receptor-associated Factor 3 (TRAF3, Accession XM_007256) is another VGAM2538 host target gene. TRAF3 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by TRAF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAF3 BINDING SITE, designated SEQ ID:30040, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86137] Another function of VGAM2538 is therefore inhibition of TNF Receptor-associated Factor 3 (TRAF3, Accession XM_007256). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF3. LOC220575 (Accession XM_083991) is another VGAM2538 host target gene. LOC220575 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220575, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220575 BINDING SITE, designated SEQ ID:37528, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86138] Another function of VGAM2538 is therefore inhibition of LOC220575 (Accession XM_083991). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220575. LOC90593 (Accession XM_032815) is another VGAM2538 host target gene. LOC90593 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90593, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90593 BINDING SITE, designated SEQ ID:31765, to the nucleotide sequence of VGAM2538 RNA, herein designated VGAM RNA, also designated SEQ ID:5249.

[86139] Another function of VGAM2538 is therefore inhibition of LOC90593 (Accession XM_032815). Accordingly, utilities of VGAM2538 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90593. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2539 (VGAM2539) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[86140] VGAM2539 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2539 was detected is described hereinabove with reference to Figs. 1-8.

[86141] VGAM2539 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pestivirus Giraffe-1. VGAM2539 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86142] VGAM2539 gene encodes a VGAM2539 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2539 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2539 precursor RNA is designated SEQ ID:2525, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2525 is located at position 1159 relative to the genome of Pestivirus Giraffe-1.

[86143] VGAM2539 precursor RNA folds onto itself, forming VGAM2539 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86144] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2539 folded precursor RNA into VGAM2539 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2539 RNA is designated SEQ ID:5250, and is provided hereinbelow with reference to the sequence listing part.

[86145] VGAM2539 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2539 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86146] VGAM2539 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2539 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2539 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86147] The complementary binding of VGAM2539 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2539 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2539 host target RNA into VGAM2539 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86148] It is appreciated that VGAM2539 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2539 host target genes. The mRNA of each one of this plurality of VGAM2539 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2539 RNA, herein designated VGAM RNA, and which when bound by VGAM2539 RNA causes inhibition of translation of respective one or more VGAM2539 host target proteins.

[86149] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2539 gene, herein designated VGAM GENE, on one or more VGAM2539 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86150] It is yet further appreciated that a function of VGAM2539 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of viral infection by Pestivirus Giraffe-1. Specific functions, and accordingly utilities, of VGAM2539 correlate with, and may be deduced from, the identity of the host target genes which VGAM2539 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[86151] Nucleotide sequences of the VGAM2539 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2539 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2539 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2539 are further described hereinbelow with reference to Table 1.

[86152] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2539 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2539 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86153] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2539 gene, herein designated VGAM is inhibition of expression of VGAM2539 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2539 correlate with, and may be deduced from, the identity of the target genes which VGAM2539 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86154] Adenosine Deaminase, RNA-specific (ADAR, Accession NM_001111) is a VGAM2539 host target gene. ADAR BINDING SITE1 through ADAR BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADAR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAR BINDING SITE1 through ADAR BINDING SITE3, designated SEQ ID:6775, SEQ ID:17961 and SEQ ID:17968 respectively, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86155] A function of VGAM2539 is therefore inhibition of Adenosine Deaminase, RNA-specific (ADAR, Accession NM_001111), a gene which converts adenosine to inosine in double-stranded RNA. Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAR. The function of ADAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.CXYorf1 (Accession XM_088704) is another VGAM2539 host target gene. CXYorf1 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXYorf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXYorf1 BINDING SITE, designated SEQ ID:39907, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86156] Another function of VGAM2539 is therefore inhibition of CXYorf1 (Accession XM_088704). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXYorf1. Eukaryotic Translation Initiation Factor 4 Gamma, 3 (EIF4G3, Accession NM_003760) is another VGAM2539 host target gene. EIF4G3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EIF4G3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF4G3 BINDING SITE, designated SEQ ID:9841, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86157] Another function of VGAM2539 is therefore inhibition of Eukaryotic Translation Initiation Factor 4 Gamma, 3 (EIF4G3, Accession NM_003760). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF4G3. FLJ20584 (Accession NM_017891) is another VGAM2539 host target gene. FLJ20584 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20584, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20584 BINDING SITE, designated SEQ ID:19560, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86158] Another function of VGAM2539 is therefore inhibition of FLJ20584 (Accession NM_017891). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20584. FLJ22390 (Accession NM_022746) is another VGAM2539 host target gene. FLJ22390 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22390, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22390 BINDING SITE, designated SEQ ID:22957, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86159] Another function of VGAM2539 is therefore inhibition of FLJ22390 (Accession NM_022746). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22390. KIAA1453 (Accession NM_025090) is another VGAM2539 host target gene. KIAA1453 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1453, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1453 BINDING SITE, designated SEQ ID:24714, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86160] Another function of VGAM2539 is therefore inhibition of KIAA1453 (Accession NM_025090). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1453. MGC14859 (Accession XM_030295) is another VGAM2539 host target gene. MGC14859 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC14859, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14859 BINDING SITE, designated SEQ ID:31005, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86161] Another function of VGAM2539 is therefore inhibition of MGC14859 (Accession XM_030295). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14859. PRO1048 (Accession NM_018497) is another VGAM2539 host target gene. PRO1048 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:20559, to the nucleotide

sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86162] Another function of VGAM2539 is therefore inhibition of PRO1048 (Accession NM_018497). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048. RPH3A (Accession NM_014954) is another VGAM2539 host target gene. RPH3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPH3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPH3A BINDING SITE, designated SEQ ID:17306, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86163] Another function of VGAM2539 is therefore inhibition of RPH3A (Accession NM_014954). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPH3A. Syntaphilin (SNPH, Accession NM_014723) is another VGAM2539 host target gene. SNPH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by SNPH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE, designated SEQ ID:16293, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86164] Another function of VGAM2539 is therefore inhibition of Syntaphilin (SNPH, Accession NM_014723). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH. SPEC1 (Accession NM_020239) is another VGAM2539 host target gene. SPEC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPEC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPEC1 BINDING SITE, designated SEQ ID:21511, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86165] Another function of VGAM2539 is therefore inhibition of SPEC1 (Accession NM_020239). Accordingly, utilities of

VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPEC1. Zinc Finger Protein 300 (ZNF300, Accession NM_052860) is another VGAM2539 host target gene. ZNF300 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF300, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF300 BINDING SITE, designated SEQ ID:27440, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86166] Another function of VGAM2539 is therefore inhibition of Zinc Finger Protein 300 (ZNF300, Accession NM_052860). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF300. LOC146756 (Accession XM_097085) is another VGAM2539 host target gene. LOC146756 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146756, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC146756 BINDING SITE, designated SEQ ID:40737, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86167] Another function of VGAM2539 is therefore inhibition of LOC146756 (Accession XM_097085). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146756. LOC92661 (Accession XM_046465) is another VGAM2539 host target gene. LOC92661 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92661, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92661 BINDING SITE, designated SEQ ID:34722, to the nucleotide sequence of VGAM2539 RNA, herein designated VGAM RNA, also designated SEQ ID:5250.

[86168] Another function of VGAM2539 is therefore inhibition of LOC92661 (Accession XM_046465). Accordingly, utilities of VGAM2539 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92661. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2540 (VGAM2540) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86169] VGAM2540 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2540 was detected is described hereinabove with reference to Figs. 1-8.

[86170] VGAM2540 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Pestivirus Giraffe-1. VGAM2540 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86171] VGAM2540 gene encodes a VGAM2540 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2540 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2540 precursor RNA is designated SEQ ID:2526, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2526 is located at position 4480 relative to the genome of Pestivirus Giraffe-1.

[86172] VGAM2540 precursor RNA folds onto itself, forming VGAM2540 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86173] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2540 folded precursor RNA into VGAM2540 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2540 RNA is designated SEQ ID:5251, and is provided hereinbelow with reference to the sequence listing part.

[86174] VGAM2540 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2540 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86175] VGAM2540 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2540 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2540 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2540 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86176] The complementary binding of VGAM2540 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2540 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2540 host target RNA into VGAM2540 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86177] It is appreciated that VGAM2540 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2540 host target genes. The mRNA of each one of this plurality of VGAM2540 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2540 RNA, herein designated VGAM RNA, and which when bound by VGAM2540 RNA causes inhibition of translation of respective one or more

VGAM2540 host target proteins.

[86178] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2540 gene, herein designated VGAM GENE, on one or more VGAM2540 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86179] It is yet further appreciated that a function of VGAM2540 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2540 include diagnosis, prevention and treatment of viral infection by Pestivirus Giraffe-1. Specific

functions, and accordingly utilities, of VGAM2540 correlate with, and may be deduced from, the identity of the host target genes which VGAM2540 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86180] Nucleotide sequences of the VGAM2540 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2540 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2540 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2540 are further described hereinbelow with reference to Table 1.

[86181] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2540 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2540 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86182] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2540 gene, herein designated VGAM is inhibition of expression of VGAM2540 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2540 correlate with, and may be deduced from, the identity of the target genes which VGAM2540 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86183] FLJ13659 (Accession NM_025189) is a VGAM2540 host target gene. FLJ13659 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13659, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13659 BINDING SITE, designated SEQ ID:24833, to the nucleotide sequence of VGAM2540 RNA, herein designated VGAM RNA, also designated SEQ ID:5251.

[86184] A function of VGAM2540 is therefore inhibition of FLJ13659 (Accession NM_025189). Accordingly, utilities of VGAM2540 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13659. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2541 (VGAM2541) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[86185] VGAM2541 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2541 was detected is described hereinabove with reference to Figs. 1-8.

[86186] VGAM2541 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat Virus. VGAM2541 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86187] VGAM2541 gene encodes a VGAM2541 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2541 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2541 precursor RNA is designated SEQ ID:2527, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2527 is located at position 1698 relative to the genome of Langat Virus.

[86188] VGAM2541 precursor RNA folds onto itself, forming VGAM2541 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86189] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2541 folded precursor RNA into VGAM2541 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2541 RNA is designated SEQ ID:5252, and is provided hereinbelow with reference to the sequence listing part.

[86190] VGAM2541 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2541 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86191] VGAM2541 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2541 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2541 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[86192] The complementary binding of VGAM2541 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2541 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2541 host target RNA into VGAM2541 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86193] It is appreciated that VGAM2541 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2541 host target genes. The mRNA of each one of this plurality of VGAM2541 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2541 RNA, herein designated VGAM RNA, and which when bound by VGAM2541 RNA causes inhibition of translation of respective one or more VGAM2541 host target proteins.

[86194] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2541 gene, herein designated VGAM GENE, on one

or more VGAM2541 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86195] It is yet further appreciated that a function of VGAM2541 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of viral infection by Langat Virus. Specific functions, and accordingly utilities, of VGAM2541 correlate with, and may be deduced from, the identity of the host target genes which VGAM2541 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86196] Nucleotide sequences of the VGAM2541 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2541 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2541 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2541 are further described hereinbelow with reference to Table 1.

[86197] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2541 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2541 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86198] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2541 gene, herein designated VGAM is inhibition of expression of VGAM2541 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2541 correlate with, and may be deduced from, the identity of the target genes which VGAM2541 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86199] Sel-1 Suppressor of Lin-12-like (C. elegans) (SEL1L, Ac-

cession NM_005065) is a VGAM2541 host target gene. SEL1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEL1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEL1L BINDING SITE, designated SEQ ID:11501, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86200] A function of VGAM2541 is therefore inhibition of Sel-1 Suppressor of Lin-12-like (C. elegans) (SEL1L, Accession NM_005065), a gene which may play a role in notch signaling (by similarity). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEL1L. The function of SEL1L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM245.DKFZP434E2135 (Accession NM_030804) is another VGAM2541 host target gene. DKFZP434E2135 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434E2135, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434E2135 BINDING SITE, designated SEQ ID:25114, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86201] Another function of VGAM2541 is therefore inhibition of DKFZP434E2135 (Accession NM_030804). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434E2135. FLJ20958 (Accession NM_022102) is another VGAM2541 host target gene. FLJ20958 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20958, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20958 BINDING SITE, designated SEQ ID:22646, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86202] Another function of VGAM2541 is therefore inhibition of FLJ20958 (Accession NM_022102). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20958. FLJ22833 (Accession NM_022837) is another VGAM2541 host target gene. FLJ22833 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22833, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22833 BINDING SITE, designated SEQ ID:23121, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86203] Another function of VGAM2541 is therefore inhibition of FLJ22833 (Accession NM_022837). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22833. Glutamate Receptor, Ionotropic, N-methyl-D-aspartate 3A (GRIN3A, Accession NM_133445) is another VGAM2541 host target gene. GRIN3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRIN3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

GRIN3A BINDING SITE, designated SEQ ID:28528, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86204] Another function of VGAM2541 is therefore inhibition of Glutamate Receptor, Ionotropic, N-methyl-D-aspartate 3A (GRIN3A, Accession NM_133445). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN3A. KIAA0240 (Accession XM_166479) is another VGAM2541 host target gene. KIAA0240 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0240, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0240 BINDING SITE, designated SEQ ID:44405, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86205] Another function of VGAM2541 is therefore inhibition of KIAA0240 (Accession XM_166479). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0240. KIAA1247 (Accession XM_030036) is another

VGAM2541 host target gene. KIAA1247 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1247 BINDING SITE, designated SEQ ID:30987, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86206] Another function of VGAM2541 is therefore inhibition of KIAA1247 (Accession XM_030036). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1247. KIAA1944 (Accession XM_062545) is another VGAM2541 host target gene. KIAA1944 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1944, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1944 BINDING SITE, designated SEQ ID:37225, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86207] Another function of VGAM2541 is therefore inhibition of KIAA1944 (Accession XM_062545). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1944. LBP-9 (Accession NM_014553) is another VGAM2541 host target gene. LBP-9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LBP-9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LBP-9 BINDING SITE, designated SEQ ID:15874, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86208] Another function of VGAM2541 is therefore inhibition of LBP-9 (Accession NM_014553). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LBP-9. RAI (Accession NM_006663) is another VGAM2541 host target gene. RAI BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of RAI BINDING SITE, designated SEQ ID:13467, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86209] Another function of VGAM2541 is therefore inhibition of RAI (Accession NM_006663). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI. RES4-25 (Accession XM_035572) is another VGAM2541 host target gene. RES4-25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RES4-25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RES4-25 BINDING SITE, designated SEQ ID:32286, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86210] Another function of VGAM2541 is therefore inhibition of RES4-25 (Accession XM_035572). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RES4-25. Syndecan 3 (N-syndecan) (SDC3, Accession

NM_014654) is another VGAM2541 host target gene. SDC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDC3 BINDING SITE, designated SEQ ID:16075, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86211] Another function of VGAM2541 is therefore inhibition of Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDC3. Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession NM_033285) is another VGAM2541 host target gene. TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TP53INP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2, designated SEQ ID:27102

and SEQ ID:36113 respectively, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86212] Another function of VGAM2541 is therefore inhibition of Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession NM_033285). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53INP1. LOC144563 (Accession XM_084897) is another VGAM2541 host target gene. LOC144563 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144563, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144563 BINDING SITE, designated SEQ ID:37766, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86213] Another function of VGAM2541 is therefore inhibition of LOC144563 (Accession XM_084897). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144563. LOC146780 (Accession XM_097086) is an-

other VGAM2541 host target gene. LOC146780 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146780, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146780 BINDING SITE, designated SEQ ID:40742, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86214] Another function of VGAM2541 is therefore inhibition of LOC146780 (Accession XM_097086). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146780. LOC151632 (Accession XM_098098) is another VGAM2541 host target gene. LOC151632 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151632, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151632 BINDING SITE, designated SEQ ID:41381, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86215] Another function of VGAM2541 is therefore inhibition of LOC151632 (Accession XM_098098). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151632. LOC161829 (Accession XM_091161) is another VGAM2541 host target gene. LOC161829 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC161829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161829 BINDING SITE, designated SEQ ID:40037, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86216] Another function of VGAM2541 is therefore inhibition of LOC161829 (Accession XM_091161). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161829. LOC164714 (Accession XM_104657) is another VGAM2541 host target gene. LOC164714 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC164714, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164714 BINDING SITE, designated SEQ ID:42173, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86217] Another function of VGAM2541 is therefore inhibition of LOC164714 (Accession XM_104657). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164714. LOC200904 (Accession XM_117291) is another VGAM2541 host target gene. LOC200904 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200904 BINDING SITE, designated SEQ ID:43360, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86218] Another function of VGAM2541 is therefore inhibition of LOC200904 (Accession XM_117291). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC200904. LOC201252 (Accession XM_113941) is another VGAM2541 host target gene. LOC201252 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201252, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201252 BINDING SITE, designated SEQ ID:42555, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86219] Another function of VGAM2541 is therefore inhibition of LOC201252 (Accession XM_113941). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201252. LOC203083 (Accession XM_117496) is another VGAM2541 host target gene. LOC203083 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203083, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203083 BINDING SITE, designated SEQ ID:43478, to the nucleotide sequence of VGAM2541 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5252.

[86220] Another function of VGAM2541 is therefore inhibition of LOC203083 (Accession XM_117496). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203083. LOC219919 (Accession XM_167785) is another VGAM2541 host target gene. LOC219919 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219919, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219919 BINDING SITE, designated SEQ ID:44800, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86221] Another function of VGAM2541 is therefore inhibition of LOC219919 (Accession XM_167785). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219919. LOC221795 (Accession XM_166491) is another VGAM2541 host target gene. LOC221795 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221795, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221795 BINDING SITE, designated SEQ ID:44423, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86222] Another function of VGAM2541 is therefore inhibition of LOC221795 (Accession XM_166491). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221795. LOC221810 (Accession XM_168222) is another VGAM2541 host target gene. LOC221810 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221810, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221810 BINDING SITE, designated SEQ ID:45081, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86223] Another function of VGAM2541 is therefore inhibition of LOC221810 (Accession XM_168222). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC221810. LOC254176 (Accession XM_173215) is another VGAM2541 host target gene. LOC254176 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254176, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254176 BINDING SITE, designated SEQ ID:46475, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86224] Another function of VGAM2541 is therefore inhibition of LOC254176 (Accession XM_173215). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254176. LOC256515 (Accession XM_172866) is another VGAM2541 host target gene. LOC256515 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256515 BINDING SITE, designated SEQ ID:46144, to

the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86225] Another function of VGAM2541 is therefore inhibition of LOC256515 (Accession XM_172866). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256515. LOC256594 (Accession XM_173127) is another VGAM2541 host target gene. LOC256594 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256594, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256594 BINDING SITE, designated SEQ ID:46377, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86226] Another function of VGAM2541 is therefore inhibition of LOC256594 (Accession XM_173127). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256594. LOC57406 (Accession NM_020676) is another VGAM2541 host target gene. LOC57406 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC57406, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57406 BINDING SITE, designated SEQ ID:21838, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86227] Another function of VGAM2541 is therefore inhibition of LOC57406 (Accession NM_020676). Accordingly, utilities of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57406. LOC92578 (Accession XM_045900) is another VGAM2541 host target gene. LOC92578 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92578, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92578 BINDING SITE, designated SEQ ID:34606, to the nucleotide sequence of VGAM2541 RNA, herein designated VGAM RNA, also designated SEQ ID:5252.

[86228] Another function of VGAM2541 is therefore inhibition of LOC92578 (Accession XM_045900). Accordingly, utilities

of VGAM2541 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92578. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2542 (VGAM2542) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86229] VGAM2542 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2542 was detected is described hereinabove with reference to Figs. 1-8.

[86230] VGAM2542 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat Virus. VGAM2542 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86231] VGAM2542 gene encodes a VGAM2542 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2542 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2542 precursor RNA is desig-

nated SEQ ID:2528, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2528 is located at position 9086 relative to the genome of Langat Virus.

[86232] VGAM2542 precursor RNA folds onto itself, forming VGAM2542 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86233] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2542 folded precursor RNA into VGAM2542 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2542 RNA is designated SEQ ID:5253, and is provided hereinbelow with reference to the sequence

listing part.

[86234] VGAM2542 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2542 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86235] VGAM2542 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2542 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2542 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86236] The complementary binding of VGAM2542 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2542 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2542 host target RNA into VGAM2542 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86237] It is appreciated that VGAM2542 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2542 host target genes. The mRNA of each one of this plurality of VGAM2542 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2542 RNA, herein designated VGAM

RNA, and which when bound by VGAM2542 RNA causes inhibition of translation of respective one or more VGAM2542 host target proteins.

[86238] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2542 gene, herein designated VGAM GENE, on one or more VGAM2542 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86239] It is yet further appreciated that a function of VGAM2542 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2542 include diagnosis, prevention and treatment of viral infection by Langat Virus. Specific functions, and accordingly utilities, of VGAM2542 correlate with, and may be deduced from, the identity of the host target genes which VGAM2542 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86240] Nucleotide sequences of the VGAM2542 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2542 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2542 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2542 are further described hereinbelow with reference to Table 1.

[86241] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2542 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2542 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86242] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2542 gene, herein designated VGAM is

inhibition of expression of VGAM2542 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2542 correlate with, and may be deduced from, the identity of the target genes which VGAM2542 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86243] Adrenergic, Alpha-2A-, Receptor (ADRA2A, Accession NM_000681) is a VGAM2542 host target gene. ADRA2A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ADRA2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADRA2A BINDING SITE, designated SEQ ID:6336, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86244] A function of VGAM2542 is therefore inhibition of Adrenergic, Alpha-2A-, Receptor (ADRA2A, Accession NM_000681), a gene which mediates the effects of epinephrine and norepinephrine. Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

ADRA2A. The function of ADRA2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM602.SMURF1 (Accession XM_166483) is another VGAM2542 host target gene. SMURF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMURF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMURF1 BINDING SITE, designated SEQ ID:44412, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86245] Another function of VGAM2542 is therefore inhibition of SMURF1 (Accession XM_166483). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMURF1. BM039 (Accession NM_018455) is another VGAM2542 host target gene. BM039 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BM039, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of BM039 BINDING SITE, designated SEQ ID:20527, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86246] Another function of VGAM2542 is therefore inhibition of BM039 (Accession NM_018455). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BM039. DKFZP434A0131 (Accession NM_018991) is another VGAM2542 host target gene. DKFZP434A0131 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434A0131, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434A0131 BINDING SITE, designated SEQ ID:21063, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86247] Another function of VGAM2542 is therefore inhibition of DKFZP434A0131 (Accession NM_018991). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP434A0131. FLJ00001 (Accession XM_088525) is another VGAM2542 host target gene. FLJ00001 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00001, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00001 BINDING SITE, designated SEQ ID:39772, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86248] Another function of VGAM2542 is therefore inhibition of FLJ00001 (Accession XM_088525). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00001. FLJ14249 (Accession NM_022460) is another VGAM2542 host target gene. FLJ14249 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14249, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14249 BINDING SITE, designated SEQ ID:22797, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM

RNA, also designated SEQ ID:5253.

[86249] Another function of VGAM2542 is therefore inhibition of FLJ14249 (Accession NM_022460). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14249. Potassium Inwardly-rectifying Channel, Subfamily J, Member 9 (KCNJ9, Accession NM_004983) is another VGAM2542 host target gene. KCNJ9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNJ9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ9 BINDING SITE, designated SEQ ID:11432, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86250] Another function of VGAM2542 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 9 (KCNJ9, Accession NM_004983). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ9. KIAA0789 (Accession XM_033113) is another VGAM2542 host target gene. KIAA0789 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0789 BINDING SITE, designated SEQ ID:31843, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86251] Another function of VGAM2542 is therefore inhibition of KIAA0789 (Accession XM_033113). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0789. Synaptotagmin XII (SYT12, Accession XM_170657) is another VGAM2542 host target gene. SYT12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYT12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYT12 BINDING SITE, designated SEQ ID:45430, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86252] Another function of VGAM2542 is therefore inhibition of Synaptotagmin XII (SYT12, Accession XM_170657). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT12. TED (Accession NM_015686) is another VGAM2542 host target gene. TED BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TED, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TED BINDING SITE, designated SEQ ID:17911, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86253] Another function of VGAM2542 is therefore inhibition of TED (Accession NM_015686). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TED. Ubiquitin Specific Protease 20 (USP20, Accession NM_006676) is another VGAM2542 host target gene. USP20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP20, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP20 BINDING SITE, designated SEQ ID:13501, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86254] Another function of VGAM2542 is therefore inhibition of Ubiquitin Specific Protease 20 (USP20, Accession NM_006676). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP20. LOC135398 (Accession XM_069333) is another VGAM2542 host target gene. LOC135398 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135398, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135398 BINDING SITE, designated SEQ ID:37384, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86255] Another function of VGAM2542 is therefore inhibition of LOC135398 (Accession XM_069333). Accordingly, utilities

of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135398. LOC164537 (Accession XM_104534) is another VGAM2542 host target gene. LOC164537 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC164537, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164537 BINDING SITE, designated SEQ ID:42171, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86256] Another function of VGAM2542 is therefore inhibition of LOC164537 (Accession XM_104534). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164537. LOC169021 (Accession XM_095459) is another VGAM2542 host target gene. LOC169021 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC169021, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC169021 BINDING SITE, designated SEQ ID:40256, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86257] Another function of VGAM2542 is therefore inhibition of LOC169021 (Accession XM_095459). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169021. LOC205095 (Accession XM_119820) is another VGAM2542 host target gene. LOC205095 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC205095, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC205095 BINDING SITE, designated SEQ ID:43601, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86258] Another function of VGAM2542 is therefore inhibition of LOC205095 (Accession XM_119820). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC205095. LOC58525 (Accession XM_086045) is another VGAM2542 host target gene. LOC58525 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC58525, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC58525 BINDING SITE, designated SEQ ID:38454, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86259] Another function of VGAM2542 is therefore inhibition of LOC58525 (Accession XM_086045). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC58525. LOC90246 (Accession XM_030283) is another VGAM2542 host target gene. LOC90246 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90246, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90246 BINDING SITE, designated SEQ ID:30998, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86260] Another function of VGAM2542 is therefore inhibition of

LOC90246 (Accession XM_030283). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90246. LOC92017 (Accession XM_042234) is another VGAM2542 host target gene. LOC92017 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92017, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92017 BINDING SITE, designated SEQ ID:33709, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86261] Another function of VGAM2542 is therefore inhibition of LOC92017 (Accession XM_042234). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92017. LOC93166 (Accession XM_049619) is another VGAM2542 host target gene. LOC93166 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC93166 BINDING SITE, designated SEQ ID:35458, to the nucleotide sequence of VGAM2542 RNA, herein designated VGAM RNA, also designated SEQ ID:5253.

[86262] Another function of VGAM2542 is therefore inhibition of LOC93166 (Accession XM_049619). Accordingly, utilities of VGAM2542 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93166. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2543 (VGAM2543) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86263] VGAM2543 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2543 was detected is described hereinabove with reference to Figs. 1-8.

[86264] VGAM2543 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat Virus. VGAM2543 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86265] VGAM2543 gene encodes a VGAM2543 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2543 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2543 precursor RNA is designated SEQ ID:2529, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2529 is located at position 976 relative to the genome of Langat Virus.

[86266] VGAM2543 precursor RNA folds onto itself, forming VGAM2543 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86267] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2543 folded precursor RNA into VGAM2543 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2543 RNA is designated SEQ ID:5254, and is provided hereinbelow with reference to the sequence listing part.

[86268] VGAM2543 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2543 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86269] VGAM2543 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2543 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2543 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86270] The complementary binding of VGAM2543 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2543 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2543 host target RNA into VGAM2543 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86271] It is appreciated that VGAM2543 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2543 host target genes. The mRNA of each one of this plurality of VGAM2543 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2543 RNA, herein designated VGAM RNA, and which when bound by VGAM2543 RNA causes inhibition of translation of respective one or more VGAM2543 host target proteins.

[86272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2543 gene, herein designated VGAM GENE, on one or more VGAM2543 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86273] It is yet further appreciated that a function of VGAM2543 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of viral infection by Langat Virus. Specific functions, and accordingly utilities, of VGAM2543 correlate with, and may be deduced from, the identity of the host target genes which VGAM2543 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86274] Nucleotide sequences of the VGAM2543 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2543 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2543 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2543 are further described hereinbelow with reference to Table 1.

[86275] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2543 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2543 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86276] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2543 gene, herein designated VGAM is inhibition of expression of VGAM2543 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2543 correlate with, and may be deduced from, the identity of the target genes which VGAM2543 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86277] Endothelin 3 (EDN3, Accession NM_000114) is a VGAM2543 host target gene. EDN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EDN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EDN3 BINDING SITE, designated SEQ ID:5580, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86278] A function of VGAM2543 is therefore inhibition of En-

dothelin 3 (EDN3, Accession NM_000114). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDN3. Inositol Polyphosphate-5-phosphatase, 145kDa (INPP5D, Accession XM_096169) is another VGAM2543 host target gene. INPP5D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by INPP5D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of INPP5D BINDING SITE, designated SEQ ID:40304, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86279] Another function of VGAM2543 is therefore inhibition of Inositol Polyphosphate-5-phosphatase, 145kDa (INPP5D, Accession XM_096169), a gene which hydrolyzes Ins(1,3,4,5)P4 and PtdIns(3,4,5)P3; contains an SH2-domain. Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INPP5D. The function of INPP5D and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to VGAM64.Lymphocyte Cytosolic Protein 1 (L-plastin) (LCP1, Accession NM_002298) is another VGAM2543 host target gene. LCP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LCP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LCP1 BINDING SITE, designated SEQ ID:8083, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86280] Another function of VGAM2543 is therefore inhibition of Lymphocyte Cytosolic Protein 1 (L-plastin) (LCP1, Accession NM_002298), a gene which is involved in t cell antigen receptor mediated signaling. Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCP1. The function of LCP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM418.Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259) is another VGAM2543 host target gene. DOCK3 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by DOCK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DOCK3 BINDING SITE, designated SEQ ID:33032, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86281] Another function of VGAM2543 is therefore inhibition of Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DOCK3. FASTK (Accession NM_025096) is another VGAM2543 host target gene. FASTK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FASTK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FASTK BINDING SITE, designated SEQ ID:24727, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86282] Another function of VGAM2543 is therefore inhibition of FASTK (Accession NM_025096). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FASTK. FLJ20004 (Accession XM_170889) is another VGAM2543 host target gene. FLJ20004 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20004, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20004 BINDING SITE, designated SEQ ID:45643, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86283] Another function of VGAM2543 is therefore inhibition of FLJ20004 (Accession XM_170889). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20004. KIAA0914 (Accession NM_014883) is another VGAM2543 host target gene. KIAA0914 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0914, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0914 BINDING SITE, designated SEQ ID:17035, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86284] Another function of VGAM2543 is therefore inhibition of KIAA0914 (Accession NM_014883). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0914. KIAA1030 (Accession XM_167789) is another VGAM2543 host target gene. KIAA1030 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1030, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1030 BINDING SITE, designated SEQ ID:44819, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86285] Another function of VGAM2543 is therefore inhibition of KIAA1030 (Accession XM_167789). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1030. l(3)mbt-like 2 (Drosophila) (L3MBTL2, Accession XM_114201) is another VGAM2543 host target gene. L3MBTL2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by L3MBTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of L3MBTL2 BINDING SITE, designated SEQ ID:42787, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86286] Another function of VGAM2543 is therefore inhibition of l(3)mbt-like 2 (Drosophila) (L3MBTL2, Accession XM_114201). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with L3MBTL2. MGC15631 (Accession NM_032753) is another VGAM2543 host target gene. MGC15631 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC15631, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15631 BINDING SITE, desig-

nated SEQ ID:26491, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86287] Another function of VGAM2543 is therefore inhibition of MGC15631 (Accession NM_032753). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15631. SCAMP5 (Accession NM_138967) is another VGAM2543 host target gene. SCAMP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAMP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAMP5 BINDING SITE, designated SEQ ID:29073, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86288] Another function of VGAM2543 is therefore inhibition of SCAMP5 (Accession NM_138967). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP5. STATI2 (Accession XM_170547) is another VGAM2543 host target gene. STATI2 BINDING SITE1 and

STATI2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by STATI2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STATI2 BINDING SITE1 and STATI2 BINDING SITE2, designated SEQ ID:45370 and SEQ ID:9959 respectively, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86289] Another function of VGAM2543 is therefore inhibition of STATI2 (Accession XM_170547). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STATI2. LOC196510 (Accession XM_113738) is another VGAM2543 host target gene. LOC196510 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196510, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196510 BINDING SITE, designated SEQ ID:42393, to the nucleotide sequence of VGAM2543 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5254.

[86290] Another function of VGAM2543 is therefore inhibition of LOC196510 (Accession XM_113738). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196510. LOC200093 (Accession XM_032184) is another VGAM2543 host target gene. LOC200093 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200093, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200093 BINDING SITE, designated SEQ ID:31596, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86291] Another function of VGAM2543 is therefore inhibition of LOC200093 (Accession XM_032184). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200093. LOC200220 (Accession XM_114157) is another VGAM2543 host target gene. LOC200220 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200220, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200220 BINDING SITE, designated SEQ ID:42742, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86292] Another function of VGAM2543 is therefore inhibition of LOC200220 (Accession XM_114157). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200220. LOC203536 (Accession XM_114716) is another VGAM2543 host target gene. LOC203536 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203536, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203536 BINDING SITE, designated SEQ ID:43056, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86293] Another function of VGAM2543 is therefore inhibition of LOC203536 (Accession XM_114716). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC203536. LOC91149 (Accession XM_036480) is another VGAM2543 host target gene. LOC91149 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91149, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91149 BINDING SITE, designated SEQ ID:32454, to the nucleotide sequence of VGAM2543 RNA, herein designated VGAM RNA, also designated SEQ ID:5254.

[86294] Another function of VGAM2543 is therefore inhibition of LOC91149 (Accession XM_036480). Accordingly, utilities of VGAM2543 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91149. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2544 (VGAM2544) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86295] VGAM2544 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2544 was detected is described hereinabove with reference to Figs. 1-8.

[86296] VGAM2544 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat Virus. VGAM2544 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86297] VGAM2544 gene encodes a VGAM2544 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2544 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2544 precursor RNA is designated SEQ ID:2530, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2530 is located at position 9387 relative to the genome of Langat Virus.

[86298] VGAM2544 precursor RNA folds onto itself, forming VGAM2544 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86299] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2544 folded precursor RNA into VGAM2544 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2544 RNA is designated SEQ ID:5255, and is provided hereinbelow with reference to the sequence listing part.

[86300] VGAM2544 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2544 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86301] VGAM2544 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2544 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2544 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86302] The complementary binding of VGAM2544 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2544 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2544 host target RNA into VGAM2544 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86303] It is appreciated that VGAM2544 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2544 host target genes. The mRNA of each one of this plurality of VGAM2544 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2544 RNA, herein designated VGAM RNA, and which when bound by VGAM2544 RNA causes inhibition of translation of respective one or more VGAM2544 host target proteins.

[86304] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2544 gene, herein designated VGAM GENE, on one or more VGAM2544 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86305] It is yet further appreciated that a function of VGAM2544 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2544 include diagnosis, prevention and treatment of viral infection by Langat Virus. Specific functions, and accordingly utilities, of VGAM2544 correlate with, and may be deduced from, the identity of the host target genes which VGAM2544 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86306] Nucleotide sequences of the VGAM2544 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2544 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2544 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2544 are further described hereinbelow with reference to Table 1.

[86307] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2544 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2544 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86308] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2544 gene, herein designated VGAM is inhibition of expression of VGAM2544 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2544 correlate with, and may be deduced from, the identity of the target genes which VGAM2544 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86309] Bullous Pemphigoid Antigen 1, 230/240kDa (BPAG1, Accession NM_015548) is a VGAM2544 host target gene. BPAG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BPAG1,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BPAG1 BINDING SITE, designated SEQ ID:17810, to the nucleotide sequence of VGAM2544 RNA, herein designated VGAM RNA, also designated SEQ ID:5255.

[86310] A function of VGAM2544 is therefore inhibition of Bullous Pemphigoid Antigen 1, 230/240kDa (BPAG1, Accession NM_015548), a gene which plays a role in cross- linking actin to other cytoskeletal proteins, binds to microtubules. Accordingly, utilities of VGAM2544 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BPAG1. The function of BPAG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM494.Notch Homolog 2 (Drosophila) (NOTCH2, Accession NM_024408) is another VGAM2544 host target gene. NOTCH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NOTCH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of NOTCH2 BINDING SITE, designated SEQ ID:23650, to the nucleotide sequence of VGAM2544 RNA, herein designated VGAM RNA, also designated SEQ ID:5255.

[86311] Another function of VGAM2544 is therefore inhibition of Notch Homolog 2 (Drosophila) (NOTCH2, Accession NM_024408), a gene which is moderately similar to a region of murine Notch1 and contains an ankyrin repeat. Accordingly, utilities of VGAM2544 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOTCH2. The function of NOTCH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM93.Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273) is another VGAM2544 host target gene. CHST3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHST3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHST3 BINDING SITE, designated SEQ ID:10475, to the nucleotide sequence of

VGAM2544 RNA, herein designated VGAM RNA, also designated SEQ ID:5255.

[86312] Another function of VGAM2544 is therefore inhibition of Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273). Accordingly, utilities of VGAM2544 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST3. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2545 (VGAM2545) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86313] VGAM2545 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2545 was detected is described hereinabove with reference to Figs. 1-8.

[86314] VGAM2545 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat Virus. VGAM2545 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86315] VGAM2545 gene encodes a VGAM2545 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2545 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2545 precursor RNA is designated SEQ ID:2531, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2531 is located at position 3636 relative to the genome of Langat Virus.

[86316] VGAM2545 precursor RNA folds onto itself, forming VGAM2545 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86317] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2545 folded precursor RNA into VGAM2545 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2545 RNA is designated SEQ ID:5256, and is provided hereinbelow with reference to the sequence listing part.

[86318] VGAM2545 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2545 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86319] VGAM2545 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2545 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2545 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86320] The complementary binding of VGAM2545 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2545 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2545 host target RNA into VGAM2545 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86321] It is appreciated that VGAM2545 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2545 host target genes. The mRNA of

each one of this plurality of VGAM2545 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2545 RNA, herein designated VGAM RNA, and which when bound by VGAM2545 RNA causes inhibition of translation of respective one or more VGAM2545 host target proteins.

[86322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2545 gene, herein designated VGAM GENE, on one or more VGAM2545 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[86323] It is yet further appreciated that a function of VGAM2545 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of viral infection by Langat Virus. Specific functions, and accordingly utilities, of VGAM2545 correlate with, and may be deduced from, the identity of the host target genes which VGAM2545 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86324] Nucleotide sequences of the VGAM2545 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2545 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2545 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2545 are further described hereinbelow with reference to Table 1.

[86325] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2545 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2545 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86326] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2545 gene, herein designated VGAM is inhibition of expression of VGAM2545 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2545 correlate with, and may be deduced from, the identity of the target genes which VGAM2545 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86327] Heat Shock Transcription Factor 2 Binding Protein (HSF2BP, Accession NM_007031) is a VGAM2545 host target gene. HSF2BP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSF2BP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSF2BP BINDING SITE, designated SEQ ID:13896, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86328] A function of VGAM2545 is therefore inhibition of Heat Shock Transcription Factor 2 Binding Protein (HSF2BP, Ac-

cession NM_007031). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSF2BP. Myeloid Differentiation Primary Response Gene (88) (MYD88, Accession NM_002468) is another VGAM2545 host target gene. MYD88 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYD88, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYD88 BINDING SITE, designated SEQ ID:8295, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86329] Another function of VGAM2545 is therefore inhibition of Myeloid Differentiation Primary Response Gene (88) (MYD88, Accession NM_002468), a gene which is involved in the toll-like receptor and il-1 receptor signaling pathway in the innate immune response. Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYD88. The function of MYD88 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM18.Protein Tyrosine Phosphatase, Non-receptor Type 7 (PTPN7, Accession NM_002832) is another VGAM2545 host target gene. PTPN7 BINDING SITE1 through PTPN7 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPN7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPN7 BINDING SITE1 through PTPN7 BINDING SITE3, designated SEQ ID:8709, SEQ ID:27887 and SEQ ID:27890 respectively, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86330] Another function of VGAM2545 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type 7 (PTPN7, Accession NM_002832). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN7. Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession XM_171090) is another VGAM2545 host target gene. SNCAIP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

SNCAIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNCAIP BINDING SITE, designated SEQ ID:45903, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86331] Another function of VGAM2545 is therefore inhibition of Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession XM_171090), a gene which promotes formation of cytosolic inclusions in neurons. Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNCAIP. The function of SNCAIP has been established by previous studies. Parkinson disease (PD) is a neurodegenerative disease characterized by tremor, bradykinesia, rigidity, and postural instability. Postmortem examination shows loss of neurons and Lewy bodies, which are cytoplasmic eosinophilic inclusions, in the substantia nigra and other brain regions. A few families have been found to have PD on the basis of mutations, A53T (163890.0001) or A30P (163890.0002), in the gene encoding alpha-synuclein (SNCA). Alpha-synuclein is present in Lewy bodies of pa-

tients with sporadic PD, suggesting that alpha-synuclein may be involved in the pathogenesis of PD. To determine the protein-interaction partners of alpha-synuclein, Engelender et al. (1999) screened human brain libraries in the yeast 2-hybrid system. They identified a novel interacting protein they designated synphilin-1, encoded by the gene SNCAIP. The predicted 919-amino acid synphilin-1 protein contains several protein-protein interaction domains, such as ankyrin-like repeats and a coiled-coil domain. An approximately 4-kb SNCAIP transcript was detected in many human tissues by Northern blot analysis and was particularly enriched in brain, heart, and placenta. Synphilin-1 was present in many regions in brain, including substantia nigra. In immunoblot analyses of human brain, synphilin-1 appeared as a single band of approximately 90 kD in several brain regions, with no differences in the level of expression in controls, patients with PD, or patients with Alzheimer disease (OMIM Ref. No. 104300). They found that alpha-synuclein interacts in vivo with synphilin-1 in neurons. Cotransfection of both proteins (but not control proteins) in HEK293 cells yielded cytoplasmic eosinophilic inclusions. Engelender et al. (2000) determined that the human SNCAIP gene contains 10 ex-

ons and has a highly polymorphic GT repeat within intron 5 that is suitable for linkage analysis in families with Parkinson disease. Using immunohistochemistry in human postmortem brain tissue, they found that synphilin-1 protein, like alpha-synuclein protein, is present in neuropil.

[86332] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[86333] Engelender, S.; Kaminsky, Z.; Guo, X.; Sharp, A. H.; Amaravi, R. K.; Kleiderlein, J. J.; Margolis, R. L.; Troncoso, J. C.; Lanahan, A. A.; Worley, P. F.; Dawson, V. L.; Dawson, T. M.; Ross, C. A. : Synphilin-1 associates with alpha-synuclein and promotes the formation of cytosolic inclusions. Nature Genet. 22: 110-114, 1999. ; and

[86334] Engelender, S.; Wanner, T.; Kleiderlein, J. J.; Wakabayashi, K.; Tsuji, S.; Takahashi, H.; Ashworth, R.; Margolis, R. L.; Ross, C. A. : Organization of the human synphilin-1 gene, a ca.

[86335] Further studies establishing the function and utilities of SNCAIP are found in John Hopkins OMIM database record ID 603779, and in sited publications numbered 244 and 8193 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Butyrophilin,

Subfamily 2, Member A2 (BTN2A2, Accession NM_006995) is another VGAM2545 host target gene. BTN2A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTN2A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTN2A2 BINDING SITE, designated SEQ ID:13857, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86336] Another function of VGAM2545 is therefore inhibition of Butyrophilin, Subfamily 2, Member A2 (BTN2A2, Accession NM_006995). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN2A2. DKFZP434A0131 (Accession NM_018991) is another VGAM2545 host target gene. DKFZP434A0131 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434A0131, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434A0131 BINDING SITE, designated SEQ ID:21061, to the nucleotide

sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86337] Another function of VGAM2545 is therefore inhibition of DKFZP434A0131 (Accession NM_018991). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434A0131. F-box Only Protein 27 (FBXO27, Accession XM_059045) is another VGAM2545 host target gene. FBXO27 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXO27, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXO27 BINDING SITE, designated SEQ ID:36833, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86338] Another function of VGAM2545 is therefore inhibition of F-box Only Protein 27 (FBXO27, Accession XM_059045). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO27. FLJ31762 (Accession NM_144601) is another VGAM2545 host target gene.

FLJ31762 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ31762, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ31762 BINDING SITE, designated SEQ ID:29417, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86339] Another function of VGAM2545 is therefore inhibition of FLJ31762 (Accession NM_144601). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31762. KIAA0057 (Accession NM_012288) is another VGAM2545 host target gene. KIAA0057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0057 BINDING SITE, designated SEQ ID:14620, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86340] Another function of VGAM2545 is therefore inhibition of KIAA0057 (Accession NM_012288). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0057. PAX Transcription Activation Domain Interacting Protein 1 Like (PAXIP1L, Accession XM_046538) is another VGAM2545 host target gene. PAXIP1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAXIP1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAXIP1L BINDING SITE, designated SEQ ID:34738, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86341] Another function of VGAM2545 is therefore inhibition of PAX Transcription Activation Domain Interacting Protein 1 Like (PAXIP1L, Accession XM_046538). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAXIP1L. PRO0456 (Accession NM_014127) is another VGAM2545 host target gene. PRO0456 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by PRO0456, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0456 BINDING SITE, designated SEQ ID:15394, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86342] Another function of VGAM2545 is therefore inhibition of PRO0456 (Accession NM_014127). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0456. PRO2964 (Accession NM_018547) is another VGAM2545 host target gene. PRO2964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2964 BINDING SITE, designated SEQ ID:20630, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86343] Another function of VGAM2545 is therefore inhibition of PRO2964 (Accession NM_018547). Accordingly, utilities of

VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2964. Serine Palmitoyltransferase, Long Chain Base Subunit 2 (SPTLC2, Accession NM_004863) is another VGAM2545 host target gene. SPTLC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPTLC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPTLC2 BINDING SITE, designated SEQ ID:11276, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86344] Another function of VGAM2545 is therefore inhibition of Serine Palmitoyltransferase, Long Chain Base Subunit 2 (SPTLC2, Accession NM_004863). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPTLC2. Signal Sequence Receptor, Gamma (translocon-associated protein gamma) (SSR3, Accession NM_007107) is another VGAM2545 host target gene. SSR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSR3, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSR3 BINDING SITE, designated SEQ ID:13970, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86345] Another function of VGAM2545 is therefore inhibition of Signal Sequence Receptor, Gamma (translocon-associated protein gamma) (SSR3, Accession NM_007107). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSR3. Zinc Finger Protein 145 (Kruppel-like, expressed in promyelocytic leukemia) (ZNF145, Accession NM_006006) is another VGAM2545 host target gene. ZNF145 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF145, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF145 BINDING SITE, designated SEQ ID:12617, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86346] Another function of VGAM2545 is therefore inhibition of Zinc Finger Protein 145 (Kruppel-like, expressed in promyelocytic leukemia) (ZNF145, Accession NM_006006). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF145. LOC115073 (Accession XM_055193) is another VGAM2545 host target gene. LOC115073 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC115073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115073 BINDING SITE, designated SEQ ID:36238, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86347] Another function of VGAM2545 is therefore inhibition of LOC115073 (Accession XM_055193). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115073. LOC145719 (Accession XM_096848) is another VGAM2545 host target gene. LOC145719 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC145719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145719 BINDING SITE, designated SEQ ID:40570, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86348] Another function of VGAM2545 is therefore inhibition of LOC145719 (Accession XM_096848). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145719. LOC145720 (Accession XM_096846) is another VGAM2545 host target gene. LOC145720 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145720, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145720 BINDING SITE, designated SEQ ID:40560, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86349] Another function of VGAM2545 is therefore inhibition of LOC145720 (Accession XM_096846). Accordingly, utilities

of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145720. LOC197114 (Accession XM_116987) is another VGAM2545 host target gene. LOC197114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197114 BINDING SITE, designated SEQ ID:43184, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86350] Another function of VGAM2545 is therefore inhibition of LOC197114 (Accession XM_116987). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197114. LOC197117 (Accession XM_116989) is another VGAM2545 host target gene. LOC197117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC197117 BINDING SITE, designated SEQ ID:43193, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86351] Another function of VGAM2545 is therefore inhibition of LOC197117 (Accession XM_116989). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197117. LOC222252 (Accession XM_168640) is another VGAM2545 host target gene. LOC222252 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222252, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222252 BINDING SITE, designated SEQ ID:45286, to the nucleotide sequence of VGAM2545 RNA, herein designated VGAM RNA, also designated SEQ ID:5256.

[86352] Another function of VGAM2545 is therefore inhibition of LOC222252 (Accession XM_168640). Accordingly, utilities of VGAM2545 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222252. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2546 (VGAM2546) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86353] VGAM2546 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2546 was detected is described hereinabove with reference to Figs. 1-8.

[86354] VGAM2546 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat Virus. VGAM2546 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86355] VGAM2546 gene encodes a VGAM2546 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2546 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2546 precursor RNA is designated SEQ ID:2532, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2532 is located at position 3420 relative to the genome of Langat Virus.

[86356] VGAM2546 precursor RNA folds onto itself, forming VGAM2546 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86357] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2546 folded precursor RNA into VGAM2546 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2546 RNA is designated SEQ ID:5257, and is provided hereinbelow with reference to the sequence listing part.

[86358] VGAM2546 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2546 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2546 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86359] VGAM2546 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2546 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2546 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86360] The complementary binding of VGAM2546 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2546 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2546 host target RNA into VGAM2546 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86361] It is appreciated that VGAM2546 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2546 host target genes. The mRNA of each one of this plurality of VGAM2546 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2546 RNA, herein designated VGAM RNA, and which when bound by VGAM2546 RNA causes inhibition of translation of respective one or more VGAM2546 host target proteins.

[86362] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2546 gene, herein designated VGAM GENE, on one or more VGAM2546 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86363] It is yet further appreciated that a function of VGAM2546 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of viral infection by Langat Virus. Specific functions, and accordingly utilities, of VGAM2546 correlate with, and may be deduced from, the identity of the host

target genes which VGAM2546 binds and inhibits, and the function of these host target genes, as elaborated herein-below.

[86364] Nucleotide sequences of the VGAM2546 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2546 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2546 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2546 are further described hereinbelow with reference to Table 1.

[86365] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2546 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2546 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86366] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2546 gene, herein designated VGAM is inhibition of expression of VGAM2546 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2546 correlate with, and may be deduced from, the identity of the target genes which VGAM2546

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86367] CGTHBA (Accession NM_012075) is a VGAM2546 host target gene. CGTHBA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CGTHBA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGTHBA BINDING SITE, designated SEQ ID:14358, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86368] A function of VGAM2546 is therefore inhibition of CGTHBA (Accession NM_012075). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGTHBA. Collagen, Type XI, Alpha 2 (COL11A2, Accession NM_080680) is another VGAM2546 host target gene. COL11A2 BINDING SITE1 and COL11A2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COL11A2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the comple-

mentarity of the nucleotide sequences of COL11A2 BINDING SITE1 and COL11A2 BINDING SITE2, designated SEQ ID:27975 and SEQ ID:27980 respectively, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86369] Another function of VGAM2546 is therefore inhibition of Collagen, Type XI, Alpha 2 (COL11A2, Accession NM_080680). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL11A2. FLJ20464 (Accession NM_017834) is another VGAM2546 host target gene. FLJ20464 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20464 BINDING SITE, designated SEQ ID:19500, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86370] Another function of VGAM2546 is therefore inhibition of FLJ20464 (Accession NM_017834). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20464. KIAA0515 (Accession XM_033380) is another VGAM2546 host target gene. KIAA0515 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0515 BINDING SITE, designated SEQ ID:31920, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86371] Another function of VGAM2546 is therefore inhibition of KIAA0515 (Accession XM_033380). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0515. KIAA0542 (Accession XM_038520) is another VGAM2546 host target gene. KIAA0542 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0542, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0542 BINDING SITE, designated SEQ ID:32857, to the

nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86372] Another function of VGAM2546 is therefore inhibition of KIAA0542 (Accession XM_038520). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0542. VRP (Accession NM_007063) is another VGAM2546 host target gene. VRP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by VRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VRP BINDING SITE, designated SEQ ID:13926, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86373] Another function of VGAM2546 is therefore inhibition of VRP (Accession NM_007063). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VRP. LOC148756 (Accession XM_097516) is another VGAM2546 host target gene. LOC148756 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC148756, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148756 BINDING SITE, designated SEQ ID:40902, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86374] Another function of VGAM2546 is therefore inhibition of LOC148756 (Accession XM_097516). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148756. LOC254413 (Accession XM_173141) is another VGAM2546 host target gene. LOC254413 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254413, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254413 BINDING SITE, designated SEQ ID:46399, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86375] Another function of VGAM2546 is therefore inhibition of LOC254413 (Accession XM_173141). Accordingly, utilities

of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254413. LOC255974 (Accession XM_173706) is another VGAM2546 host target gene. LOC255974 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255974, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255974 BINDING SITE, designated SEQ ID:46555, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86376] Another function of VGAM2546 is therefore inhibition of LOC255974 (Accession XM_173706). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255974. LOC256306 (Accession XM_172976) is another VGAM2546 host target gene. LOC256306 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256306, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC256306 BINDING SITE, designated SEQ ID:46235, to the nucleotide sequence of VGAM2546 RNA, herein designated VGAM RNA, also designated SEQ ID:5257.

[86377] Another function of VGAM2546 is therefore inhibition of LOC256306 (Accession XM_172976). Accordingly, utilities of VGAM2546 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256306. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2547 (VGAM2547) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86378] VGAM2547 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2547 was detected is described hereinabove with reference to Figs. 1-8.

[86379] VGAM2547 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Langat Virus. VGAM2547 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86380] VGAM2547 gene encodes a VGAM2547 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2547 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2547 precursor RNA is designated SEQ ID:2533, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2533 is located at position 6689 relative to the genome of Langat Virus.

[86381] VGAM2547 precursor RNA folds onto itself, forming VGAM2547 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86382] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2547 folded precursor RNA into VGAM2547 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2547 RNA is designated SEQ ID:5258, and is provided hereinbelow with reference to the sequence listing part.

[86383] VGAM2547 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2547 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86384] VGAM2547 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2547 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2547 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86385] The complementary binding of VGAM2547 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2547 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2547 host target RNA into VGAM2547 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86386] It is appreciated that VGAM2547 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2547 host target genes. The mRNA of each one of this plurality of VGAM2547 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2547 RNA, herein designated VGAM RNA, and which when bound by VGAM2547 RNA causes inhibition of translation of respective one or more VGAM2547 host target proteins.

[86387] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2547 gene, herein designated VGAM GENE, on one or more VGAM2547 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86388] It is yet further appreciated that a function of VGAM2547 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of viral infection by Langat Virus. Specific functions, and accordingly utilities, of VGAM2547 correlate with, and may be deduced from, the identity of the host target genes which VGAM2547 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86389] Nucleotide sequences of the VGAM2547 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2547 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2547 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2547 are further described hereinbelow with reference to Table 1.

[86390] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2547 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2547 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86391] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2547 gene, herein designated VGAM is inhibition of expression of VGAM2547 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2547 correlate with, and may be deduced from, the identity of the target genes which VGAM2547 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86392] Guanylate Cyclase 1, Soluble, Alpha 3 (GUCY1A3, Accession XM_032838) is a VGAM2547 host target gene. GUCY1A3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GUCY1A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GUCY1A3 BINDING SITE, designated SEQ ID:31779, to the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, also designated SEQ ID:5258.

[86393] A function of VGAM2547 is therefore inhibition of Guany-

late Cyclase 1, Soluble, Alpha 3 (GUCY1A3, Accession XM_032838), a gene which is alpha 1 (alpha 3) subunit of soluble guanylate cyclase and forms a heterodimer with GUCY1B3 that converts GTP to cGMP. Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GUCY1A3. The function of GUCY1A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Baculoviral IAP Repeat-containing 8 (BIRC8, Accession NM_033341) is another VGAM2547 host target gene. BIRC8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BIRC8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIRC8 BINDING SITE, designated SEQ ID:27197, to the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, also designated SEQ ID:5258.

[86394] Another function of VGAM2547 is therefore inhibition of Baculoviral IAP Repeat-containing 8 (BIRC8, Accession NM_033341). Accordingly, utilities of VGAM2547 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC8. Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273) is another VGAM2547 host target gene. CHST3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHST3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHST3 BINDING SITE, designated SEQ ID:10477, to the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, also designated SEQ ID:5258.

[86395] Another function of VGAM2547 is therefore inhibition of Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273). Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST3. FLJ10201 (Accession NM_018023) is another VGAM2547 host target gene. FLJ10201 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10201, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10201 BINDING SITE, designated SEQ ID:19761, to the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, also designated SEQ ID:5258.

[86396] Another function of VGAM2547 is therefore inhibition of FLJ10201 (Accession NM_018023). Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10201. FLJ33069 (Accession NM_144649) is another VGAM2547 host target gene. FLJ33069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ33069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ33069 BINDING SITE, designated SEQ ID:29475, to the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, also designated SEQ ID:5258.

[86397] Another function of VGAM2547 is therefore inhibition of FLJ33069 (Accession NM_144649). Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ33069. KIAA0478 (Accession NM_014870) is another VGAM2547 host target gene. KIAA0478 BINDING SITE1 and KIAA0478 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0478, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0478 BINDING SITE1 and KIAA0478 BINDING SITE2, designated SEQ ID:16974 and SEQ ID:16975 respectively, to the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, also designated SEQ ID:5258.

[86398] Another function of VGAM2547 is therefore inhibition of KIAA0478 (Accession NM_014870). Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0478. LOC130271 (Accession XM_059415) is another VGAM2547 host target gene. LOC130271 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC130271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC130271 BINDING SITE, designated SEQ ID:36986, to the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, also designated SEQ ID:5258.

[86399] Another function of VGAM2547 is therefore inhibition of LOC130271 (Accession XM_059415). Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130271. LOC143943 (Accession XM_096504) is another VGAM2547 host target gene. LOC143943 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143943, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143943 BINDING SITE, designated SEQ ID:40382, to the nucleotide sequence of VGAM2547 RNA, herein designated VGAM RNA, also designated SEQ ID:5258.

[86400] Another function of VGAM2547 is therefore inhibition of LOC143943 (Accession XM_096504). Accordingly, utilities of VGAM2547 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143943. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2548 (VGAM2548) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86401] VGAM2548 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2548 was detected is described hereinabove with reference to Figs. 1-8.

[86402] VGAM2548 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saccharomyces Cerevisiae Virus L-A. VGAM2548 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86403] VGAM2548 gene encodes a VGAM2548 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2548 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2548 precursor RNA is designated SEQ ID:2534, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2534 is located at position 4007 relative to the

genome of Saccharomyces Cerevisiae Virus L-A.

[86404] VGAM2548 precursor RNA folds onto itself, forming VGAM2548 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86405] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2548 folded precursor RNA into VGAM2548 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2548 RNA is designated SEQ ID:5259, and is provided hereinbelow with reference to the sequence listing part.

[86406] VGAM2548 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2548 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86407] VGAM2548 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2548 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2548 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86408] The complementary binding of VGAM2548 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2548 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2548 host target RNA into VGAM2548 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86409] It is appreciated that VGAM2548 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2548 host target genes. The mRNA of each one of this plurality of VGAM2548 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2548 RNA, herein designated VGAM RNA, and which when bound by VGAM2548 RNA causes inhibition of translation of respective one or more VGAM2548 host target proteins.

[86410] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2548 gene, herein designated VGAM GENE, on one or more VGAM2548 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86411] It is yet further appreciated that a function of VGAM2548 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2548 include diagnosis, prevention and treatment of viral infection by Saccharomyces Cerevisiae Virus L-A. Specific functions, and accordingly utilities, of

VGAM2548 correlate with, and may be deduced from, the identity of the host target genes which VGAM2548 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86412] Nucleotide sequences of the VGAM2548 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2548 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2548 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2548 are further described hereinbelow with reference to Table 1.

[86413] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2548 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2548 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86414] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2548 gene, herein designated VGAM is inhibition of expression of VGAM2548 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2548 correlate with, and may be deduced

from, the identity of the target genes which VGAM2548 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86415] DKFZP434P0721 (Accession XM_033181) is a VGAM2548 host target gene. DKFZP434P0721 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434P0721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434P0721 BINDING SITE, designated SEQ ID:31867, to the nucleotide sequence of VGAM2548 RNA, herein designated VGAM RNA, also designated SEQ ID:5259.

[86416] A function of VGAM2548 is therefore inhibition of DKFZP434P0721 (Accession XM_033181). Accordingly, utilities of VGAM2548 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P0721. LOC149386 (Accession XM_097631) is another VGAM2548 host target gene. LOC149386 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149386, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149386 BINDING SITE, designated SEQ ID:40984, to the nucleotide sequence of VGAM2548 RNA, herein designated VGAM RNA, also designated SEQ ID:5259.

[86417] Another function of VGAM2548 is therefore inhibition of LOC149386 (Accession XM_097631). Accordingly, utilities of VGAM2548 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149386. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2549 (VGAM2549) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86418] VGAM2549 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2549 was detected is described hereinabove with reference to Figs. 1-8.

[86419] VGAM2549 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saccharomyces Cerevisiae Virus L-A. VGAM2549 host target gene, herein des-

ignated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86420] VGAM2549 gene encodes a VGAM2549 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2549 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2549 precursor RNA is designated SEQ ID:2535, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2535 is located at position 2612 relative to the genome of Saccharomyces Cerevisiae Virus L-A.

[86421] VGAM2549 precursor RNA folds onto itself, forming VGAM2549 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86422] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2549 folded precursor RNA into VGAM2549

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2549 RNA is designated SEQ ID:5260, and is provided hereinbelow with reference to the sequence listing part.

[86423] VGAM2549 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2549 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86424] VGAM2549 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2549 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2549 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86425] The complementary binding of VGAM2549 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2549 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2549 host target RNA into VGAM2549 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[86426] It is appreciated that VGAM2549 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2549 host target genes. The mRNA of each one of this plurality of VGAM2549 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2549 RNA, herein designated VGAM RNA, and which when bound by VGAM2549 RNA causes inhibition of translation of respective one or more VGAM2549 host target proteins.

[86427] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2549 gene, herein designated VGAM GENE, on one or more VGAM2549 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86428] It is yet further appreciated that a function of VGAM2549 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of viral infection by Saccharomyces Cerevisiae Virus L-A. Specific functions, and accordingly utilities, of VGAM2549 correlate with, and may be deduced from, the identity of the host target genes which VGAM2549 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86429] Nucleotide sequences of the VGAM2549 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2549 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2549 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2549 are further described hereinbelow with reference to Table 1.

[86430] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2549 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2549 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86431] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2549 gene, herein designated VGAM is inhibition of expression of VGAM2549 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2549 correlate with, and may be deduced from, the identity of the target genes which VGAM2549 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86432] DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 6 (RNA helicase, 54kDa) (DDX6, Accession NM_004397) is a VGAM2549 host target gene. DDX6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DDX6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDX6 BINDING SITE, designated SEQ ID:10645, to the nucleotide sequence of

VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86433] A function of VGAM2549 is therefore inhibition of DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 6 (RNA helicase, 54kDa) (DDX6, Accession NM_004397), a gene which is putative RNA helicases. Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX6. The function of DDX6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM179.Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NM_004513) is another VGAM2549 host target gene. IL16 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IL16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL16 BINDING SITE, designated SEQ ID:10840, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86434] Another function of VGAM2549 is therefore inhibition of

Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NM_004513), a gene which modulates T-cell activation. Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL16. The function of IL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM819.Kinesin Family Member 5B (KIF5B, Accession NM_004521) is another VGAM2549 host target gene. KIF5B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIF5B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIF5B BINDING SITE, designated SEQ ID:10850, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86435] Another function of VGAM2549 is therefore inhibition of Kinesin Family Member 5B (KIF5B, Accession NM_004521), a gene which is a microtubule-associated force-producing protein that may play a role in organelle transport. Accordingly, utilities of VGAM2549 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with KIF5B. The function of KIF5B has been established by previous studies. Kinesins are microtubule-based motor proteins involved in the transport of organelles in eukaryotic cells. They typically consist of 2 identical, approximately 110- to 120-kD heavy chains and 2 identical, approximately 60- to 70-kD light chains. The heavy chain contains 3 domains: a globular N-terminal motor domain, which converts the chemical energy of ATP into a motile force along microtubules in 1 fixed direction; a central alpha-helical rod domain, which enables the 2 heavy chains to dimerize; and a globular C-terminal domain, which interacts with light chains and possibly an organelle receptor. By screening a human placenta cDNA library with a probe based on a conserved region of the Drosophila and squid kinesin heavy chains (KHCs), Navone et al. (1992) isolated cDNAs encoding KNS1. The predicted 963-amino acid protein has 63% sequence identity to the Drosophila KHC. Immunoblot analysis using antibodies against squid KHC detected a 120-kD protein in CV-1 monkey kidney epithelial cells. Immunofluorescence studies showed that KNS1 expressed in CV-1 cells had both a diffuse distribution and a fila-

mentous staining pattern that coaligned with microtubules but not vimentin (VIM; 193060) intermediate filaments; the KNS1 N- and C-terminal domains, but not the alpha-helical rod domain, also colocalized with microtubules. Kamal et al. (2000) demonstrated that the axonal transport of APP in neurons is mediated by the direct binding of APP to the kinesin light chain (OMIM Ref. No. 600025) subunit of kinesin-I. Kamal et al. (2001) identified an axonal membrane compartment that contains APP, beta-secretase (OMIM Ref. No. 604252), and presenilin-1 (OMIM Ref. No. 104311). The fast anterograde axonal transport of this compartment is mediated by APP and kinesin-I. Proteolytic processing of APP can occur in the compartment in vitro and in vivo in axons. This proteolysis generates amyloid-beta and a carboxy-terminal fragment of APP, and liberates kinesin-I from the membrane. Kamal et al. (2001) concluded that APP functions as a kinesin-I membrane receptor, mediating the axonal transport of beta-secretase and presenilin-1, and that processing of APP to amyloid-beta by secretases can occur in an axonal membrane compartment transported by kinesin-I. Animal model experiments lend further support to the function of KIF5B. Tanaka et al. (1998) disrupted

the mouse kif5B gene by homologous recombination. The kif5B -/- mice were embryonic lethal with a severe growth retardation at 9.5 to 11.5 days postcoitum. To analyze the significance of this conventional kinesin heavy chain in organelle transport, the authors studied the distribution of major organelles in the extraembryonic cells. The null mutant cells impaired lysosomal dispersion, while brefeldin A could normally induce the breakdown of their Golgi apparatus. More prominently, their mitochondria abnormally clustered in the perinuclear region. This mitochondrial phenotype was reversed by an exogenous expression of KIF5B, and a subcellular fractionation revealed that KIF5B was associated with mitochondria. These data indicated that kinesin is essential for mitochondrial and lysosomal dispersion rather than for the Golgi-to-endoplasmic reticulum traffic in these cells.

[86436] It is appreciated that the abovementioned animal model for KIF5B is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[86437] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[86438] Kamal, A.; Stokin, G. B.; Yang, Z.; Xia, C.; Goldstein, L. S. : Axonal transport of amyloid precursor protein is mediated by direct binding to the kinesin light chain subunit of kinesin-I. Neuron 28: 449-459, 2000. ; and

[86439] Navone, F.; Niclas, J.; Hom-Booher, N.; Sparks, L.; Bernstein, H. D.; McCaffrey, G.; Vale, R. D. : Cloning and expression of a human kinesin heavy chain gene: interaction of the COOH-te.

[86440] Further studies establishing the function and utilities of KIF5B are found in John Hopkins OMIM database record ID 602809, and in sited publications numbered 12307-1055 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Oxidative-stress Responsive 1 (OSR1, Accession NM_005109) is another VGAM2549 host target gene. OSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSR1 BINDING SITE, designated SEQ ID:11587, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86441] Another function of VGAM2549 is therefore inhibition of Oxidative-stress Responsive 1 (OSR1, Accession NM_005109), a gene which mediats stress-activated signals. Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSR1. The function of OSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM538.APEG1 (Accession XM_050966) is another VGAM2549 host target gene. APEG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APEG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APEG1 BINDING SITE, designated SEQ ID:35694, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86442] Another function of VGAM2549 is therefore inhibition of APEG1 (Accession XM_050966). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APEG1.

Doublecortin and CaM Kinase-like 1 (DCAMKL1, Accession NM_004734) is another VGAM2549 host target gene. DCAMKL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DCAMKL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCAMKL1 BINDING SITE, designated SEQ ID:11115, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86443] Another function of VGAM2549 is therefore inhibition of Doublecortin and CaM Kinase-like 1 (DCAMKL1, Accession NM_004734). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCAMKL1. FLJ10853 (Accession NM_018246) is another VGAM2549 host target gene. FLJ10853 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10853, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10853 BINDING SITE, designated

SEQ ID:20211, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86444] Another function of VGAM2549 is therefore inhibition of FLJ10853 (Accession NM_018246). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10853. KIAA0397 (Accession XM_029438) is another VGAM2549 host target gene. KIAA0397 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0397 BINDING SITE, designated SEQ ID:30896, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86445] Another function of VGAM2549 is therefore inhibition of KIAA0397 (Accession XM_029438). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0397. KIAA1344 (Accession XM_051699) is another VGAM2549 host target gene. KIAA1344 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1344, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1344 BINDING SITE, designated SEQ ID:35869, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86446] Another function of VGAM2549 is therefore inhibition of KIAA1344 (Accession XM_051699). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1344. TED (Accession NM_015686) is another VGAM2549 host target gene. TED BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TED, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TED BINDING SITE, designated SEQ ID:17919, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86447] Another function of VGAM2549 is therefore inhibition of

TED (Accession NM_015686). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TED. LOC147229 (Accession XM_085742) is another VGAM2549 host target gene. LOC147229 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147229 BINDING SITE, designated SEQ ID:38319, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86448] Another function of VGAM2549 is therefore inhibition of LOC147229 (Accession XM_085742). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147229. LOC219722 (Accession XM_167593) is another VGAM2549 host target gene. LOC219722 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219722, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC219722 BINDING SITE, designated SEQ ID:44710, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86449] Another function of VGAM2549 is therefore inhibition of LOC219722 (Accession XM_167593). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219722. LOC253758 (Accession XM_173067) is another VGAM2549 host target gene. LOC253758 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253758, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253758 BINDING SITE, designated SEQ ID:46321, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86450] Another function of VGAM2549 is therefore inhibition of LOC253758 (Accession XM_173067). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253758. LOC253955 (Accession XM_170486) is an-

other VGAM2549 host target gene. LOC253955 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253955 BINDING SITE, designated SEQ ID:45327, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86451] Another function of VGAM2549 is therefore inhibition of LOC253955 (Accession XM_170486). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253955. LOC51026 (Accession NM_016072) is another VGAM2549 host target gene. LOC51026 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51026 BINDING SITE, designated SEQ ID:18140, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86452] Another function of VGAM2549 is therefore inhibition of LOC51026 (Accession NM_016072). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51026. LOC91574 (Accession XM_039310) is another VGAM2549 host target gene. LOC91574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91574, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91574 BINDING SITE, designated SEQ ID:33047, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86453] Another function of VGAM2549 is therefore inhibition of LOC91574 (Accession XM_039310). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91574. LOC92231 (Accession XM_043734) is another VGAM2549 host target gene. LOC92231 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92231, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92231 BINDING SITE, designated SEQ ID:34010, to the nucleotide sequence of VGAM2549 RNA, herein designated VGAM RNA, also designated SEQ ID:5260.

[86454] Another function of VGAM2549 is therefore inhibition of LOC92231 (Accession XM_043734). Accordingly, utilities of VGAM2549 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92231. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2550 (VGAM2550) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86455] VGAM2550 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2550 was detected is described hereinabove with reference to Figs. 1-8.

[86456] VGAM2550 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Saccharomyces Cerevisiae Virus L-A. VGAM2550 host target gene, herein des-

ignated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86457] VGAM2550 gene encodes a VGAM2550 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2550 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2550 precursor RNA is designated SEQ ID:2536, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2536 is located at position 4405 relative to the genome of Saccharomyces Cerevisiae Virus L-A.

[86458] VGAM2550 precursor RNA folds onto itself, forming VGAM2550 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86459] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2550 folded precursor RNA into VGAM2550

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2550 RNA is designated SEQ ID:5261, and is provided hereinbelow with reference to the sequence listing part.

[86460] VGAM2550 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2550 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86461] VGAM2550 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2550 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2550 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86462] The complementary binding of VGAM2550 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2550 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2550 host target RNA into VGAM2550 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[86463] It is appreciated that VGAM2550 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2550 host target genes. The mRNA of each one of this plurality of VGAM2550 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2550 RNA, herein designated VGAM RNA, and which when bound by VGAM2550 RNA causes inhibition of translation of respective one or more VGAM2550 host target proteins.

[86464] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2550 gene, herein designated VGAM GENE, on one or more VGAM2550 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86465] It is yet further appreciated that a function of VGAM2550 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2550 include diagnosis, prevention and treatment of viral infection by Saccharomyces Cerevisiae Virus L-A. Specific functions, and accordingly utilities, of VGAM2550 correlate with, and may be deduced from, the identity of the host target genes which VGAM2550 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86466] Nucleotide sequences of the VGAM2550 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2550 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2550 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2550 are further described hereinbelow with reference to Table 1.

[86467] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2550 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2550 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86468] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2550 gene, herein designated VGAM is inhibition of expression of VGAM2550 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2550 correlate with, and may be deduced from, the identity of the target genes which VGAM2550 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86469] Cyclic Nucleotide Gated Channel Beta 3 (CNGB3, Accession NM_019098) is a VGAM2550 host target gene. CNGB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNGB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNGB3 BINDING SITE, designated SEQ ID:21176, to the nucleotide sequence of VGAM2550 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5261.

[86470] A function of VGAM2550 is therefore inhibition of Cyclic Nucleotide Gated Channel Beta 3 (CNGB3, Accession NM_019098). Accordingly, utilities of VGAM2550 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNGB3. FK506 Binding Protein 5 (FKBP5, Accession NM_004117) is another VGAM2550 host target gene. FKBP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FKBP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKBP5 BINDING SITE, designated SEQ ID:10324, to the nucleotide sequence of VGAM2550 RNA, herein designated VGAM RNA, also designated SEQ ID:5261.

[86471] Another function of VGAM2550 is therefore inhibition of FK506 Binding Protein 5 (FKBP5, Accession NM_004117). Accordingly, utilities of VGAM2550 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKBP5. KIAA0939 (Accession XM_030524) is another VGAM2550 host target gene. KIAA0939 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by KIAA0939, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0939 BINDING SITE, designated SEQ ID:31065, to the nucleotide sequence of VGAM2550 RNA, herein designated VGAM RNA, also designated SEQ ID:5261.

[86472] Another function of VGAM2550 is therefore inhibition of KIAA0939 (Accession XM_030524). Accordingly, utilities of VGAM2550 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0939. LOC200010 (Accession XM_117174) is another VGAM2550 host target gene. LOC200010 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200010 BINDING SITE, designated SEQ ID:43277, to the nucleotide sequence of VGAM2550 RNA, herein designated VGAM RNA, also designated SEQ ID:5261.

[86473] Another function of VGAM2550 is therefore inhibition of

LOC200010 (Accession XM_117174). Accordingly, utilities of VGAM2550 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200010. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2551 (VGAM2551) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86474] VGAM2551 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2551 was detected is described hereinabove with reference to Figs. 1-8.

[86475] VGAM2551 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice Yellow Stunt Virus. VGAM2551 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86476] VGAM2551 gene encodes a VGAM2551 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2551 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2551 precursor RNA is designated SEQ ID:2537, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2537 is located at position 11536 relative to the genome of Rice Yellow Stunt Virus.

[86477] VGAM2551 precursor RNA folds onto itself, forming VGAM2551 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86478] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2551 folded precursor RNA into VGAM2551 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide se-

quence of VGAM2551 RNA is designated SEQ ID:5262, and is provided hereinbelow with reference to the sequence listing part.

[86479] VGAM2551 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2551 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86480] VGAM2551 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2551 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2551 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86481] The complementary binding of VGAM2551 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2551 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2551 host target RNA into VGAM2551 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86482] It is appreciated that VGAM2551 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2551 host target genes. The mRNA of each one of this plurality of VGAM2551 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2551 RNA, herein designated VGAM RNA, and which when bound by VGAM2551 RNA causes inhibition of translation of respective one or more VGAM2551 host target proteins.

[86483] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2551 gene, herein designated VGAM GENE, on one or more VGAM2551 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86484] It is yet further appreciated that a function of VGAM2551

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of viral infection by Rice Yellow Stunt Virus. Specific functions, and accordingly utilities, of VGAM2551 correlate with, and may be deduced from, the identity of the host target genes which VGAM2551 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86485] Nucleotide sequences of the VGAM2551 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2551 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2551 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2551 are further described hereinbelow with reference to Table 1.

[86486] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2551 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2551 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86487] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2551 gene, herein designated VGAM is inhibition of expression of VGAM2551 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2551 correlate with, and may be deduced from, the identity of the target genes which VGAM2551 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86488] Aryl-hydrocarbon Receptor Nuclear Translocator 2 (ARNT2, Accession NM_014862) is a VGAM2551 host target gene. ARNT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARNT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARNT2 BINDING SITE, designated SEQ ID:16936, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86489] A function of VGAM2551 is therefore inhibition of Aryl-hydrocarbon Receptor Nuclear Translocator 2 (ARNT2, Accession NM_014862), a gene which specifically recognizes the xenobiotic response element (xre). Accordingly, utili-

ties of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARNT2. The function of ARNT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM345.Bromodomain Adjacent to Zinc Finger Domain, 1B (BAZ1B, Accession NM_032408) is another VGAM2551 host target gene. BAZ1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAZ1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAZ1B BINDING SITE, designated SEQ ID:26190, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86490] Another function of VGAM2551 is therefore inhibition of Bromodomain Adjacent to Zinc Finger Domain, 1B (BAZ1B, Accession NM_032408). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ1B. Chromosome 1 Open Reading Frame 6 (C1orf6, Accession NM_020131) is another VGAM2551 host target gene.

C1orf6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf6 BINDING SITE, designated SEQ ID:21327, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86491] Another function of VGAM2551 is therefore inhibition of Chromosome 1 Open Reading Frame 6 (C1orf6, Accession NM_020131), a gene which may link ataxin-1 with the chaperone and ubiquitin/proteasome pathways . Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf6. The function of C1orf6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1286.Centromere Protein F, 350/400ka (mitosin) (CENPF, Accession NM_016343) is another VGAM2551 host target gene. CENPF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CENPF, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENPF BINDING SITE, designated SEQ ID:18470, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86492] Another function of VGAM2551 is therefore inhibition of Centromere Protein F, 350/400ka (mitosin) (CENPF, Accession NM_016343), a gene which is a protein of the nuclear matrix and regulates mitosis. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPF. The function of CENPF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1709.Chediak-Higashi Syndrome 1 (CHS1, Accession NM_000081) is another VGAM2551 host target gene. CHS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHS1 BINDING SITE, designated SEQ ID:5523,

to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86493] Another function of VGAM2551 is therefore inhibition of Chediak-Higashi Syndrome 1 (CHS1, Accession NM_000081), a gene which may sort endosomal resident proteins into late multivesicular endosome. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHS1. The function of CHS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.Cartilage Linking Protein 1 (CRTL1, Accession NM_001884) is another VGAM2551 host target gene. CRTL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CRTL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRTL1 BINDING SITE, designated SEQ ID:7615, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86494] Another function of VGAM2551 is therefore inhibition of

Cartilage Linking Protein 1 (CRTL1, Accession NM_001884), a gene which stabilize the aggregates of proteoglycan monomers with hyaluronic acid. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTL1. The function of CRTL1 has been established by previous studies. Using a cDNA for the chicken protein, Osborne-Lawrence et al. (1990) isolated 2 overlapping clones that encode the entire human cartilage link protein. The deduced amino acid sequence is 354 residues long and shows a striking degree of similarity to porcine, rat, and chicken link protein sequences. By in situ hybridization, they mapped the gene to 5q13-q14.1. Dudhia et al. (1994) found that the CRTL1 gene comprises 5 exons and is spread over more than 60 kb. Primer extension and S1 nuclease protection analysis revealed transcription initiation to be 315 bases upstream from the translation initiation codon Cartilage link protein stabilizes aggregates of aggrecan and hyaluronan, giving cartilage its tensile strength and elasticity. Cartilage provides the template for endochondral ossification and is crucial for determining the length and width of the skeleton. During endochondral bone formation, hypertrophic chondrocytes die and

the cartilage is replaced with bone matrix. Watanabe and Yamada (1999) generated targeted mutations in cartilage link protein of mice (Crtl1). Homozygotes showed defects in cartilage development and delayed bone formation with short limbs and craniofacial anomalies. Most homozygous Crtl1 mutant mice died shortly after birth due to respiratory failure, but some survived and developed progressive dwarfism and lordosis of the cervical spine. They showed small epiphyses, slightly flared metaphyses of long bones, and flattened vertebrae, characteristic of spondyloepiphyseal dysplasias. The cartilage contained significantly reduced aggrecan depositions in the hypertrophic zone and decreased numbers of prehypertrophic and hypertrophic chondrocytes. Reduced Indian hedgehog (OMIM Ref. No. 600726) expression was observed in prehypertrophic chondrocytes, and apoptosis was inhibited in hypertrophic chondrocytes. The results indicated that cartilage link protein is important for the formation of proteoglycan aggregates and normal organization of hypertrophic chondrocytes, and suggested that cartilage matrix has a role in chondrocyte differentiation and maturation

[86495] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[86496] Osborne-Lawrence, S. L.; Sinclair, A. K.; Hicks, R. C.; Lacey, S. W.; Eddy, R. L., Jr.; Byers, M. G.; Shows, T. B.; Duby, A. D. : Complete amino acid sequence of human cartilage link protein (CRTL1) deduced from cDNA clones and chromosomal assignment of the gene. Genomics 8: 562-567, 1990. ; and

[86497] Watanabe, H.; Yamada, Y. : Mice lacking link protein develop dwarfism and craniofacial abnormalities. Nature Genet. 21: 225-229, 1999.

[86498] Further studies establishing the function and utilities of CRTL1 are found in John Hopkins OMIM database record ID 115435, and in sited publications numbered 3 and 12584-12586 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Death-associated Protein Kinase 1 (DAPK1, Accession NM_004938) is another VGAM2551 host target gene. DAPK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAPK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAPK1 BINDING SITE, designated SEQ

ID:11386, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86499] Another function of VGAM2551 is therefore inhibition of Death-associated Protein Kinase 1 (DAPK1, Accession NM_004938). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAPK1. Heterogeneous Nuclear Ribonucleoprotein D-like (HNRPDL, Accession NM_005463) is another VGAM2551 host target gene. HNRPDL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HNRPDL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPDL BINDING SITE, designated SEQ ID:11954, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86500] Another function of VGAM2551 is therefore inhibition of Heterogeneous Nuclear Ribonucleoprotein D-like (HNRPDL, Accession NM_005463), a gene which binds to rna molecules that contain au-rich elements. Accordingly,

utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPDL. The function of HNRPDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM144.Neuronal Pentraxin I (NPTX1, Accession NM_002522) is another VGAM2551 host target gene. NPTX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPTX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPTX1 BINDING SITE, designated SEQ ID:8356, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86501] Another function of VGAM2551 is therefore inhibition of Neuronal Pentraxin I (NPTX1, Accession NM_002522), a gene which may be involved in synaptic uptake of extracellular material and is very strongly similar to rat NP1. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTX1. The function of NPTX1 and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.Perilipin (PLIN, Accession NM_002666) is another VGAM2551 host target gene. PLIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLIN BINDING SITE, designated SEQ ID:8535, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86502] Another function of VGAM2551 is therefore inhibition of Perilipin (PLIN, Accession NM_002666). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLIN. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 12A (PPP1R12A, Accession NM_002480) is another VGAM2551 host target gene. PPP1R12A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R12A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of PPP1R12A BINDING SITE, designated SEQ ID:8304, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86503] Another function of VGAM2551 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 12A (PPP1R12A, Accession NM_002480), a gene which regulates the interaction of actin and myosin. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12A. The function of PPP1R12A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM838.Prostaglandin F2 Receptor Negative Regulator (PTGFRN, Accession XM_040709) is another VGAM2551 host target gene. PTGFRN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTGFRN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGFRN BINDING SITE, designated SEQ ID:33361, to the nucleotide sequence of VGAM2551 RNA,

herein designated VGAM RNA, also designated SEQ ID:5262.

[86504] Another function of VGAM2551 is therefore inhibition of Prostaglandin F2 Receptor Negative Regulator (PTGFRN, Accession XM_040709), a gene which inhibits the binding of prostaglandin f2-alpha (pgf2- alpha) to its specific fp receptor. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGFRN. The function of PTGFRN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.Paxillin (PXN, Accession NM_002859) is another VGAM2551 host target gene. PXN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PXN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PXN BINDING SITE, designated SEQ ID:8759, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86505] Another function of VGAM2551 is therefore inhibition of Paxillin (PXN, Accession NM_002859), a gene which may

be involved in p53-dependent apoptosis. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PXN. The function of PXN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM132.SMURF1 (Accession XM_166483) is another VGAM2551 host target gene. SMURF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMURF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMURF1 BINDING SITE, designated SEQ ID:44409, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86506] Another function of VGAM2551 is therefore inhibition of SMURF1 (Accession XM_166483). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMURF1. Src Homology Three (SH3) and Cysteine Rich Domain (STAC, Accession NM_003149) is another VGAM2551 host target gene. STAC BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by STAC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAC BINDING SITE, designated SEQ ID:9119, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86507] Another function of VGAM2551 is therefore inhibition of Src Homology Three (SH3) and Cysteine Rich Domain (STAC, Accession NM_003149), a gene which is probably involved in a neuron-specific signal transduction. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAC. The function of STAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM331.TEM8 (Accession NM_032208) is another VGAM2551 host target gene. TEM8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates

the complementarity of the nucleotide sequences of TEM8 BINDING SITE, designated SEQ ID:25917, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86508] Another function of VGAM2551 is therefore inhibition of TEM8 (Accession NM_032208), a gene which is a tumor-specific endothelial marker. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEM8. The function of TEM8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1489.Tenascin C (hexabrachion) (TNC, Accession NM_002160) is another VGAM2551 host target gene. TNC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNC BINDING SITE, designated SEQ ID:7934, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86509] Another function of VGAM2551 is therefore inhibition of

Tenascin C (hexabrachion) (TNC, Accession NM_002160), a gene which has epidermal growth factor-like repeats. Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNC. The function of TNC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM808.Tropomyosin 4 (TPM4, Accession NM_003290) is another VGAM2551 host target gene. TPM4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TPM4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TPM4 BINDING SITE, designated SEQ ID:9300, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86510] Another function of VGAM2551 is therefore inhibition of Tropomyosin 4 (TPM4, Accession NM_003290), a gene which plays a central role, in association with the troponin complex, in the calcium dependent regulation of vertebrate striated muscle contraction. Accordingly, utilities of

VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TPM4. The function of TPM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM744.X-prolyl Aminopeptidase (aminopeptidase P) 2, Membrane-bound (XPNPEP2, Accession NM_003399) is another VGAM2551 host target gene. XPNPEP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XPNPEP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XPNPEP2 BINDING SITE, designated SEQ ID:9433, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86511] Another function of VGAM2551 is therefore inhibition of X-prolyl Aminopeptidase (aminopeptidase P) 2, Membrane-bound (XPNPEP2, Accession NM_003399), a gene which is a membrane-associated X-prolyl metallopeptidase . Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XPNPEP2. The function of XPNPEP2

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2108.BRAG (Accession NM_014863) is another VGAM2551 host target gene. BRAG BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BRAG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRAG BINDING SITE, designated SEQ ID:16940, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86512] Another function of VGAM2551 is therefore inhibition of BRAG (Accession NM_014863). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRAG. Chromosome 20 Open Reading Frame 98 (C20orf98, Accession XM_049398) is another VGAM2551 host target gene. C20orf98 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf98, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of C20orf98 BINDING SITE, designated SEQ ID:35416, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86513] Another function of VGAM2551 is therefore inhibition of Chromosome 20 Open Reading Frame 98 (C20orf98, Accession XM_049398). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf98. ENDO180 (Accession NM_006039) is another VGAM2551 host target gene. ENDO180 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENDO180, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENDO180 BINDING SITE, designated SEQ ID:12674, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86514] Another function of VGAM2551 is therefore inhibition of ENDO180 (Accession NM_006039). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

ENDO180. F-box Only Protein 4 (FBXO4, Accession NM_033484) is another VGAM2551 host target gene. FBXO4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXO4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXO4 BINDING SITE, designated SEQ ID:27262, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86515] Another function of VGAM2551 is therefore inhibition of F-box Only Protein 4 (FBXO4, Accession NM_033484). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO4. FLJ10512 (Accession NM_018121) is another VGAM2551 host target gene. FLJ10512 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10512, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10512 BINDING SITE, designated SEQ ID:19902, to the

nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86516] Another function of VGAM2551 is therefore inhibition of FLJ10512 (Accession NM_018121). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10512. FLJ11457 (Accession NM_024753) is another VGAM2551 host target gene. FLJ11457 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11457, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11457 BINDING SITE, designated SEQ ID:24094, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86517] Another function of VGAM2551 is therefore inhibition of FLJ11457 (Accession NM_024753). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11457. FLJ14146 (Accession NM_024709) is another VGAM2551 host target gene. FLJ14146 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ14146, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14146 BINDING SITE, designated SEQ ID:24029, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86518] Another function of VGAM2551 is therefore inhibition of FLJ14146 (Accession NM_024709). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14146. FLJ20034 (Accession NM_017630) is another VGAM2551 host target gene. FLJ20034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20034 BINDING SITE, designated SEQ ID:19128, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86519] Another function of VGAM2551 is therefore inhibition of FLJ20034 (Accession NM_017630). Accordingly, utilities of

VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20034. FLJ20094 (Accession NM_017665) is another VGAM2551 host target gene. FLJ20094 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20094, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20094 BINDING SITE, designated SEQ ID:19208, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86520] Another function of VGAM2551 is therefore inhibition of FLJ20094 (Accession NM_017665). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20094. GBTS1 (Accession NM_145173) is another VGAM2551 host target gene. GBTS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GBTS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GBTS1 BINDING SITE,

designated SEQ ID:29725, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86521] Another function of VGAM2551 is therefore inhibition of GBTS1 (Accession NM_145173). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBTS1. HCC-4 (Accession NM_138611) is another VGAM2551 host target gene. HCC-4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HCC-4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCC-4 BINDING SITE, designated SEQ ID:28896, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86522] Another function of VGAM2551 is therefore inhibition of HCC-4 (Accession NM_138611). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCC-4. HRIHFB2072 (Accession NM_032547) is another VGAM2551 host target gene. HRIHFB2072 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRIHFB2072, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRI-HFB2072 BINDING SITE, designated SEQ ID:26271, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86523] Another function of VGAM2551 is therefore inhibition of HRIHFB2072 (Accession NM_032547). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRIHFB2072. KIAA0255 (Accession NM_014742) is another VGAM2551 host target gene. KIAA0255 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0255 BINDING SITE, designated SEQ ID:16413, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86524] Another function of VGAM2551 is therefore inhibition of

KIAA0255 (Accession NM_014742). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0255. KIAA1198 (Accession XM_032674) is another VGAM2551 host target gene. KIAA1198 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1198, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE, designated SEQ ID:31702, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86525] Another function of VGAM2551 is therefore inhibition of KIAA1198 (Accession XM_032674). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198. KIAA1473 (Accession XM_047550) is another VGAM2551 host target gene. KIAA1473 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1473, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1473 BINDING SITE, designated SEQ ID:34995, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86526] Another function of VGAM2551 is therefore inhibition of KIAA1473 (Accession XM_047550). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1473. KIAA1538 (Accession XM_049474) is another VGAM2551 host target gene. KIAA1538 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1538 BINDING SITE, designated SEQ ID:35431, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86527] Another function of VGAM2551 is therefore inhibition of KIAA1538 (Accession XM_049474). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1538. MGC15906 (Accession NM_032885) is another

VGAM2551 host target gene. MGC15906 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC15906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15906 BINDING SITE, designated SEQ ID:26707, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86528] Another function of VGAM2551 is therefore inhibition of MGC15906 (Accession NM_032885). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15906. MGC22014 (Accession XM_035307) is another VGAM2551 host target gene. MGC22014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC22014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC22014 BINDING SITE, designated SEQ ID:32218, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86529] Another function of VGAM2551 is therefore inhibition of MGC22014 (Accession XM_035307). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC22014. MGC5466 (Accession XM_054436) is another VGAM2551 host target gene. MGC5466 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC5466, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5466 BINDING SITE, designated SEQ ID:36159, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86530] Another function of VGAM2551 is therefore inhibition of MGC5466 (Accession XM_054436). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5466. Pellino Homolog 1 (Drosophila) (PELI1, Accession NM_020651) is another VGAM2551 host target gene. PELI1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PELI1, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PELI1 BINDING SITE, designated SEQ ID:21815, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86531] Another function of VGAM2551 is therefore inhibition of Pellino Homolog 1 (Drosophila) (PELI1, Accession NM_020651). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PELI1. RAB3GAP (Accession XM_040048) is another VGAM2551 host target gene. RAB3GAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB3GAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB3GAP BINDING SITE, designated SEQ ID:33245, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86532] Another function of VGAM2551 is therefore inhibition of RAB3GAP (Accession XM_040048). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with RAB3GAP. SEC31B-1 (Accession NM_015490) is another VGAM2551 host target gene. SEC31B-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC31B-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC31B-1 BINDING SITE, designated SEQ ID:17760, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86533] Another function of VGAM2551 is therefore inhibition of SEC31B-1 (Accession NM_015490). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC31B-1. Solute Carrier Family 38, Member 4 (SLC38A4, Accession NM_018018) is another VGAM2551 host target gene. SLC38A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC38A4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC38A4 BINDING SITE, designated SEQ

ID:19756, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86534] Another function of VGAM2551 is therefore inhibition of Solute Carrier Family 38, Member 4 (SLC38A4, Accession NM_018018). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC38A4. T-box 4 (TBX4, Accession NM_018488) is another VGAM2551 host target gene. TBX4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBX4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBX4 BINDING SITE, designated SEQ ID:20544, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86535] Another function of VGAM2551 is therefore inhibition of T-box 4 (TBX4, Accession NM_018488). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX4. Transducer of ERBB2, 2 (TOB2, Accession XM_170995) is another VGAM2551 host target gene.

TOB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOB2 BINDING SITE, designated SEQ ID:45762, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86536] Another function of VGAM2551 is therefore inhibition of Transducer of ERBB2, 2 (TOB2, Accession XM_170995). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOB2. Zinc Finger Protein 221 (ZNF221, Accession NM_013359) is another VGAM2551 host target gene. ZNF221 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF221, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF221 BINDING SITE, designated SEQ ID:15008, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86537] Another function of VGAM2551 is therefore inhibition of Zinc Finger Protein 221 (ZNF221, Accession NM_013359). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF221. LOC144395 (Accession XM_084850) is another VGAM2551 host target gene. LOC144395 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144395, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144395 BINDING SITE, designated SEQ ID:37732, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86538] Another function of VGAM2551 is therefore inhibition of LOC144395 (Accession XM_084850). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144395. LOC145719 (Accession XM_096848) is another VGAM2551 host target gene. LOC145719 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145719, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145719 BINDING SITE, designated SEQ ID:40577, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86539] Another function of VGAM2551 is therefore inhibition of LOC145719 (Accession XM_096848). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145719. LOC145720 (Accession XM_096846) is another VGAM2551 host target gene. LOC145720 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145720, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145720 BINDING SITE, designated SEQ ID:40566, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86540] Another function of VGAM2551 is therefore inhibition of LOC145720 (Accession XM_096846). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145720. LOC146802 (Accession XM_085595) is another VGAM2551 host target gene. LOC146802 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146802, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146802 BINDING SITE, designated SEQ ID:38245, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86541] Another function of VGAM2551 is therefore inhibition of LOC146802 (Accession XM_085595). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146802. LOC148198 (Accession XM_047554) is another VGAM2551 host target gene. LOC148198 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148198, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148198 BINDING SITE, designated SEQ ID:34999, to

the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86542] Another function of VGAM2551 is therefore inhibition of LOC148198 (Accession XM_047554). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148198. LOC150203 (Accession XM_018294) is another VGAM2551 host target gene. LOC150203 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150203, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150203 BINDING SITE, designated SEQ ID:30349, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86543] Another function of VGAM2551 is therefore inhibition of LOC150203 (Accession XM_018294). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150203. LOC150350 (Accession XM_086861) is another VGAM2551 host target gene. LOC150350 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC150350, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150350 BINDING SITE, designated SEQ ID:38929, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86544] Another function of VGAM2551 is therefore inhibition of LOC150350 (Accession XM_086861). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150350. LOC151647 (Accession XM_087261) is another VGAM2551 host target gene. LOC151647 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151647, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151647 BINDING SITE, designated SEQ ID:39156, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86545] Another function of VGAM2551 is therefore inhibition of LOC151647 (Accession XM_087261). Accordingly, utilities

of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151647. LOC197114 (Accession XM_116987) is another VGAM2551 host target gene. LOC197114 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC197114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197114 BINDING SITE, designated SEQ ID:43189, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86546] Another function of VGAM2551 is therefore inhibition of LOC197114 (Accession XM_116987). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197114. LOC197117 (Accession XM_116989) is another VGAM2551 host target gene. LOC197117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC197117 BINDING SITE, designated SEQ ID:43196, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86547] Another function of VGAM2551 is therefore inhibition of LOC197117 (Accession XM_116989). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197117. LOC221178 (Accession XM_167936) is another VGAM2551 host target gene. LOC221178 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221178 BINDING SITE, designated SEQ ID:44925, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86548] Another function of VGAM2551 is therefore inhibition of LOC221178 (Accession XM_167936). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221178. LOC221398 (Accession XM_165762) is another VGAM2551 host target gene. LOC221398 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221398, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221398 BINDING SITE, designated SEQ ID:43749, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86549] Another function of VGAM2551 is therefore inhibition of LOC221398 (Accession XM_165762). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221398. LOC221656 (Accession XM_166418) is another VGAM2551 host target gene. LOC221656 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221656, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221656 BINDING SITE, designated SEQ ID:44292, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86550] Another function of VGAM2551 is therefore inhibition of

LOC221656 (Accession XM_166418). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221656. LOC254018 (Accession XM_173066) is another VGAM2551 host target gene. LOC254018 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254018, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254018 BINDING SITE, designated SEQ ID:46317, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86551] Another function of VGAM2551 is therefore inhibition of LOC254018 (Accession XM_173066). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254018. LOC91012 (Accession XM_035503) is another VGAM2551 host target gene. LOC91012 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91012, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC91012 BINDING SITE, designated SEQ ID:32285, to the nucleotide sequence of VGAM2551 RNA, herein designated VGAM RNA, also designated SEQ ID:5262.

[86552] Another function of VGAM2551 is therefore inhibition of LOC91012 (Accession XM_035503). Accordingly, utilities of VGAM2551 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91012. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2552 (VGAM2552) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86553] VGAM2552 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2552 was detected is described hereinabove with reference to Figs. 1-8.

[86554] VGAM2552 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice Ragged Stunt Virus. VGAM2552 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[86555] VGAM2552 gene encodes a VGAM2552 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2552 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2552 precursor RNA is designated SEQ ID:2538, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2538 is located at position 3478 relative to the genome of Rice Ragged Stunt Virus.

[86556] VGAM2552 precursor RNA folds onto itself, forming VGAM2552 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86557] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2552 folded precursor RNA into VGAM2552 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2552 RNA is designated SEQ ID:5263, and is provided hereinbelow with reference to the sequence listing part.

[86558] VGAM2552 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2552 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86559] VGAM2552 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2552 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2552 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86560] The complementary binding of VGAM2552 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2552 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2552 host target RNA into VGAM2552 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86561] It is appreciated that VGAM2552 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2552 host target genes. The mRNA of each one of this plurality of VGAM2552 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2552 RNA, herein designated VGAM RNA, and which when bound by VGAM2552 RNA causes inhibition of translation of respective one or more VGAM2552 host target proteins.

[86562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2552 gene, herein designated VGAM GENE, on one or more VGAM2552 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86563] It is yet further appreciated that a function of VGAM2552 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2552 include diagnosis, prevention and treatment of viral infection by Rice Ragged Stunt Virus. Specific functions, and accordingly utilities, of VGAM2552 correlate with, and may be deduced from, the identity of the host target genes which VGAM2552 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86564] Nucleotide sequences of the VGAM2552 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2552 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2552 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2552 are further described hereinbelow with reference to Table 1.

[86565] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2552 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2552 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86566] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2552 gene, herein designated VGAM is inhibition of expression of VGAM2552 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2552 correlate with, and may be deduced from, the identity of the target genes which VGAM2552 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86567] Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841) is a VGAM2552 host target gene. OSBPL8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL8 BINDING SITE, designated SEQ ID:21909, to the nucleotide sequence of VGAM2552 RNA, herein designated VGAM RNA, also designated SEQ ID:5263.

[86568] A function of VGAM2552 is therefore inhibition of Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841). Accordingly, utilities of VGAM2552 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL8. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2553 (VGAM2553) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86569] VGAM2553 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2553 was detected is described hereinabove with reference to Figs. 1-8.

[86570] VGAM2553 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rice Ragged Stunt Virus. VGAM2553 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86571] VGAM2553 gene encodes a VGAM2553 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2553 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2553 precursor RNA is designated SEQ ID:2539, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2539 is located at position 271 relative to the genome of Rice Ragged Stunt Virus.

[86572] VGAM2553 precursor RNA folds onto itself, forming VGAM2553 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86573] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2553 folded precursor RNA into VGAM2553 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2553 RNA is designated SEQ ID:5264, and is provided hereinbelow with reference to the sequence listing part.

[86574] VGAM2553 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2553 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86575] VGAM2553 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2553 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2553 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86576] The complementary binding of VGAM2553 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2553 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2553 host target RNA into VGAM2553 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86577] It is appreciated that VGAM2553 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2553 host target genes. The mRNA of each one of this plurality of VGAM2553 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2553 RNA, herein designated VGAM RNA, and which when bound by VGAM2553 RNA causes inhibition of translation of respective one or more VGAM2553 host target proteins.

[86578] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2553 gene, herein designated VGAM GENE, on one or more VGAM2553 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86579] It is yet further appreciated that a function of VGAM2553 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2553 include diagnosis, prevention and treatment of viral infection by Rice Ragged Stunt Virus. Specific functions, and accordingly utilities, of VGAM2553 correlate with, and may be deduced from, the identity of the host target genes which VGAM2553 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86580] Nucleotide sequences of the VGAM2553 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2553 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2553 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2553 are further described hereinbelow with reference to Table 1.

[86581] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2553 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2553 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[86582] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2553 gene, herein designated VGAM is inhibition of expression of VGAM2553 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2553 correlate with, and may be deduced from, the identity of the target genes which VGAM2553 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86583] Cytochrome P450, Subfamily XXIV (vitamin D 24-hydroxylase) (CYP24, Accession NM_000782) is a VGAM2553 host target gene. CYP24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP24 BINDING SITE, designated SEQ ID:6426, to the nucleotide sequence of VGAM2553 RNA, herein designated VGAM RNA, also designated SEQ ID:5264.

[86584] A function of VGAM2553 is therefore inhibition of Cytochrome P450, Subfamily XXIV (vitamin D 24-hydroxylase) (CYP24, Accession NM_000782), a gene

which induces the differentiation of promyelocytes into monocytes/macrophages. Accordingly, utilities of VGAM2553 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP24. The function of CYP24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1204.C1q and Tumor Necrosis Factor Related Protein 7 (C1QTNF7, Accession NM_031911) is another VGAM2553 host target gene. C1QTNF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1QTNF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1QTNF7 BINDING SITE, designated SEQ ID:25665, to the nucleotide sequence of VGAM2553 RNA, herein designated VGAM RNA, also designated SEQ ID:5264.

[86585] Another function of VGAM2553 is therefore inhibition of C1q and Tumor Necrosis Factor Related Protein 7 (C1QTNF7, Accession NM_031911). Accordingly, utilities of VGAM2553 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

C1QTNF7. KIAA1274 (Accession XM_166125) is another VGAM2553 host target gene. KIAA1274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1274 BINDING SITE, designated SEQ ID:43910, to the nucleotide sequence of VGAM2553 RNA, herein designated VGAM RNA, also designated SEQ ID:5264.

[86586] Another function of VGAM2553 is therefore inhibition of KIAA1274 (Accession XM_166125). Accordingly, utilities of VGAM2553 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1274. RAS-like, Estrogen-regulated, Growth-inhibitor (RERG, Accession NM_032918) is another VGAM2553 host target gene. RERG BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RERG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RERG BINDING SITE, designated SEQ ID:26739, to the nucleotide sequence of

VGAM2553 RNA, herein designated VGAM RNA, also designated SEQ ID:5264.

[86587] Another function of VGAM2553 is therefore inhibition of RAS-like, Estrogen-regulated, Growth-inhibitor (RERG, Accession NM_032918). Accordingly, utilities of VGAM2553 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RERG. LOC256940 (Accession XM_172879) is another VGAM2553 host target gene. LOC256940 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256940 BINDING SITE, designated SEQ ID:46155, to the nucleotide sequence of VGAM2553 RNA, herein designated VGAM RNA, also designated SEQ ID:5264.

[86588] Another function of VGAM2553 is therefore inhibition of LOC256940 (Accession XM_172879). Accordingly, utilities of VGAM2553 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256940. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2554 (VGAM2554) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86589] VGAM2554 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2554 was detected is described hereinabove with reference to Figs. 1-8.

[86590] VGAM2554 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Plautia Stali Intestine Virus. VGAM2554 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86591] VGAM2554 gene encodes a VGAM2554 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2554 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2554 precursor RNA is designated SEQ ID:2540, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2540 is located at position 685 relative to the

genome of Plautia Stali Intestine Virus.

[86592] VGAM2554 precursor RNA folds onto itself, forming VGAM2554 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86593] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2554 folded precursor RNA into VGAM2554 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM2554 RNA is designated SEQ ID:5265, and is provided hereinbelow with reference to the sequence listing part.

[86594] VGAM2554 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2554 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86595] VGAM2554 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2554 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2554 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86596] The complementary binding of VGAM2554 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2554 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2554 host target RNA into VGAM2554 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86597] It is appreciated that VGAM2554 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2554 host target genes. The mRNA of each one of this plurality of VGAM2554 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2554 RNA, herein designated VGAM RNA, and which when bound by VGAM2554 RNA causes inhibition of translation of respective one or more VGAM2554 host target proteins.

[86598] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2554 gene, herein designated VGAM GENE, on one or more VGAM2554 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86599] It is yet further appreciated that a function of VGAM2554 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of viral infection by Plautia Stali Intestine Virus. Specific functions, and accordingly utilities, of VGAM2554

correlate with, and may be deduced from, the identity of the host target genes which VGAM2554 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86600] Nucleotide sequences of the VGAM2554 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2554 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2554 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2554 are further described hereinbelow with reference to Table 1.

[86601] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2554 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2554 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86602] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2554 gene, herein designated VGAM is inhibition of expression of VGAM2554 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2554 correlate with, and may be deduced

from, the identity of the target genes which VGAM2554 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86603] ATP-binding Cassette, Sub-family D (ALD), Member 4 (ABCD4, Accession NM_020326) is a VGAM2554 host target gene. ABCD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCD4 BINDING SITE, designated SEQ ID:21592, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86604] A function of VGAM2554 is therefore inhibition of ATP-binding Cassette, Sub-family D (ALD), Member 4 (ABCD4, Accession NM_020326), a gene which Putative peroxisomal ATP binding cassette transporter. Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCD4. The function of ABCD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM1924.Cannabinoid Receptor 1 (brain) (CNR1, Accession NM_016083) is another VGAM2554 host target gene. CNR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNR1 BINDING SITE, designated SEQ ID:18162, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86605] Another function of VGAM2554 is therefore inhibition of Cannabinoid Receptor 1 (brain) (CNR1, Accession NM_016083), a gene which is involved in the cannabinoid-induced CNS effects. Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNR1. The function of CNR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM533.Fc Fragment of IgG, Low Affinity IIa, Receptor For (CD32) (FCGR2A, Accession XM_086483) is another VGAM2554 host target gene. FCGR2A BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FCGR2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCGR2A BINDING SITE, designated SEQ ID:38697, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86606] Another function of VGAM2554 is therefore inhibition of Fc Fragment of IgG, Low Affinity IIa, Receptor For (CD32) (FCGR2A, Accession XM_086483), a gene which binds IgG immune complexes; member of the immunoglobulin superfamily. Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCGR2A. The function of FCGR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM444.Mitogen-activated Protein Kinase 1 (MAPK1, Accession NM_002745) is another VGAM2554 host target gene. MAPK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPK1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK1 BINDING SITE, designated SEQ ID:8614, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86607] Another function of VGAM2554 is therefore inhibition of Mitogen-activated Protein Kinase 1 (MAPK1, Accession NM_002745), a gene which phosphorylates microtubule-associated protein-2 (map2). myelin basic protein (mbp), and elk-1; may promote entry in the cell cycle. Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK1. The function of MAPK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.Retinitis Pigmentosa 2 (X-linked recessive) (RP2, Accession NM_006915) is another VGAM2554 host target gene. RP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of RP2 BINDING SITE, designated SEQ ID:13792, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86608] Another function of VGAM2554 is therefore inhibition of Retinitis Pigmentosa 2 (X-linked recessive) (RP2, Accession NM_006915). Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RP2. DKFZP434C1715 (Accession XM_098421) is another VGAM2554 host target gene. DKFZP434C1715 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C1715, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434C1715 BINDING SITE, designated SEQ ID:41673, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86609] Another function of VGAM2554 is therefore inhibition of DKFZP434C1715 (Accession XM_098421). Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP434C1715. KIAA1416 (Accession XM_098762) is another VGAM2554 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41807, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86610] Another function of VGAM2554 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. MGC9912 (Accession NM_080664) is another VGAM2554 host target gene. MGC9912 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC9912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC9912 BINDING SITE, designated SEQ ID:27952, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM

RNA, also designated SEQ ID:5265.

[86611] Another function of VGAM2554 is therefore inhibition of MGC9912 (Accession NM_080664). Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9912. LOC154222 (Accession XM_098497) is another VGAM2554 host target gene. LOC154222 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154222, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154222 BINDING SITE, designated SEQ ID:41689, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86612] Another function of VGAM2554 is therefore inhibition of LOC154222 (Accession XM_098497). Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154222. LOC222060 (Accession XM_168427) is another VGAM2554 host target gene. LOC222060 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222060, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222060 BINDING SITE, designated SEQ ID:45156, to the nucleotide sequence of VGAM2554 RNA, herein designated VGAM RNA, also designated SEQ ID:5265.

[86613] Another function of VGAM2554 is therefore inhibition of LOC222060 (Accession XM_168427). Accordingly, utilities of VGAM2554 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222060. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2555 (VGAM2555) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86614] VGAM2555 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2555 was detected is described hereinabove with reference to Figs. 1-8.

[86615] VGAM2555 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Plautia Stali Intestine

Virus. VGAM2555 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86616] VGAM2555 gene encodes a VGAM2555 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2555 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2555 precursor RNA is designated SEQ ID:2541, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2541 is located at position 3272 relative to the genome of Plautia Stali Intestine Virus.

[86617] VGAM2555 precursor RNA folds onto itself, forming VGAM2555 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86618] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2555 folded precursor RNA into VGAM2555 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2555 RNA is designated SEQ ID:5266, and is provided hereinbelow with reference to the sequence listing part.

[86619] VGAM2555 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2555 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86620] VGAM2555 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2555 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2555 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86621] The complementary binding of VGAM2555 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2555 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2555 host target RNA into VGAM2555 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86622] It is appreciated that VGAM2555 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2555 host target genes. The mRNA of each one of this plurality of VGAM2555 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2555 RNA, herein designated VGAM RNA, and which when bound by VGAM2555 RNA causes inhibition of translation of respective one or more VGAM2555 host target proteins.

[86623] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2555 gene, herein designated VGAM GENE, on one or more VGAM2555 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86624] It is yet further appreciated that a function of VGAM2555 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of viral infection by Plautia Stali Intestine Virus. Specific functions, and accordingly utilities, of VGAM2555 correlate with, and may be deduced from, the identity of the host target genes which VGAM2555 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86625] Nucleotide sequences of the VGAM2555 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2555 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2555 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2555 are further described hereinbelow with reference to Table 1.

[86626] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2555 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2555 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86627] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2555 gene, herein designated VGAM is inhibition of expression of VGAM2555 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2555 correlate with, and may be deduced from, the identity of the target genes which VGAM2555 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86628] GM2 Ganglioside Activator Protein (GM2A, Accession XM_041978) is a VGAM2555 host target gene. GM2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GM2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE, designated SEQ ID:33659, to the

nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86629] A function of VGAM2555 is therefore inhibition of GM2 Ganglioside Activator Protein (GM2A, Accession XM_041978). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A. HCS (Accession NM_018947) is another VGAM2555 host target gene. HCS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCS BINDING SITE, designated SEQ ID:21014, to the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86630] Another function of VGAM2555 is therefore inhibition of HCS (Accession NM_018947). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCS. WD Repeat Domain 4 (WDR4, Accession NM_033662) is another VGAM2555 host target gene. WDR4 BINDING SITE1 and WDR4 BINDING SITE2 are HOST TARGET binding

sites found in untranslated regions of mRNA encoded by WDR4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WDR4 BINDING SITE1 and WDR4 BINDING SITE2, designated SEQ ID:27391 and SEQ ID:20744 respectively, to the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86631] Another function of VGAM2555 is therefore inhibition of WD Repeat Domain 4 (WDR4, Accession NM_033662). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR4. KIAA1755 (Accession XM_028810) is another VGAM2555 host target gene. KIAA1755 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1755, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1755 BINDING SITE, designated SEQ ID:30748, to the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86632] Another function of VGAM2555 is therefore inhibition of KIAA1755 (Accession XM_028810). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1755. Mitochondrial Ribosomal Protein L35 (MRPL35, Accession NM_016622) is another VGAM2555 host target gene. MRPL35 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL35, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL35 BINDING SITE, designated SEQ ID:18735, to the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86633] Another function of VGAM2555 is therefore inhibition of Mitochondrial Ribosomal Protein L35 (MRPL35, Accession NM_016622). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL35. Mitochondrial Ribosomal Protein S27 (MRPS27, Accession NM_015084) is another VGAM2555 host target gene. MRPS27 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPS27, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPS27 BINDING SITE, designated SEQ ID:17475, to the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86634] Another function of VGAM2555 is therefore inhibition of Mitochondrial Ribosomal Protein S27 (MRPS27, Accession

NM_015084). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS27. RAP140 (Accession NM_015224) is another VGAM2555 host target gene. RAP140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAP140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP140 BINDING SITE, designated SEQ ID:17554, to the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86635] Another function of VGAM2555 is therefore inhibition of RAP140 (Accession NM_015224). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP140. LOC152373 (Accession XM_087449) is another VGAM2555 host target gene. LOC152373 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152373, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC152373 BINDING SITE, designated SEQ ID:39270, to the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86636] Another function of VGAM2555 is therefore inhibition of LOC152373 (Accession XM_087449). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152373. LOC90155 (Accession XM_029487) is another VGAM2555 host target gene. LOC90155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90155 BINDING SITE, designated SEQ ID:30899, to the nucleotide sequence of VGAM2555 RNA, herein designated VGAM RNA, also designated SEQ ID:5266.

[86637] Another function of VGAM2555 is therefore inhibition of LOC90155 (Accession XM_029487). Accordingly, utilities of VGAM2555 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90155. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2556 (VGAM2556) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86638] VGAM2556 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2556 was detected is described hereinabove with reference to Figs. 1-8.

[86639] VGAM2556 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Plautia Stali Intestine Virus. VGAM2556 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86640] VGAM2556 gene encodes a VGAM2556 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2556 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2556 precursor RNA is designated SEQ ID:2542, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2542 is located at position 4204 relative to the genome of Plautia Stali Intestine Virus.

[86641] VGAM2556 precursor RNA folds onto itself, forming VGAM2556 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86642] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2556 folded precursor RNA into VGAM2556 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2556 RNA is designated SEQ ID:5267, and is provided hereinbelow with reference to the sequence listing part.

[86643] VGAM2556 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2556 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86644] VGAM2556 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2556 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2556 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2556 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86645] The complementary binding of VGAM2556 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2556 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2556 host target RNA into VGAM2556 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86646] It is appreciated that VGAM2556 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2556 host target genes. The mRNA of each one of this plurality of VGAM2556 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2556 RNA, herein designated VGAM RNA, and which when bound by VGAM2556 RNA causes inhibition of translation of respective one or more

VGAM2556 host target proteins.

[86647] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2556 gene, herein designated VGAM GENE, on one or more VGAM2556 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86648] It is yet further appreciated that a function of VGAM2556 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2556 include diagnosis, prevention and treatment of viral infection by Plautia Stali Intestine Virus.

Specific functions, and accordingly utilities, of VGAM2556 correlate with, and may be deduced from, the identity of the host target genes which VGAM2556 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86649] Nucleotide sequences of the VGAM2556 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2556 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2556 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2556 are further described hereinbelow with reference to Table 1.

[86650] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2556 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2556 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86651] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2556 gene, herein designated VGAM is inhibition of expression of VGAM2556 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2556 correlate with, and may be deduced from, the identity of the target genes which VGAM2556 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86652] Aryl Hydrocarbon Receptor (AHR, Accession NM_001621) is a VGAM2556 host target gene. AHR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AHR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AHR BINDING SITE, designated SEQ ID:7330, to the nucleotide sequence of VGAM2556 RNA, herein designated VGAM RNA, also designated SEQ ID:5267.

[86653] A function of VGAM2556 is therefore inhibition of Aryl Hydrocarbon Receptor (AHR, Accession NM_001621), a gene which plays a role in modulating carcinogenesis through the induction of xenobiotic-metabolizing enzymes. Accordingly, utilities of VGAM2556 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AHR. The function of AHR and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM368.Coagulation Factor VIII, Procoagulant Component (hemophilia A) (F8, Accession NM_000132) is another VGAM2556 host target gene. F8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by F8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of F8 BINDING SITE, designated SEQ ID:5612, to the nucleotide sequence of VGAM2556 RNA, herein designated VGAM RNA, also designated SEQ ID:5267.

[86654] Another function of VGAM2556 is therefore inhibition of Coagulation Factor VIII, Procoagulant Component (hemophilia A) (F8, Accession NM_000132). Accordingly, utilities of VGAM2556 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F8. FLJ10697 (Accession NM_018181) is another VGAM2556 host target gene. FLJ10697 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ10697 BINDING SITE, designated SEQ ID:20015, to the nucleotide sequence of VGAM2556 RNA, herein designated VGAM RNA, also designated SEQ ID:5267.

[86655] Another function of VGAM2556 is therefore inhibition of FLJ10697 (Accession NM_018181). Accordingly, utilities of VGAM2556 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10697. LOC114971 (Accession XM_054936) is another VGAM2556 host target gene. LOC114971 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC114971, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC114971 BINDING SITE, designated SEQ ID:36205, to the nucleotide sequence of VGAM2556 RNA, herein designated VGAM RNA, also designated SEQ ID:5267.

[86656] Another function of VGAM2556 is therefore inhibition of LOC114971 (Accession XM_054936). Accordingly, utilities of VGAM2556 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC114971. LOC158158 (Accession XM_088494) is an-

other VGAM2556 host target gene. LOC158158 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158158 BINDING SITE, designated SEQ ID:39731, to the nucleotide sequence of VGAM2556 RNA, herein designated VGAM RNA, also designated SEQ ID:5267.

[86657] Another function of VGAM2556 is therefore inhibition of LOC158158 (Accession XM_088494). Accordingly, utilities of VGAM2556 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158158. LOC257319 (Accession XM_171049) is another VGAM2556 host target gene. LOC257319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257319 BINDING SITE, designated SEQ ID:45833, to the nucleotide sequence of VGAM2556 RNA, herein designated VGAM RNA, also designated SEQ ID:5267.

[86658] Another function of VGAM2556 is therefore inhibition of LOC257319 (Accession XM_171049). Accordingly, utilities of VGAM2556 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257319. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2557 (VGAM2557) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86659] VGAM2557 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2557 was detected is described hereinabove with reference to Figs. 1-8.

[86660] VGAM2557 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P Virus. VGAM2557 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86661] VGAM2557 gene encodes a VGAM2557 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2557 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2557 precursor RNA is designated SEQ ID:2543, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2543 is located at position 8347 relative to the genome of Himetobi P Virus.

[86662] VGAM2557 precursor RNA folds onto itself, forming VGAM2557 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86663] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2557 folded precursor RNA into VGAM2557 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2557 RNA is designated SEQ ID:5268, and is provided hereinbelow with reference to the sequence listing part.

[86664] VGAM2557 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2557 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86665] VGAM2557 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2557 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2557 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86666] The complementary binding of VGAM2557 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2557 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2557 host target RNA into VGAM2557 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86667] It is appreciated that VGAM2557 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2557 host target genes. The mRNA of each one of this plurality of VGAM2557 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2557 RNA, herein designated VGAM RNA, and which when bound by VGAM2557 RNA causes inhibition of translation of respective one or more VGAM2557 host target proteins.

[86668] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2557 gene, herein designated VGAM GENE, on one or more VGAM2557 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86669] It is yet further appreciated that a function of VGAM2557 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2557 include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGAM2557 correlate with, and may be deduced from, the identity of the host target genes which VGAM2557 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86670] Nucleotide sequences of the VGAM2557 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2557 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2557 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2557 are further described hereinbelow with reference to Table 1.

[86671] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2557 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2557 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[86672] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2557 gene, herein designated VGAM is inhibition of expression of VGAM2557 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2557 correlate with, and may be deduced from, the identity of the target genes which VGAM2557 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86673] Potassium Voltage-gated Channel, Shal-related Subfamily, Member 2 (KCND2, Accession NM_012281) is a VGAM2557 host target gene. KCND2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCND2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCND2 BINDING SITE, designated SEQ ID:14611, to the nucleotide sequence of VGAM2557 RNA, herein designated VGAM RNA, also designated SEQ ID:5268.

[86674] A function of VGAM2557 is therefore inhibition of Potassium Voltage-gated Channel, Shal-related Subfamily, Member 2 (KCND2, Accession NM_012281), a gene which

is prominent in the repolarization phase of the action potential. Accordingly, utilities of VGAM2557 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCND2. The function of KCND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM449.RAS Guanyl Releasing Protein 1 (calcium and DAG-regulated) (RASGRP1, Accession NM_005739) is another VGAM2557 host target gene. RASGRP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASGRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASGRP1 BINDING SITE, designated SEQ ID:12301, to the nucleotide sequence of VGAM2557 RNA, herein designated VGAM RNA, also designated SEQ ID:5268.

[86675] Another function of VGAM2557 is therefore inhibition of RAS Guanyl Releasing Protein 1 (calcium and DAG-regulated) (RASGRP1, Accession NM_005739). Accordingly, utilities of VGAM2557 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with RASGRP1. FLJ14166 (Accession NM_024565) is another VGAM2557 host target gene. FLJ14166 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14166 BINDING SITE, designated SEQ ID:23793, to the nucleotide sequence of VGAM2557 RNA, herein designated VGAM RNA, also designated SEQ ID:5268.

[86676] Another function of VGAM2557 is therefore inhibition of FLJ14166 (Accession NM_024565). Accordingly, utilities of VGAM2557 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14166. FLJ33069 (Accession NM_144649) is another VGAM2557 host target gene. FLJ33069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ33069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ33069 BINDING SITE, designated SEQ ID:29473, to the nucleotide sequence of VGAM2557 RNA, herein designated VGAM

RNA, also designated SEQ ID:5268.

[86677] Another function of VGAM2557 is therefore inhibition of FLJ33069 (Accession NM_144649). Accordingly, utilities of VGAM2557 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33069. KIAA0152 (Accession NM_014730) is another VGAM2557 host target gene. KIAA0152 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0152, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0152 BINDING SITE, designated SEQ ID:16331, to the nucleotide sequence of VGAM2557 RNA, herein designated VGAM RNA, also designated SEQ ID:5268.

[86678] Another function of VGAM2557 is therefore inhibition of KIAA0152 (Accession NM_014730). Accordingly, utilities of VGAM2557 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0152. LOC148195 (Accession XM_097419) is another VGAM2557 host target gene. LOC148195 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148195, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148195 BINDING SITE, designated SEQ ID:40879, to the nucleotide sequence of VGAM2557 RNA, herein designated VGAM RNA, also designated SEQ ID:5268.

[86679] Another function of VGAM2557 is therefore inhibition of LOC148195 (Accession XM_097419). Accordingly, utilities of VGAM2557 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148195. LOC148562 (Accession XM_086240) is another VGAM2557 host target gene. LOC148562 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148562, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148562 BINDING SITE, designated SEQ ID:38565, to the nucleotide sequence of VGAM2557 RNA, herein designated VGAM RNA, also designated SEQ ID:5268.

[86680] Another function of VGAM2557 is therefore inhibition of LOC148562 (Accession XM_086240). Accordingly, utilities of VGAM2557 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC148562. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2558 (VGAM2558) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86681] VGAM2558 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2558 was detected is described hereinabove with reference to Figs. 1-8.

[86682] VGAM2558 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P Virus. VGAM2558 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86683] VGAM2558 gene encodes a VGAM2558 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2558 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2558 precursor RNA is desig-

nated SEQ ID:2544, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2544 is located at position 7354 relative to the genome of Himetobi P Virus.

[86684] VGAM2558 precursor RNA folds onto itself, forming VGAM2558 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86685] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2558 folded precursor RNA into VGAM2558 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2558 RNA is designated SEQ ID:5269, and is provided hereinbelow with reference to the sequence

listing part.

[86686] VGAM2558 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2558 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86687] VGAM2558 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2558 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2558 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86688] The complementary binding of VGAM2558 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2558 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2558 host target RNA into VGAM2558 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86689] It is appreciated that VGAM2558 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2558 host target genes. The mRNA of each one of this plurality of VGAM2558 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2558 RNA, herein designated VGAM

RNA, and which when bound by VGAM2558 RNA causes inhibition of translation of respective one or more VGAM2558 host target proteins.

[86690] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2558 gene, herein designated VGAM GENE, on one or more VGAM2558 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86691] It is yet further appreciated that a function of VGAM2558 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2558 include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGAM2558 correlate with, and may be deduced from, the identity of the host target genes which VGAM2558 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86692] Nucleotide sequences of the VGAM2558 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2558 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2558 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2558 are further described hereinbelow with reference to Table 1.

[86693] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2558 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2558 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86694] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2558 gene, herein designated VGAM is

inhibition of expression of VGAM2558 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2558 correlate with, and may be deduced from, the identity of the target genes which VGAM2558 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86695] DNAM-1 (Accession NM_006566) is a VGAM2558 host target gene. DNAM-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNAM-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNAM-1 BINDING SITE, designated SEQ ID:13338, to the nucleotide sequence of VGAM2558 RNA, herein designated VGAM RNA, also designated SEQ ID:5269.

[86696] A function of VGAM2558 is therefore inhibition of DNAM-1 (Accession NM_006566). Accordingly, utilities of VGAM2558 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAM-1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Mes-

senger 2559 (VGAM2559) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86697] VGAM2559 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2559 was detected is described hereinabove with reference to Figs. 1-8.

[86698] VGAM2559 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P Virus. VGAM2559 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86699] VGAM2559 gene encodes a VGAM2559 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2559 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2559 precursor RNA is designated SEQ ID:2545, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2545 is located at position 8220 relative to the genome of Himetobi P Virus.

[86700] VGAM2559 precursor RNA folds onto itself, forming VGAM2559 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86701] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2559 folded precursor RNA into VGAM2559 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2559 RNA is designated SEQ ID:5270, and is provided hereinbelow with reference to the sequence listing part.

[86702] VGAM2559 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2559 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2559 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86703] VGAM2559 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2559 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2559 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2559 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2559 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86704] The complementary binding of VGAM2559 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2559 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2559 host target RNA into VGAM2559 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86705] It is appreciated that VGAM2559 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2559 host target genes. The mRNA of each one of this plurality of VGAM2559 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2559 RNA, herein designated VGAM RNA, and which when bound by VGAM2559 RNA causes inhibition of translation of respective one or more VGAM2559 host target proteins.

[86706] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2559 gene, herein designated VGAM GENE, on one or more VGAM2559 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86707] It is yet further appreciated that a function of VGAM2559 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2559 include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGAM2559 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2559 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86708] Nucleotide sequences of the VGAM2559 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2559 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2559 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2559 are further described hereinbelow with reference to Table 1.

[86709] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2559 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2559 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86710] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2559 gene, herein designated VGAM is inhibition of expression of VGAM2559 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2559 correlate with, and may be deduced from, the identity of the target genes which VGAM2559

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86711] Dystrophia Myotonica-containing WD Repeat Motif (DMWD, Accession XM_027569) is a VGAM2559 host target gene. DMWD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DMWD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMWD BINDING SITE, designated SEQ ID:30529, to the nucleotide sequence of VGAM2559 RNA, herein designated VGAM RNA, also designated SEQ ID:5270.

[86712] A function of VGAM2559 is therefore inhibition of Dystrophia Myotonica-containing WD Repeat Motif (DMWD, Accession XM_027569). Accordingly, utilities of VGAM2559 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMWD. KIAA0450 (Accession NM_014638) is another VGAM2559 host target gene. KIAA0450 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0450, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0450 BINDING SITE, designated SEQ ID:16029, to the nucleotide sequence of VGAM2559 RNA, herein designated VGAM RNA, also designated SEQ ID:5270.

[86713] Another function of VGAM2559 is therefore inhibition of KIAA0450 (Accession NM_014638). Accordingly, utilities of VGAM2559 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0450. KIAA0594 (Accession XM_036117) is another VGAM2559 host target gene. KIAA0594 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0594, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0594 BINDING SITE, designated SEQ ID:32386, to the nucleotide sequence of VGAM2559 RNA, herein designated VGAM RNA, also designated SEQ ID:5270.

[86714] Another function of VGAM2559 is therefore inhibition of KIAA0594 (Accession XM_036117). Accordingly, utilities of VGAM2559 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0594. KIAA1940 (Accession XM_086981) is another VGAM2559 host target gene. KIAA1940 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1940 BINDING SITE, designated SEQ ID:39005, to the nucleotide sequence of VGAM2559 RNA, herein designated VGAM RNA, also designated SEQ ID:5270.

[86715] Another function of VGAM2559 is therefore inhibition of KIAA1940 (Accession XM_086981). Accordingly, utilities of VGAM2559 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1940. MGC11257 (Accession NM_032350) is another VGAM2559 host target gene. MGC11257 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC11257, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11257 BINDING SITE, designated SEQ ID:26139, to the nucleotide sequence of VGAM2559 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5270.

[86716] Another function of VGAM2559 is therefore inhibition of MGC11257 (Accession NM_032350). Accordingly, utilities of VGAM2559 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11257. LOC154739 (Accession XM_098602) is another VGAM2559 host target gene. LOC154739 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154739 BINDING SITE, designated SEQ ID:41717, to the nucleotide sequence of VGAM2559 RNA, herein designated VGAM RNA, also designated SEQ ID:5270.

[86717] Another function of VGAM2559 is therefore inhibition of LOC154739 (Accession XM_098602). Accordingly, utilities of VGAM2559 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154739. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2560 (VGAM2560) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86718] VGAM2560 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2560 was detected is described hereinabove with reference to Figs. 1-8.

[86719] VGAM2560 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P Virus. VGAM2560 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86720] VGAM2560 gene encodes a VGAM2560 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2560 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2560 precursor RNA is designated SEQ ID:2546, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2546 is located at position 8011 relative to the genome of Himetobi P Virus.

[86721] VGAM2560 precursor RNA folds onto itself, forming

VGAM2560 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86722] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2560 folded precursor RNA into VGAM2560 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2560 RNA is designated SEQ ID:5271, and is provided hereinbelow with reference to the sequence listing part.

[86723] VGAM2560 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2560 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86724] VGAM2560 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2560 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2560 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86725] The complementary binding of VGAM2560 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2560 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2560 host target RNA into VGAM2560 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86726] It is appreciated that VGAM2560 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2560 host target genes. The mRNA of each one of this plurality of VGAM2560 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2560 RNA, herein designated VGAM RNA, and which when bound by VGAM2560 RNA causes inhibition of translation of respective one or more VGAM2560 host target proteins.

[86727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2560 gene, herein designated VGAM GENE, on one or more VGAM2560 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86728] It is yet further appreciated that a function of VGAM2560 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGAM2560 correlate with, and may be deduced from, the identity of the host target genes which VGAM2560 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[86729] Nucleotide sequences of the VGAM2560 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2560 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2560 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2560 are further described hereinbelow with reference to Table 1.

[86730] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2560 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2560 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86731] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2560 gene, herein designated VGAM is inhibition of expression of VGAM2560 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2560 correlate with, and may be deduced from, the identity of the target genes which VGAM2560 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[86732] Hormonally Upregulated Neu-associated Kinase (HUNK, Accession NM_014586) is a VGAM2560 host target gene. HUNK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HUNK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HUNK BINDING SITE, designated SEQ ID:15949, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86733] A function of VGAM2560 is therefore inhibition of Hormonally Upregulated Neu-associated Kinase (HUNK, Accession NM_014586). Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUNK. Interleukin 1, Beta (IL1B, Accession NM_000576) is another VGAM2560 host target gene. IL1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1B BINDING SITE, desig-

nated SEQ ID:6175, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86734] Another function of VGAM2560 is therefore inhibition of Interleukin 1, Beta (IL1B, Accession NM_000576), a gene which stimulates thymocyte proliferation. Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1B. The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2007.Mucin 4, Tracheobronchial (MUC4, Accession NM_138298) is another VGAM2560 host target gene. MUC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MUC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MUC4 BINDING SITE, designated SEQ ID:28711, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86735] Another function of VGAM2560 is therefore inhibition of

Mucin 4, Tracheobronchial (MUC4, Accession NM_138298), a gene which may act as a ligand for ErbB2 mediated cell signalling. Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MUC4. The function of MUC4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1290.Peripheral Myelin Protein 2 (PMP2, Accession NM_002677) is another VGAM2560 host target gene. PMP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PMP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMP2 BINDING SITE, designated SEQ ID:8545, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86736] Another function of VGAM2560 is therefore inhibition of Peripheral Myelin Protein 2 (PMP2, Accession NM_002677), a gene which is a lipid transport protein in schwann cells. Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PMP2. The function of PMP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.SWAP70 (Accession XM_049197) is another VGAM2560 host target gene. SWAP70 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SWAP70, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SWAP70 BINDING SITE, designated SEQ ID:35350, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86737] Another function of VGAM2560 is therefore inhibition of SWAP70 (Accession XM_049197), a gene which is involved not only in nuclear events but also in signaling in B-cell activation. Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SWAP70. The function of SWAP70 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM1090.Sulfotransferase Family 4A, Member 1 (SULT4A1, Accession XM_043609) is another VGAM2560 host target gene. SULT4A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SULT4A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SULT4A1 BINDING SITE, designated SEQ ID:33976, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86738] Another function of VGAM2560 is therefore inhibition of Sulfotransferase Family 4A, Member 1 (SULT4A1, Accession XM_043609). Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SULT4A1. LOC202934 (Accession XM_117486) is another VGAM2560 host target gene. LOC202934 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, desig-

nated SEQ ID:43463, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86739] Another function of VGAM2560 is therefore inhibition of LOC202934 (Accession XM_117486). Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934. LOC255465 (Accession XM_173206) is another VGAM2560 host target gene. LOC255465 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255465 BINDING SITE, designated SEQ ID:46455, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86740] Another function of VGAM2560 is therefore inhibition of LOC255465 (Accession XM_173206). Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255465. LOC54505 (Accession XM_042110) is another VGAM2560 host target gene. LOC54505 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC54505, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC54505 BINDING SITE, designated SEQ ID:33697, to the nucleotide sequence of VGAM2560 RNA, herein designated VGAM RNA, also designated SEQ ID:5271.

[86741] Another function of VGAM2560 is therefore inhibition of LOC54505 (Accession XM_042110). Accordingly, utilities of VGAM2560 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC54505. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2561 (VGAM2561) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86742] VGAM2561 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2561 was detected is described hereinabove with reference to Figs. 1-8.

[86743] VGAM2561 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P Virus. VGAM2561 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86744] VGAM2561 gene encodes a VGAM2561 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2561 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2561 precursor RNA is designated SEQ ID:2547, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2547 is located at position 8473 relative to the genome of Himetobi P Virus.

[86745] VGAM2561 precursor RNA folds onto itself, forming VGAM2561 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[86746] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2561 folded precursor RNA into VGAM2561 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2561 RNA is designated SEQ ID:5272, and is provided hereinbelow with reference to the sequence listing part.

[86747] VGAM2561 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2561 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2561 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86748] VGAM2561 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2561 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2561 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2561 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2561 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86749] The complementary binding of VGAM2561 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2561 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2561 host target RNA into VGAM2561 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86750] It is appreciated that VGAM2561 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2561 host target genes. The mRNA of each one of this plurality of VGAM2561 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2561 RNA, herein designated VGAM RNA, and which when bound by VGAM2561 RNA causes inhibition of translation of respective one or more VGAM2561 host target proteins.

[86751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2561 gene, herein designated VGAM GENE, on one or more VGAM2561 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86752] It is yet further appreciated that a function of VGAM2561 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2561 include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGAM2561 correlate with, and may be deduced from, the identity of the host target genes which VGAM2561 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86753] Nucleotide sequences of the VGAM2561 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2561 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2561 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2561 are further described hereinbelow with reference to Table 1.

[86754] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2561 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2561 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86755] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2561 gene, herein designated VGAM is inhibition of expression of VGAM2561 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2561 correlate with, and may be deduced from, the identity of the target genes which VGAM2561 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86756] Myotubular Myopathy 1 (MTM1, Accession NM_000252) is a VGAM2561 host target gene. MTM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of MTM1 BINDING SITE, designated SEQ ID:5791, to the nucleotide sequence of VGAM2561 RNA, herein designated VGAM RNA, also designated SEQ ID:5272.

[86757] A function of VGAM2561 is therefore inhibition of Myotubular Myopathy 1 (MTM1, Accession NM_000252). Accordingly, utilities of VGAM2561 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTM1. Reversion-inducing-cysteine-rich Protein with Kazal Motifs (RECK, Accession NM_021111) is another VGAM2561 host target gene. RECK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RECK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RECK BINDING SITE, designated SEQ ID:22091, to the nucleotide sequence of VGAM2561 RNA, herein designated VGAM RNA, also designated SEQ ID:5272.

[86758] Another function of VGAM2561 is therefore inhibition of Reversion-inducing-cysteine-rich Protein with Kazal Motifs (RECK, Accession NM_021111), a gene which plays a role in regulation of cancer progression and tumor angio-

genesis. Accordingly, utilities of VGAM2561 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RECK. The function of RECK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM75.KIAA1915 (Accession XM_055481) is another VGAM2561 host target gene. KIAA1915 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1915, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1915 BINDING SITE, designated SEQ ID:36270, to the nucleotide sequence of VGAM2561 RNA, herein designated VGAM RNA, also designated SEQ ID:5272.

[86759] Another function of VGAM2561 is therefore inhibition of KIAA1915 (Accession XM_055481). Accordingly, utilities of VGAM2561 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1915. PRO1617 (Accession NM_018587) is another VGAM2561 host target gene. PRO1617 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by PRO1617, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1617 BINDING SITE, designated SEQ ID:20664, to the nucleotide sequence of VGAM2561 RNA, herein designated VGAM RNA, also designated SEQ ID:5272.

[86760] Another function of VGAM2561 is therefore inhibition of PRO1617 (Accession NM_018587). Accordingly, utilities of VGAM2561 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1617. SE70-2 (Accession NM_022118) is another VGAM2561 host target gene. SE70-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SE70-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SE70-2 BINDING SITE, designated SEQ ID:22664, to the nucleotide sequence of VGAM2561 RNA, herein designated VGAM RNA, also designated SEQ ID:5272.

[86761] Another function of VGAM2561 is therefore inhibition of SE70-2 (Accession NM_022118). Accordingly, utilities of

VGAM2561 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SE70-2. Solute Carrier Family 26, Member 10 (SLC26A10, Accession NM_133489) is another VGAM2561 host target gene. SLC26A10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC26A10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC26A10 BINDING SITE, designated SEQ ID:28561, to the nucleotide sequence of VGAM2561 RNA, herein designated VGAM RNA, also designated SEQ ID:5272.

[86762] Another function of VGAM2561 is therefore inhibition of Solute Carrier Family 26, Member 10 (SLC26A10, Accession NM_133489). Accordingly, utilities of VGAM2561 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC26A10. LOC157273 (Accession XM_098743) is another VGAM2561 host target gene. LOC157273 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157273, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157273 BINDING SITE, designated SEQ ID:41787, to the nucleotide sequence of VGAM2561 RNA, herein designated VGAM RNA, also designated SEQ ID:5272.

[86763] Another function of VGAM2561 is therefore inhibition of LOC157273 (Accession XM_098743). Accordingly, utilities of VGAM2561 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157273. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2562 (VGAM2562) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86764] VGAM2562 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2562 was detected is described hereinabove with reference to Figs. 1-8.

[86765] VGAM2562 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Himetobi P Virus. VGAM2562 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[86766] VGAM2562 gene encodes a VGAM2562 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2562 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2562 precursor RNA is designated SEQ ID:2548, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2548 is located at position 7594 relative to the genome of Himetobi P Virus.

[86767] VGAM2562 precursor RNA folds onto itself, forming VGAM2562 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86768] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2562 folded precursor RNA into VGAM2562

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2562 RNA is designated SEQ ID:5273, and is provided hereinbelow with reference to the sequence listing part.

[86769] VGAM2562 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2562 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86770] VGAM2562 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2562 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2562 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86771] The complementary binding of VGAM2562 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2562 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2562 host target RNA into VGAM2562 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[86772] It is appreciated that VGAM2562 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2562 host target genes. The mRNA of each one of this plurality of VGAM2562 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2562 RNA, herein designated VGAM RNA, and which when bound by VGAM2562 RNA causes inhibition of translation of respective one or more VGAM2562 host target proteins.

[86773] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2562 gene, herein designated VGAM GENE, on one or more VGAM2562 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86774] It is yet further appreciated that a function of VGAM2562 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGAM2562 correlate with, and may be deduced from, the identity of the host target genes which VGAM2562 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86775] Nucleotide sequences of the VGAM2562 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2562 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2562 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2562 are further described hereinbelow with reference to Table 1.

[86776] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2562 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2562 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86777] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2562 gene, herein designated VGAM is inhibition of expression of VGAM2562 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2562 correlate with, and may be deduced from, the identity of the target genes which VGAM2562 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86778] AS3 (Accession NM_015928) is a VGAM2562 host target gene. AS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AS3 BINDING SITE, designated SEQ ID:18050, to the nucleotide sequence of VGAM2562 RNA, herein designated VGAM RNA, also designated SEQ ID:5273.

[86779] A function of VGAM2562 is therefore inhibition of AS3 (Accession NM_015928), a gene which inhibits cell proloferation. Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AS3. The function of AS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM393.CD164 Antigen, Sialomucin (CD164, Accession NM_006016) is another VGAM2562 host target gene. CD164 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD164, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD164 BINDING SITE, designated SEQ ID:12630, to the nucleotide sequence of VGAM2562 RNA, herein designated VGAM RNA, also designated SEQ ID:5273.

[86780] Another function of VGAM2562 is therefore inhibition of CD164 Antigen, Sialomucin (CD164, Accession NM_006016), a gene which plays a role in hematopoiesis by facilitating the adhesion of CD34+ cells to bone marrow stroma and negatively regulates CD34+ hematopoi-

etic progenitor cell growth. Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD164. The function of CD164 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM75.Cytosolic Ovarian Carcinoma Antigen 1 (COVA1, Accession XM_055323) is another VGAM2562 host target gene. COVA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COVA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COVA1 BINDING SITE, designated SEQ ID:36265, to the nucleotide sequence of VGAM2562 RNA, herein designated VGAM RNA, also designated SEQ ID:5273.

[86781] Another function of VGAM2562 is therefore inhibition of Cytosolic Ovarian Carcinoma Antigen 1 (COVA1, Accession XM_055323). Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COVA1. FLJ11273 (Accession NM_018374) is another VGAM2562 host target

gene. FLJ11273 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11273, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11273 BINDING SITE, designated SEQ ID:20392, to the nucleotide sequence of VGAM2562 RNA, herein designated VGAM RNA, also designated SEQ ID:5273.

[86782] Another function of VGAM2562 is therefore inhibition of FLJ11273 (Accession NM_018374). Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11273. KIAA0092 (Accession NM_014679) is another VGAM2562 host target gene. KIAA0092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0092 BINDING SITE, designated SEQ ID:16152, to the nucleotide sequence of VGAM2562 RNA, herein designated VGAM RNA, also designated SEQ ID:5273.

[86783] Another function of VGAM2562 is therefore inhibition of KIAA0092 (Accession NM_014679). Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0092. LIN-28 (Accession NM_024674) is another VGAM2562 host target gene. LIN-28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIN-28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIN-28 BINDING SITE, designated SEQ ID:23978, to the nucleotide sequence of VGAM2562 RNA, herein designated VGAM RNA, also designated SEQ ID:5273.

[86784] Another function of VGAM2562 is therefore inhibition of LIN-28 (Accession NM_024674). Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-28. Nudix (nucleoside diphosphate linked moiety X)-type Motif 12 (NUDT12, Accession NM_031438) is another VGAM2562 host target gene. NUDT12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUDT12, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUDT12 BINDING SITE, designated SEQ ID:25448, to the nucleotide sequence of VGAM2562 RNA, herein designated VGAM RNA, also designated SEQ ID:5273.

[86785] Another function of VGAM2562 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety X)-type Motif 12 (NUDT12, Accession NM_031438). Accordingly, utilities of VGAM2562 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT12. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2563 (VGAM2563) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86786] VGAM2563 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2563 was detected is described hereinabove with reference to Figs. 1-8.

[86787] VGAM2563 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Himetobi P Virus. VGAM2563 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86788] VGAM2563 gene encodes a VGAM2563 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2563 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2563 precursor RNA is designated SEQ ID:2549, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2549 is located at position 8878 relative to the genome of Himetobi P Virus.

[86789] VGAM2563 precursor RNA folds onto itself, forming VGAM2563 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86790] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2563 folded precursor RNA into VGAM2563 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2563 RNA is designated SEQ ID:5274, and is provided hereinbelow with reference to the sequence listing part.

[86791] VGAM2563 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2563 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86792] VGAM2563 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2563 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2563 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86793] The complementary binding of VGAM2563 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2563 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2563

host target RNA into VGAM2563 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86794] It is appreciated that VGAM2563 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2563 host target genes. The mRNA of each one of this plurality of VGAM2563 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2563 RNA, herein designated VGAM RNA, and which when bound by VGAM2563 RNA causes inhibition of translation of respective one or more VGAM2563 host target proteins.

[86795] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2563 gene, herein designated VGAM GENE, on one or more VGAM2563 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86796] It is yet further appreciated that a function of VGAM2563 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2563 include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGAM2563 correlate with, and may be deduced from, the identity of the host target genes which VGAM2563 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86797] Nucleotide sequences of the VGAM2563 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2563 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2563 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2563 are further

described hereinbelow with reference to Table 1.

[86798] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2563 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2563 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86799] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2563 gene, herein designated VGAM is inhibition of expression of VGAM2563 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2563 correlate with, and may be deduced from, the identity of the target genes which VGAM2563 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86800] LOC222484 (Accession XM_169424) is a VGAM2563 host target gene. LOC222484 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222484, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222484 BINDING SITE,

designated SEQ ID:45297, to the nucleotide sequence of VGAM2563 RNA, herein designated VGAM RNA, also designated SEQ ID:5274.

[86801] A function of VGAM2563 is therefore inhibition of LOC222484 (Accession XM_169424). Accordingly, utilities of VGAM2563 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222484. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2564 (VGAM2564) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86802] VGAM2564 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2564 was detected is described hereinabove with reference to Figs. 1-8.

[86803] VGAM2564 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2564 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86804] VGAM2564 gene encodes a VGAM2564 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2564 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2564 precursor RNA is designated SEQ ID:2550, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2550 is located at position 3567 relative to the genome of Triatoma Virus.

[86805] VGAM2564 precursor RNA folds onto itself, forming VGAM2564 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86806] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2564 folded precursor RNA into VGAM2564 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2564 RNA is designated SEQ ID:5275, and is provided hereinbelow with reference to the sequence listing part.

[86807] VGAM2564 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2564 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86808] VGAM2564 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2564 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2564 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86809] The complementary binding of VGAM2564 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2564 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2564 host target RNA into VGAM2564 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86810] It is appreciated that VGAM2564 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2564 host target genes. The mRNA of each one of this plurality of VGAM2564 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2564 RNA, herein designated VGAM RNA, and which when bound by VGAM2564 RNA causes inhibition of translation of respective one or more VGAM2564 host target proteins.

[86811] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2564 gene, herein designated VGAM GENE, on one or more VGAM2564 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86812] It is yet further appreciated that a function of VGAM2564 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2564 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2564 correlate with, and may be deduced from, the identity of the host target genes which VGAM2564 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86813] Nucleotide sequences of the VGAM2564 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2564 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2564 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2564 are further described hereinbelow with reference to Table 1.

[86814] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2564 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2564 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86815] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2564 gene, herein designated VGAM is inhibition of expression of VGAM2564 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2564 correlate with, and may be deduced from, the identity of the target genes which VGAM2564 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86816] Active BCR-related Gene (ABR, Accession NM_001092) is a VGAM2564 host target gene. ABR BINDING SITE1 and ABR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ABR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABR BINDING SITE1 and ABR BINDING SITE2, designated SEQ ID:6749 and SEQ ID:22494 respectively, to the nucleotide sequence of VGAM2564 RNA, herein designated VGAM RNA, also designated SEQ ID:5275.

[86817] A function of VGAM2564 is therefore inhibition of Active BCR-related Gene (ABR, Accession NM_001092), a gene which gtpase-activating protein for rac and cdc42. Accordingly, utilities of VGAM2564 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABR. The function of ABR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM489.Profilin 2 (PFN2, Accession NM_002628) is another VGAM2564 host target gene. PFN2 BINDING SITE1 and PFN2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PFN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFN2 BINDING SITE1 and PFN2 BINDING SITE2, designated SEQ ID:8488 and SEQ ID:27581 respectively, to the nucleotide sequence of VGAM2564 RNA, herein designated VGAM RNA, also designated SEQ ID:5275.

[86818] Another function of VGAM2564 is therefore inhibition of Profilin 2 (PFN2, Accession NM_002628). Accordingly, utilities of VGAM2564 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with PFN2. DKFZP434P211 (Accession NM_014549) is another VGAM2564 host target gene. DKFZP434P211 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P211, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434P211 BINDING SITE, designated SEQ ID:15870, to the nucleotide sequence of VGAM2564 RNA, herein designated VGAM RNA, also designated SEQ ID:5275.

[86819] Another function of VGAM2564 is therefore inhibition of DKFZP434P211 (Accession NM_014549). Accordingly, utilities of VGAM2564 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P211. DKFZP586F1318 (Accession NM_015677) is another VGAM2564 host target gene. DKFZP586F1318 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP586F1318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of DKFZP586F1318 BINDING SITE, designated SEQ ID:17904, to the nucleotide sequence of VGAM2564 RNA, herein designated VGAM RNA, also designated SEQ ID:5275.

[86820] Another function of VGAM2564 is therefore inhibition of DKFZP586F1318 (Accession NM_015677). Accordingly, utilities of VGAM2564 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586F1318. LOC145009 (Accession XM_016472) is another VGAM2564 host target gene. LOC145009 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145009 BINDING SITE, designated SEQ ID:30261, to the nucleotide sequence of VGAM2564 RNA, herein designated VGAM RNA, also designated SEQ ID:5275.

[86821] Another function of VGAM2564 is therefore inhibition of LOC145009 (Accession XM_016472). Accordingly, utilities of VGAM2564 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC145009. LOC150213 (Accession XM_059324) is another VGAM2564 host target gene. LOC150213 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150213, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150213 BINDING SITE, designated SEQ ID:36961, to the nucleotide sequence of VGAM2564 RNA, herein designated VGAM RNA, also designated SEQ ID:5275.

[86822] Another function of VGAM2564 is therefore inhibition of LOC150213 (Accession XM_059324). Accordingly, utilities of VGAM2564 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150213. LOC255027 (Accession XM_170806) is another VGAM2564 host target gene. LOC255027 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255027, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255027 BINDING SITE, designated SEQ ID:45572, to the nucleotide sequence of VGAM2564 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5275.

[86823] Another function of VGAM2564 is therefore inhibition of LOC255027 (Accession XM_170806). Accordingly, utilities of VGAM2564 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255027. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2565 (VGAM2565) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86824] VGAM2565 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2565 was detected is described hereinabove with reference to Figs. 1-8.

[86825] VGAM2565 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2565 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86826] VGAM2565 gene encodes a VGAM2565 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2565 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2565 precursor RNA is designated SEQ ID:2551, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2551 is located at position 1775 relative to the genome of Triatoma Virus.

[86827] VGAM2565 precursor RNA folds onto itself, forming VGAM2565 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86828] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2565 folded precursor RNA into VGAM2565 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2565 RNA is designated SEQ ID:5276, and is provided hereinbelow with reference to the sequence listing part.

[86829] VGAM2565 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2565 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86830] VGAM2565 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2565 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2565 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86831] The complementary binding of VGAM2565 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2565 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2565 host target RNA into VGAM2565 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86832] It is appreciated that VGAM2565 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2565 host target genes. The mRNA of

each one of this plurality of VGAM2565 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2565 RNA, herein designated VGAM RNA, and which when bound by VGAM2565 RNA causes inhibition of translation of respective one or more VGAM2565 host target proteins.

[86833] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2565 gene, herein designated VGAM GENE, on one or more VGAM2565 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[86834] It is yet further appreciated that a function of VGAM2565 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2565 correlate with, and may be deduced from, the identity of the host target genes which VGAM2565 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86835] Nucleotide sequences of the VGAM2565 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2565 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2565 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2565 are further described hereinbelow with reference to Table 1.

[86836] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2565 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2565 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86837] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2565 gene, herein designated VGAM is inhibition of expression of VGAM2565 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2565 correlate with, and may be deduced from, the identity of the target genes which VGAM2565 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86838] Egl Nine Homolog 1 (C. elegans) (EGLN1, Accession NM_022051) is a VGAM2565 host target gene. EGLN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EGLN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGLN1 BINDING SITE, designated SEQ ID:22578, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86839] A function of VGAM2565 is therefore inhibition of Egl Nine Homolog 1 (C. elegans) (EGLN1, Accession NM_022051), a gene which is expressed in the cytoplasm of arterial

smooth muscle cells. Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGLN1. The function of EGLN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM216.Lysosomal-associated Membrane Protein 1 (LAMP1, Accession NM_005561) is another VGAM2565 host target gene. LAMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LAMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAMP1 BINDING SITE, designated SEQ ID:12089, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86840] Another function of VGAM2565 is therefore inhibition of Lysosomal-associated Membrane Protein 1 (LAMP1, Accession NM_005561), a gene which presents carbohydrate ligands to selectins. Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP1. The func-

tion of LAMP1 has been established by previous studies. The 120-kD lysosomal membrane glycoprotein is an acidic, heavily glycosylated membrane protein enriched in the lysosomal membrane. By using an oligonucleotide probe corresponding to the amino terminus of rat lgp120, Howe et al. (1988) isolated and characterized cDNA clones containing the entire coding region. The deduced amino acid sequence demonstrated that the rat LGP120 contains a putative signal peptide, 18 sites for N-linked glycosylation, a single membrane-spanning segment, and a short (11 amino acid) cytosolic tail. LGP120 showed similarity to 2 other lysosomal membrane proteins and showed a high degree of conservation in domain organization and primary structure with the proteins in other species. Viitala et al. (1988) reported the complete amino acid sequence for the human lysosome-associated membrane glycoprotein with M(r) about 120,000. The amino acid sequence, which was deduced from analysis of the cDNA, contains 385 amino acid residues. By means of in situ hybridization, Mattei et al. (1990) assigned the LAMP1 gene to 13q34. A related gene, which may be a pseudogene, mapped to 12p13.3. The hybridization of LAMP1 cDNA to 12p13.3 was observed even when probes representing

different portions of the LAMP1 cDNA were used. Although LAMP1 contains a functional hinge region, it has a disulfide arrangement different from that observed in members of the immunoglobulin superfamily and thus may represent a new family of membrane glycoproteins. The amino acid sequence of LAMP1 is more homologous to corresponding molecules from other species than it is to LAMP2 (OMIM Ref. No. 309060). Furthermore, LAMP1 and LAMP2 are immunologically distinguishable from each other. Thus it was proposed that LAMP1 and LAMP2 diverged relatively early in evolution but that LAMP1 (and possibly LAMP2) structures have been strongly conserved. Using Southern hybridization in hamster/human hybrid cell panels, Schleutker et al. (1991) confirmed the assignment of the LAMP1 gene to chromosome 13. Furthermore, Schleutker et al. (1991) demonstrated absence of genetic linkage of either LAMP1 or LAMP2 with Salla disease (OMIM Ref. No. 604369), a condition in which defective function of a lysosomal membrane transporter protein is the probable cause of accumulation of sialic acid in lysosomes. Bermingham et al. (1996) demonstrated that the Lamp1 gene is located on mouse chromosome 8. They could find no evidence that it is the site of the mutation in

mnd (motorneuron degeneration) mice.

[86841] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[86842] Bermingham, N. A.; Martin, J. E.; Fisher, E. M. C. : The mouse lysosomal membrane protein 1 gene as a candidate for the motorneuron degeneration (mnd) locus. Genomics 32: 266-271, 1996. ; and

[86843] Howe, C. L.; Granger, B. L.; Hull, M.; Green, S. A.; Gabel, C. A.; Helenius, A.; Mellman, I. : Derived protein sequence, oligosaccharides, and membrane insertion of the 120-kDa lysosomal.

[86844] Further studies establishing the function and utilities of LAMP1 are found in John Hopkins OMIM database record ID 153330, and in sited publications numbered 2951-2955 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Leukemia Inhibitory Factor (cholinergic differentiation factor) (LIF, Accession NM_002309) is another VGAM2565 host target gene. LIF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of LIF BINDING SITE, designated SEQ ID:8093, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86845] Another function of VGAM2565 is therefore inhibition of Leukemia Inhibitory Factor (cholinergic differentiation factor) (LIF, Accession NM_002309). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIF. SET Translocation (myeloid leukemia-associated) (SET, Accession NM_003011) is another VGAM2565 host target gene. SET BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SET, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SET BINDING SITE, designated SEQ ID:8921, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86846] Another function of VGAM2565 is therefore inhibition of SET Translocation (myeloid leukemia-associated) (SET, Accession NM_003011). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SET. Vacuolar Protein Sorting 41 (yeast) (VPS41, Accession NM_014396) is another VGAM2565 host target gene. VPS41 BINDING SITE1 and VPS41 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by VPS41, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS41 BINDING SITE1 and VPS41 BINDING SITE2, designated SEQ ID:15734 and SEQ ID:27934 respectively, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86847] Another function of VGAM2565 is therefore inhibition of Vacuolar Protein Sorting 41 (yeast) (VPS41, Accession NM_014396). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS41. CDV-1 (Accession NM_031473) is another VGAM2565 host target gene. CDV-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDV-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of CDV-1 BINDING SITE, designated SEQ ID:25539, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86848] Another function of VGAM2565 is therefore inhibition of CDV-1 (Accession NM_031473). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDV-1. Cysteine Sulfinic Acid Decarboxylase (CSAD, Accession NM_015989) is another VGAM2565 host target gene. CSAD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSAD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSAD BINDING SITE, designated SEQ ID:18082, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86849] Another function of VGAM2565 is therefore inhibition of Cysteine Sulfinic Acid Decarboxylase (CSAD, Accession NM_015989). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with CSAD. CSL4 (Accession NM_016046) is another VGAM2565 host target gene. CSL4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSL4 BINDING SITE, designated SEQ ID:18124, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86850] Another function of VGAM2565 is therefore inhibition of CSL4 (Accession NM_016046). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSL4. ENDOFIN (Accession NM_014733) is another VGAM2565 host target gene. ENDOFIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENDOFIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENDOFIN BINDING SITE, designated SEQ ID:16367, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5276.

[86851] Another function of VGAM2565 is therefore inhibition of ENDOFIN (Accession NM_014733). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENDOFIN. FLJ11160 (Accession NM_018344) is another VGAM2565 host target gene. FLJ11160 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11160 BINDING SITE, designated SEQ ID:20351, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86852] Another function of VGAM2565 is therefore inhibition of FLJ11160 (Accession NM_018344). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11160. KIAA0527 (Accession XM_171054) is another VGAM2565 host target gene. KIAA0527 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0527, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE, designated SEQ ID:45840, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86853] Another function of VGAM2565 is therefore inhibition of KIAA0527 (Accession XM_171054). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527. KIAA1900 (Accession XM_055299) is another VGAM2565 host target gene. KIAA1900 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1900, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1900 BINDING SITE, designated SEQ ID:36258, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86854] Another function of VGAM2565 is therefore inhibition of KIAA1900 (Accession XM_055299). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1900. Mitochondrial Ribosomal Protein L35 (MRPL35, Accession NM_016622) is another VGAM2565 host target gene. MRPL35 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL35, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL35 BINDING SITE, designated SEQ ID:18732, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86855] Another function of VGAM2565 is therefore inhibition of Mitochondrial Ribosomal Protein L35 (MRPL35, Accession NM_016622). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL35. Phospholipid Scramblase 4 (PLSCR4, Accession NM_020353) is another VGAM2565 host target gene. PLSCR4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLSCR4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PLSCR4 BINDING SITE, designated SEQ ID:21620, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86856] Another function of VGAM2565 is therefore inhibition of Phospholipid Scramblase 4 (PLSCR4, Accession NM_020353). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLSCR4. PR Domain Containing 8 (PRDM8, Accession NM_020226) is another VGAM2565 host target gene. PRDM8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRDM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM8 BINDING SITE, designated SEQ ID:21489, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86857] Another function of VGAM2565 is therefore inhibition of PR Domain Containing 8 (PRDM8, Accession NM_020226). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with PRDM8. Tripartite Motif-containing 2 (TRIM2, Accession NM_015271) is another VGAM2565 host target gene. TRIM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM2 BINDING SITE, designated SEQ ID:17595, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86858] Another function of VGAM2565 is therefore inhibition of Tripartite Motif-containing 2 (TRIM2, Accession NM_015271). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM2. LOC118611 (Accession XM_061055) is another VGAM2565 host target gene. LOC118611 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC118611, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118611 BINDING SITE, desig-

nated SEQ ID:37185, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86859] Another function of VGAM2565 is therefore inhibition of LOC118611 (Accession XM_061055). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118611. LOC130026 (Accession NM_138468) is another VGAM2565 host target gene. LOC130026 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130026 BINDING SITE, designated SEQ ID:28817, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86860] Another function of VGAM2565 is therefore inhibition of LOC130026 (Accession NM_138468). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130026. LOC153810 (Accession XM_087778) is another VGAM2565 host target gene. LOC153810 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153810, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153810 BINDING SITE, designated SEQ ID:39410, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86861] Another function of VGAM2565 is therefore inhibition of LOC153810 (Accession XM_087778). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153810. LOC221312 (Accession XM_166314) is another VGAM2565 host target gene. LOC221312 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221312, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221312 BINDING SITE, designated SEQ ID:44138, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86862] Another function of VGAM2565 is therefore inhibition of

LOC221312 (Accession XM_166314). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221312. LOC256080 (Accession XM_174235) is another VGAM2565 host target gene. LOC256080 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256080, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256080 BINDING SITE, designated SEQ ID:46584, to the nucleotide sequence of VGAM2565 RNA, herein designated VGAM RNA, also designated SEQ ID:5276.

[86863] Another function of VGAM2565 is therefore inhibition of LOC256080 (Accession XM_174235). Accordingly, utilities of VGAM2565 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256080. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2566 (VGAM2566) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[86864] VGAM2566 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2566 was detected is described hereinabove with reference to Figs. 1-8.

[86865] VGAM2566 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2566 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86866] VGAM2566 gene encodes a VGAM2566 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2566 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2566 precursor RNA is designated SEQ ID:2552, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2552 is located at position 2022 relative to the genome of Triatoma Virus.

[86867] VGAM2566 precursor RNA folds onto itself, forming VGAM2566 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86868] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2566 folded precursor RNA into VGAM2566 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2566 RNA is designated SEQ ID:5277, and is provided hereinbelow with reference to the sequence listing part.

[86869] VGAM2566 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2566 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86870] VGAM2566 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2566 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2566 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[86871] The complementary binding of VGAM2566 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2566 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2566 host target RNA into VGAM2566 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86872] It is appreciated that VGAM2566 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2566 host target genes. The mRNA of each one of this plurality of VGAM2566 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2566 RNA, herein designated VGAM RNA, and which when bound by VGAM2566 RNA causes inhibition of translation of respective one or more VGAM2566 host target proteins.

[86873] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2566 gene, herein designated VGAM GENE, on one

or more VGAM2566 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86874] It is yet further appreciated that a function of VGAM2566 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2566 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2566 correlate with, and may be deduced from, the identity of the host target genes which VGAM2566 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86875] Nucleotide sequences of the VGAM2566 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2566 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2566 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2566 are further described hereinbelow with reference to Table 1.

[86876] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2566 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2566 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86877] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2566 gene, herein designated VGAM is inhibition of expression of VGAM2566 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2566 correlate with, and may be deduced from, the identity of the target genes which VGAM2566 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86878] Unc-119 Homolog (C. elegans) (UNC119, Accession

NM_054035) is a VGAM2566 host target gene. UNC119 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UNC119, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UNC119 BINDING SITE, designated SEQ ID:27647, to the nucleotide sequence of VGAM2566 RNA, herein designated VGAM RNA, also designated SEQ ID:5277.

[86879] A function of VGAM2566 is therefore inhibition of Unc-119 Homolog (C. elegans) (UNC119, Accession NM_054035), a gene which is expressed in the retina and may play a role in the mechanism of photoreceptor neurotransmitter release through the synaptic vesicle cycle. Accordingly, utilities of VGAM2566 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC119. The function of UNC119 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1044.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention,

referred to here as Viral Genomic Address Messenger 2567 (VGAM2567) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86880] VGAM2567 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2567 was detected is described hereinabove with reference to Figs. 1-8.

[86881] VGAM2567 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2567 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86882] VGAM2567 gene encodes a VGAM2567 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2567 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2567 precursor RNA is designated SEQ ID:2553, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2553 is located at position 3811 relative to the genome of Triatoma Virus.

[86883] VGAM2567 precursor RNA folds onto itself, forming VGAM2567 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86884] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2567 folded precursor RNA into VGAM2567 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2567 RNA is designated SEQ ID:5278, and is provided hereinbelow with reference to the sequence listing part.

[86885] VGAM2567 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2567 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2567 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86886] VGAM2567 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2567 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2567 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86887] The complementary binding of VGAM2567 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2567 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2567 host target RNA into VGAM2567 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86888] It is appreciated that VGAM2567 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2567 host target genes. The mRNA of each one of this plurality of VGAM2567 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2567 RNA, herein designated VGAM RNA, and which when bound by VGAM2567 RNA causes inhibition of translation of respective one or more VGAM2567 host target proteins.

[86889] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2567 gene, herein designated VGAM GENE, on one or more VGAM2567 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86890] It is yet further appreciated that a function of VGAM2567 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2567 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2567 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2567 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86891] Nucleotide sequences of the VGAM2567 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2567 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2567 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2567 are further described hereinbelow with reference to Table 1.

[86892] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2567 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2567 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86893] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2567 gene, herein designated VGAM is inhibition of expression of VGAM2567 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2567 correlate with, and may be deduced from, the identity of the target genes which VGAM2567

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86894] Amiloride-sensitive Cation Channel 1, Neuronal (degenerin) (ACCN1, Accession NM_001094) is a VGAM2567 host target gene. ACCN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACCN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACCN1 BINDING SITE, designated SEQ ID:6752, to the nucleotide sequence of VGAM2567 RNA, herein designated VGAM RNA, also designated SEQ ID:5278.

[86895] A function of VGAM2567 is therefore inhibition of Amiloride-sensitive Cation Channel 1, Neuronal (degenerin) (ACCN1, Accession NM_001094), a gene which non-voltage-gated amiloride-sensitive cation channel permeable for sodium, potassium and lithium. Accordingly, utilities of VGAM2567 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACCN1. The function of ACCN1 and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM1095.PB1 (Accession NM_018313) is another VGAM2567 host target gene. PB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PB1 BINDING SITE, designated SEQ ID:20308, to the nucleotide sequence of VGAM2567 RNA, herein designated VGAM RNA, also designated SEQ ID:5278.

[86896] Another function of VGAM2567 is therefore inhibition of PB1 (Accession NM_018313). Accordingly, utilities of VGAM2567 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PB1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2568 (VGAM2568) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86897] VGAM2568 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2568 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[86898] VGAM2568 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2568 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86899] VGAM2568 gene encodes a VGAM2568 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2568 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2568 precursor RNA is designated SEQ ID:2554, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2554 is located at position 4293 relative to the genome of Triatoma Virus.

[86900] VGAM2568 precursor RNA folds onto itself, forming VGAM2568 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86901] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2568 folded precursor RNA into VGAM2568 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2568 RNA is designated SEQ ID:5279, and is provided hereinbelow with reference to the sequence listing part.

[86902] VGAM2568 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2568 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2568 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86903] VGAM2568 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2568 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2568 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2568 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2568 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86904] The complementary binding of VGAM2568 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2568 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2568 host target RNA into VGAM2568 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86905] It is appreciated that VGAM2568 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2568 host target genes. The mRNA of each one of this plurality of VGAM2568 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2568 RNA, herein designated VGAM RNA, and which when bound by VGAM2568 RNA causes inhibition of translation of respective one or more VGAM2568 host target proteins.

[86906] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2568 gene, herein designated VGAM GENE, on one or more VGAM2568 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86907] It is yet further appreciated that a function of VGAM2568 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2568 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2568 correlate with, and may be deduced from, the identity of the host target genes which VGAM2568 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86908] Nucleotide sequences of the VGAM2568 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2568 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2568 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2568 are further described hereinbelow with reference to Table 1.

[86909] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2568 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2568 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86910] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2568 gene, herein designated VGAM is inhibition of expression of VGAM2568 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2568 correlate with, and may be deduced from, the identity of the target genes which VGAM2568 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86911] H2A Histone Family, Member J (H2AFJ, Accession NM_018267) is a VGAM2568 host target gene. H2AFJ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H2AFJ, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H2AFJ BINDING SITE, designated SEQ ID:20239, to the nucleotide sequence of VGAM2568 RNA, herein designated VGAM RNA, also designated SEQ ID:5279.

[86912] A function of VGAM2568 is therefore inhibition of H2A Histone Family, Member J (H2AFJ, Accession NM_018267). Accordingly, utilities of VGAM2568 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AFJ. KIAA0061 (Accession XM_043094) is another VGAM2568 host target gene. KIAA0061 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0061, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0061 BINDING SITE, designated SEQ ID:33892, to the nucleotide sequence of VGAM2568 RNA, herein designated VGAM RNA, also designated SEQ ID:5279.

[86913] Another function of VGAM2568 is therefore inhibition of KIAA0061 (Accession XM_043094). Accordingly, utilities of VGAM2568 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0061. KIAA1655 (Accession XM_039442) is another VGAM2568 host target gene. KIAA1655 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1655, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1655 BINDING SITE, designated SEQ ID:33083, to the nucleotide sequence of VGAM2568 RNA, herein designated VGAM RNA, also designated SEQ ID:5279.

[86914] Another function of VGAM2568 is therefore inhibition of KIAA1655 (Accession XM_039442). Accordingly, utilities of VGAM2568 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1655. Kelch-like 6 (Drosophila) (KLHL6, Accession NM_130446) is another VGAM2568 host target gene. KLHL6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLHL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLHL6 BINDING SITE, designated SEQ

ID:28215, to the nucleotide sequence of VGAM2568 RNA, herein designated VGAM RNA, also designated SEQ ID:5279.

[86915] Another function of VGAM2568 is therefore inhibition of Kelch-like 6 (Drosophila) (KLHL6, Accession NM_130446). Accordingly, utilities of VGAM2568 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL6. LOC147947 (Accession XM_085974) is another VGAM2568 host target gene. LOC147947 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147947, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147947 BINDING SITE, designated SEQ ID:38424, to the nucleotide sequence of VGAM2568 RNA, herein designated VGAM RNA, also designated SEQ ID:5279.

[86916] Another function of VGAM2568 is therefore inhibition of LOC147947 (Accession XM_085974). Accordingly, utilities of VGAM2568 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147947. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2569 (VGAM2569) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86917] VGAM2569 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2569 was detected is described hereinabove with reference to Figs. 1-8.

[86918] VGAM2569 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2569 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86919] VGAM2569 gene encodes a VGAM2569 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2569 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2569 precursor RNA is designated SEQ ID:2555, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2555 is located at position 5389 relative to the genome of Triatoma Virus.

[86920] VGAM2569 precursor RNA folds onto itself, forming VGAM2569 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86921] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2569 folded precursor RNA into VGAM2569 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2569 RNA is designated SEQ ID:5280, and is provided hereinbelow with reference to the sequence listing part.

[86922] VGAM2569 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2569 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2569 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86923] VGAM2569 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2569 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2569 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2569 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2569 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86924] The complementary binding of VGAM2569 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2569 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2569 host target RNA into VGAM2569 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86925] It is appreciated that VGAM2569 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2569 host target genes. The mRNA of each one of this plurality of VGAM2569 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2569 RNA, herein designated VGAM RNA, and which when bound by VGAM2569 RNA causes inhibition of translation of respective one or more

VGAM2569 host target proteins.

[86926] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2569 gene, herein designated VGAM GENE, on one or more VGAM2569 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86927] It is yet further appreciated that a function of VGAM2569 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific

functions, and accordingly utilities, of VGAM2569 correlate with, and may be deduced from, the identity of the host target genes which VGAM2569 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86928] Nucleotide sequences of the VGAM2569 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2569 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2569 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2569 are further described hereinbelow with reference to Table 1.

[86929] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2569 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2569 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86930] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2569 gene, herein designated VGAM is inhibition of expression of VGAM2569 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2569 correlate with, and may be deduced from, the identity of the target genes which VGAM2569 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86931] Chloride Channel 3 (CLCN3, Accession NM_001829) is a VGAM2569 host target gene. CLCN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLCN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLCN3 BINDING SITE, designated SEQ ID:7564, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86932] A function of VGAM2569 is therefore inhibition of Chloride Channel 3 (CLCN3, Accession NM_001829), a gene which play a role in the neural cell function through regulation of membrane excitability. Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN3. The function of CLCN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM1332.Dual Oxidase 2 (DUOX2, Accession NM_014080) is another VGAM2569 host target gene. DUOX2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DUOX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DUOX2 BINDING SITE, designated SEQ ID:15306, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86933] Another function of VGAM2569 is therefore inhibition of Dual Oxidase 2 (DUOX2, Accession NM_014080), a gene which is a calcium-dependent flavoprotein component of thyroid NADPH oxidase. Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUOX2. The function of DUOX2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1169.Fms-related Tyrosine Kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1, Accession NM_002019) is another

VGAM2569 host target gene. FLT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLT1 BINDING SITE, designated SEQ ID:7763, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86934] Another function of VGAM2569 is therefore inhibition of Fms-related Tyrosine Kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1, Accession NM_002019). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLT1. Forkhead Box E1 (thyroid transcription factor 2) (FOXE1, Accession NM_004473) is another VGAM2569 host target gene. FOXE1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FOXE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXE1 BINDING SITE, designated SEQ

ID:10782, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86935] Another function of VGAM2569 is therefore inhibition of Forkhead Box E1 (thyroid transcription factor 2) (FOXE1, Accession NM_004473). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXE1. UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7, Accession NM_054110) is another VGAM2569 host target gene. GALNT7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALNT7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNT7 BINDING SITE, designated SEQ ID:27649, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86936] Another function of VGAM2569 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7,

Accession NM_054110). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT7. Nuclear Factor of Activated T-cells, Cytoplasmic, Calcineurin-dependent 1 (NFATC1, Accession NM_006162) is another VGAM2569 host target gene. NFATC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NFATC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFATC1 BINDING SITE, designated SEQ ID:12815, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86937] Another function of VGAM2569 is therefore inhibition of Nuclear Factor of Activated T-cells, Cytoplasmic, Calcineurin-dependent 1 (NFATC1, Accession NM_006162), a gene which regulates he activation,proliferation,differentiation and programmed death of ymphoid and nonlymphoid cells. Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

NFATC1. The function of NFATC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM123.Peroxisomal Farnesylated Protein (PXF, Accession NM_002857) is another VGAM2569 host target gene. PXF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PXF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PXF BINDING SITE, designated SEQ ID:8748, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86938] Another function of VGAM2569 is therefore inhibition of Peroxisomal Farnesylated Protein (PXF, Accession NM_002857), a gene which may function in peroxisomal biogenesis or assembly. Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PXF. The function of PXF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM193.Vacuolar Protein Sorting 26 (yeast) (VPS26,

Accession NM_004896) is another VGAM2569 host target gene. VPS26 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS26 BINDING SITE, designated SEQ ID:11323, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86939] Another function of VGAM2569 is therefore inhibition of Vacuolar Protein Sorting 26 (yeast) (VPS26, Accession NM_004896), a gene which is a sorting protein- ensures the proper delivery of organelle-specific proteins. Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS26. The function of VPS26 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM315.Agmatine Ureohydrolase (agmatinase) (AGMAT, Accession NM_024758) is another VGAM2569 host target gene. AGMAT BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by AGMAT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AGMAT BINDING SITE, designated SEQ ID:24104, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86940] Another function of VGAM2569 is therefore inhibition of Agmatine Ureohydrolase (agmatinase) (AGMAT, Accession NM_024758). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGMAT. DKFZp761O17121 (Accession NM_032287) is another VGAM2569 host target gene. DKFZp761O17121 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761O17121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761O17121 BINDING SITE, designated SEQ ID:26044, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86941] Another function of VGAM2569 is therefore inhibition of

DKFZp761O17121 (Accession NM_032287). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761O17121. Junctional Adhesion Molecule 1 (JAM1, Accession NM_144503) is another VGAM2569 host target gene. JAM1 BINDING SITE1 through JAM1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by JAM1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAM1 BINDING SITE1 through JAM1 BINDING SITE4, designated SEQ ID:29335, SEQ ID:29346, SEQ ID:29326 and SEQ ID:18859 respectively, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86942] Another function of VGAM2569 is therefore inhibition of Junctional Adhesion Molecule 1 (JAM1, Accession NM_144503). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAM1. KIAA1573 (Accession XM_031545) is another VGAM2569 host target gene. KIAA1573 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by KIAA1573, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1573 BINDING SITE, designated SEQ ID:31412, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86943] Another function of VGAM2569 is therefore inhibition of KIAA1573 (Accession XM_031545). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1573. KIAA1750 (Accession XM_043067) is another VGAM2569 host target gene. KIAA1750 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1750, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1750 BINDING SITE, designated SEQ ID:33871, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86944] Another function of VGAM2569 is therefore inhibition of

KIAA1750 (Accession XM_043067). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1750. MGC11034 (Accession NM_031453) is another VGAM2569 host target gene. MGC11034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC11034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11034 BINDING SITE, designated SEQ ID:25469, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86945] Another function of VGAM2569 is therefore inhibition of MGC11034 (Accession NM_031453). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11034. Nuclear Receptor Subfamily 6, Group A, Member 1 (NR6A1, Accession NM_001489) is another VGAM2569 host target gene. NR6A1 BINDING SITE1 through NR6A1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NR6A1, corresponding to HOST TARGET binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR6A1 BINDING SITE1 through NR6A1 BINDING SITE3, designated SEQ ID:7231, SEQ ID:27179 and SEQ ID:27185 respectively, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86946] Another function of VGAM2569 is therefore inhibition of Nuclear Receptor Subfamily 6, Group A, Member 1 (NR6A1, Accession NM_001489). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR6A1. Roundabout Homolog 4, Magic Roundabout (Drosophila) (ROBO4, Accession NM_019055) is another VGAM2569 host target gene. ROBO4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ROBO4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ROBO4 BINDING SITE, designated SEQ ID:21134, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86947] Another function of VGAM2569 is therefore inhibition of Roundabout Homolog 4, Magic Roundabout (Drosophila) (ROBO4, Accession NM_019055). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROBO4. LOC154860 (Accession XM_098623) is another VGAM2569 host target gene. LOC154860 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154860, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154860 BINDING SITE, designated SEQ ID:41733, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86948] Another function of VGAM2569 is therefore inhibition of LOC154860 (Accession XM_098623). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154860. LOC220522 (Accession XM_018306) is another VGAM2569 host target gene. LOC220522 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220522, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220522 BINDING SITE, designated SEQ ID:30350, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86949] Another function of VGAM2569 is therefore inhibition of LOC220522 (Accession XM_018306). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220522. LOC253596 (Accession XM_170934) is another VGAM2569 host target gene. LOC253596 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253596, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253596 BINDING SITE, designated SEQ ID:45721, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86950] Another function of VGAM2569 is therefore inhibition of LOC253596 (Accession XM_170934). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC253596. LOC93268 (Accession XM_050158) is another VGAM2569 host target gene. LOC93268 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93268 BINDING SITE, designated SEQ ID:35587, to the nucleotide sequence of VGAM2569 RNA, herein designated VGAM RNA, also designated SEQ ID:5280.

[86951] Another function of VGAM2569 is therefore inhibition of LOC93268 (Accession XM_050158). Accordingly, utilities of VGAM2569 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93268. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2570 (VGAM2570) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86952] VGAM2570 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2570 was detected is described hereinabove with reference to Figs. 1-8.

[86953] VGAM2570 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2570 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86954] VGAM2570 gene encodes a VGAM2570 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2570 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2570 precursor RNA is designated SEQ ID:2556, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2556 is located at position 5274 relative to the genome of Triatoma Virus.

[86955] VGAM2570 precursor RNA folds onto itself, forming VGAM2570 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86956] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2570 folded precursor RNA into VGAM2570 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM2570 RNA is designated SEQ ID:5281, and is provided hereinbelow with reference to the sequence listing part.

[86957] VGAM2570 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2570 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86958] VGAM2570 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2570 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2570 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86959] The complementary binding of VGAM2570 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2570 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2570 host target RNA into VGAM2570 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86960] It is appreciated that VGAM2570 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2570 host target genes. The mRNA of each one of this plurality of VGAM2570 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2570 RNA, herein designated VGAM RNA, and which when bound by VGAM2570 RNA causes inhibition of translation of respective one or more VGAM2570 host target proteins.

[86961] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2570 gene, herein designated VGAM GENE, on one or more VGAM2570 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86962] It is yet further appreciated that a function of VGAM2570 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2570 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2570 correlate with, and may be deduced from, the identity of the host target genes which VGAM2570 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86963] Nucleotide sequences of the VGAM2570 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2570 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2570 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2570 are further described hereinbelow with reference to Table 1.

[86964] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2570 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2570 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86965] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2570 gene, herein designated VGAM is inhibition of expression of VGAM2570 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2570 correlate with, and may be deduced from, the identity of the target genes which VGAM2570 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86966] Fibrinogen, A Alpha Polypeptide (FGA, Accession NM_000508) is a VGAM2570 host target gene. FGA BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by FGA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGA BINDING SITE, designated SEQ ID:6119, to the nucleotide sequence of VGAM2570 RNA, herein designated VGAM RNA, also designated SEQ ID:5281.

[86967] A function of VGAM2570 is therefore inhibition of Fibrinogen, A Alpha Polypeptide (FGA, Accession NM_000508). Accordingly, utilities of VGAM2570 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGA. XPO5 (Accession XM_166042) is another VGAM2570 host target gene. XPO5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XPO5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XPO5 BINDING SITE, designated SEQ ID:43839, to the nucleotide sequence of VGAM2570 RNA, herein designated VGAM RNA, also designated SEQ ID:5281.

[86968] Another function of VGAM2570 is therefore inhibition of XPO5 (Accession XM_166042). Accordingly, utilities of

VGAM2570 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XPO5. LOC51333 (Accession NM_016643) is another VGAM2570 host target gene. LOC51333 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51333 BINDING SITE, designated SEQ ID:18750, to the nucleotide sequence of VGAM2570 RNA, herein designated VGAM RNA, also designated SEQ ID:5281.

[86969] Another function of VGAM2570 is therefore inhibition of LOC51333 (Accession NM_016643). Accordingly, utilities of VGAM2570 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51333. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2571 (VGAM2571) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86970] VGAM2571 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2571 was detected is described hereinabove with reference to Figs. 1-8.

[86971] VGAM2571 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2571 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86972] VGAM2571 gene encodes a VGAM2571 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2571 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2571 precursor RNA is designated SEQ ID:2557, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2557 is located at position 5836 relative to the genome of Triatoma Virus.

[86973] VGAM2571 precursor RNA folds onto itself, forming VGAM2571 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86974] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2571 folded precursor RNA into VGAM2571 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2571 RNA is designated SEQ ID:5282, and is provided hereinbelow with reference to the sequence listing part.

[86975] VGAM2571 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2571 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[86976] VGAM2571 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2571 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2571 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[86977] The complementary binding of VGAM2571 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2571 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2571 host target RNA into VGAM2571 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[86978] It is appreciated that VGAM2571 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2571 host target genes. The mRNA of each one of this plurality of VGAM2571 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2571 RNA, herein designated VGAM RNA, and which when bound by VGAM2571 RNA causes inhibition of translation of respective one or more VGAM2571 host target proteins.

[86979] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2571 gene, herein designated VGAM GENE, on one or more VGAM2571 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[86980] It is yet further appreciated that a function of VGAM2571 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2571 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2571 correlate with, and may be deduced from, the identity of the host target genes which VGAM2571 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[86981] Nucleotide sequences of the VGAM2571 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2571 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2571 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2571 are further described hereinbelow with reference to Table 1.

[86982] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2571 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2571 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[86983] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2571 gene, herein designated VGAM is inhibition of expression of VGAM2571 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2571 correlate with, and may be deduced from, the identity of the target genes which VGAM2571 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[86984] Ring Finger Protein (C3H2C3 type) 6 (RNF6, Accession NM_005977) is a VGAM2571 host target gene. RNF6

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF6 BINDING SITE, designated SEQ ID:12603, to the nucleotide sequence of VGAM2571 RNA, herein designated VGAM RNA, also designated SEQ ID:5282.

[86985] A function of VGAM2571 is therefore inhibition of Ring Finger Protein (C3H2C3 type) 6 (RNF6, Accession NM_005977), a gene which is a RING finger protein, may be a tumor suppressor. Accordingly, utilities of VGAM2571 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF6. The function of RNF6 has been established by previous studies. By FISH and physical mapping, Macdonald et al. (1999) determined that RNF6 is located at 13q12.2 close to marker D13S1121, and that it is oriented from telomere to centromere. RNF6 was not disrupted by the t(4;13) translocation in the case of myeloproliferative disorder studied by Macdonald et al. (1999). MOLECULAR GENETICS By loss of heterozygosity (LOH) studies in esophageal squamous cell carcinoma (ESCC; 133239), Li et al. (2001)

identified an 800-kb region on chromosome 13q12.11 as the site of a potential tumor suppressor gene. Lo et al. (2002) screened the ATP8A2 (OMIM Ref. No. 605870) and RNF6 genes for mutations in 24 ESCC primary tumors and 16 tumor cell lines by direct sequencing of the PCR products that were amplified from each exon. They detected no mutations in ATP8A2, but identified 3 somatic mutations in the RNF6 gene in the ESCC primary tumors (604242.0001-604242.0003); 1 mutation was also found in a tumor cell line. Lo et al. (2002) concluded that RNF6 may be a tumor suppressor gene involved in the pathogenesis of ESCC.

[86986] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[86987] Lo, H. S.; Hu, N.; Gere, S.; Lu, N.; Su, H.; Goldstein, A. M.; Taylor, P. R.; Lee, M. P. : Identification of somatic mutations of the RNF6 gene in human esophageal squamous cell carcinoma. Cancer Res. 62: 4191-4193, 2002. ; and

[86988] Macdonald, D. H. C.; Lahiri, D.; Sampath, A.; Chase, A.; Sohal, J.; Cross, N. C. P. : Cloning and characterization of RNF6, a novel RING finger gene mapping to 13q12. Genomics 58: 94-97, 1.

[86989] Further studies establishing the function and utilities of RNF6 are found in John Hopkins OMIM database record ID 604242, and in sited publications numbered 5366-465 and 691 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.BCL2-associated Athanogene 5 (BAG5, Accession NM_004873) is another VGAM2571 host target gene. BAG5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAG5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAG5 BINDING SITE, designated SEQ ID:11301, to the nucleotide sequence of VGAM2571 RNA, herein designated VGAM RNA, also designated SEQ ID:5282.

[86990] Another function of VGAM2571 is therefore inhibition of BCL2-associated Athanogene 5 (BAG5, Accession NM_004873). Accordingly, utilities of VGAM2571 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG5. LOC143425 (Accession XM_113695) is another VGAM2571 host target gene. LOC143425 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by LOC143425, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143425 BINDING SITE, designated SEQ ID:42349, to the nucleotide sequence of VGAM2571 RNA, herein designated VGAM RNA, also designated SEQ ID:5282.

[86991] Another function of VGAM2571 is therefore inhibition of LOC143425 (Accession XM_113695). Accordingly, utilities of VGAM2571 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143425. LOC220936 (Accession XM_166137) is another VGAM2571 host target gene. LOC220936 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220936, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220936 BINDING SITE, designated SEQ ID:43931, to the nucleotide sequence of VGAM2571 RNA, herein designated VGAM RNA, also designated SEQ ID:5282.

[86992] Another function of VGAM2571 is therefore inhibition of LOC220936 (Accession XM_166137). Accordingly, utilities

of VGAM2571 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220936. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2572 (VGAM2572) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[86993] VGAM2572 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2572 was detected is described hereinabove with reference to Figs. 1-8.

[86994] VGAM2572 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2572 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[86995] VGAM2572 gene encodes a VGAM2572 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2572 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2572 precursor RNA is designated SEQ ID:2558, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2558 is located at position 3076 relative to the genome of Triatoma Virus.

[86996] VGAM2572 precursor RNA folds onto itself, forming VGAM2572 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[86997] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2572 folded precursor RNA into VGAM2572 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2572 RNA is designated SEQ ID:5283, and

is provided hereinbelow with reference to the sequence listing part.

[86998] VGAM2572 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2572 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[86999] VGAM2572 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2572 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2572 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87000] The complementary binding of VGAM2572 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2572 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2572 host target RNA into VGAM2572 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87001] It is appreciated that VGAM2572 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2572 host target genes. The mRNA of each one of this plurality of VGAM2572 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2572 RNA, herein designated VGAM RNA, and which when bound by VGAM2572 RNA causes inhibition of translation of respective one or more VGAM2572 host target proteins.

[87002] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2572 gene, herein designated VGAM GENE, on one or more VGAM2572 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87003] It is yet further appreciated that a function of VGAM2572 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2572 correlate with, and may be deduced from, the identity of the host target genes which VGAM2572 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87004] Nucleotide sequences of the VGAM2572 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2572 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2572 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2572 are further described hereinbelow with reference to Table 1.

[87005] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2572 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2572 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87006] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2572 gene, herein designated VGAM is inhibition of expression of VGAM2572 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2572 correlate with, and may be deduced from, the identity of the target genes which VGAM2572 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87007] LENG4 (Accession NM_024298) is a VGAM2572 host target gene. LENG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LENG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LENG4 BINDING SITE, designated SEQ ID:23582, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87008] A function of VGAM2572 is therefore inhibition of LENG4 (Accession NM_024298), a gene which may be a transmembrane protein. Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LENG4. The function of LENG4 and its association with various diseases and clini-

cal conditions, has been established by previous studies, as described hereinabove with reference to VGAM259.Mucin 3B (MUC3B, Accession XM_168578) is another VGAM2572 host target gene. MUC3B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MUC3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MUC3B BINDING SITE, designated SEQ ID:45255, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87009] Another function of VGAM2572 is therefore inhibition of Mucin 3B (MUC3B, Accession XM_168578), a gene which provides a protective, lubricating barrier against particles and infectious agents at mucosal surfaces. Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MUC3B. The function of MUC3B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog,

Drosophila) (PDE4D, Accession XM_056815) is another VGAM2572 host target gene. PDE4D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4D BINDING SITE, designated SEQ ID:36435, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87010] Another function of VGAM2572 is therefore inhibition of Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815), a gene which has similarity to Drosophila dnc, which is the affected protein in learning and memory mutant dunce. Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4D. The function of PDE4D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM180.Runt-related Transcription Factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1, Accession

NM_001754) is another VGAM2572 host target gene. RUNX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RUNX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RUNX1 BINDING SITE, designated SEQ ID:7502, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87011] Another function of VGAM2572 is therefore inhibition of Runt-related Transcription Factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1, Accession NM_001754). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RUNX1. Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Zeta Polypeptide (YWHAZ, Accession NM_003406) is another VGAM2572 host target gene. YWHAZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YWHAZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of YWHAZ BINDING SITE, designated SEQ ID:9444, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87012] Another function of VGAM2572 is therefore inhibition of Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Zeta Polypeptide (YWHAZ, Accession NM_003406), a gene which mediates signal transduction by binding to phosphorylated serine residues on a variety of signaling molecules. Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YWHAZ. The function of YWHAZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM43.FEM-2 (Accession NM_014634) is another VGAM2572 host target gene. FEM-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FEM-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FEM-2 BINDING SITE, designated SEQ ID:16009, to the nu-

cleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87013] Another function of VGAM2572 is therefore inhibition of FEM-2 (Accession NM_014634). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEM-2. FLJ20514 (Accession NM_017856) is another VGAM2572 host target gene. FLJ20514 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20514 BINDING SITE, designated SEQ ID:19532, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87014] Another function of VGAM2572 is therefore inhibition of FLJ20514 (Accession NM_017856). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20514. G4 (Accession XM_165712) is another VGAM2572 host target gene. G4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region

of mRNA encoded by G4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of G4 BINDING SITE, designated SEQ ID:43735, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87015] Another function of VGAM2572 is therefore inhibition of G4 (Accession XM_165712). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G4. KIAA1036 (Accession NM_014909) is another VGAM2572 host target gene. KIAA1036 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1036, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1036 BINDING SITE, designated SEQ ID:17125, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87016] Another function of VGAM2572 is therefore inhibition of KIAA1036 (Accession NM_014909). Accordingly, utilities

of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1036. KIAA1340 (Accession XM_044836) is another VGAM2572 host target gene. KIAA1340 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1340, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1340 BINDING SITE, designated SEQ ID:34298, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87017] Another function of VGAM2572 is therefore inhibition of KIAA1340 (Accession XM_044836). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1340. Protein Tyrosine Phosphatase Type IVA, Member 1 (PTP4A1, Accession NM_003463) is another VGAM2572 host target gene. PTP4A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTP4A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PTP4A1 BINDING SITE, designated SEQ ID:9534, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87018] Another function of VGAM2572 is therefore inhibition of Protein Tyrosine Phosphatase Type IVA, Member 1 (PTP4A1, Accession NM_003463). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTP4A1. Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958) is another VGAM2572 host target gene. RNF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE, designated SEQ ID:10097, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87019] Another function of VGAM2572 is therefore inhibition of Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with RNF8. LOC219376 (Accession XM_168147) is another VGAM2572 host target gene. LOC219376 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219376 BINDING SITE, designated SEQ ID:45069, to the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87020] Another function of VGAM2572 is therefore inhibition of LOC219376 (Accession XM_168147). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219376. LOC257554 (Accession XM_175149) is another VGAM2572 host target gene. LOC257554 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257554, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257554 BINDING SITE, designated SEQ ID:46642, to

the nucleotide sequence of VGAM2572 RNA, herein designated VGAM RNA, also designated SEQ ID:5283.

[87021] Another function of VGAM2572 is therefore inhibition of LOC257554 (Accession XM_175149). Accordingly, utilities of VGAM2572 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257554. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2573 (VGAM2573) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87022] VGAM2573 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2573 was detected is described hereinabove with reference to Figs. 1-8.

[87023] VGAM2573 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2573 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87024] VGAM2573 gene encodes a VGAM2573 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2573 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2573 precursor RNA is designated SEQ ID:2559, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2559 is located at position 3368 relative to the genome of Triatoma Virus.

[87025] VGAM2573 precursor RNA folds onto itself, forming VGAM2573 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87026] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2573 folded precursor RNA into VGAM2573 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2573 RNA is designated SEQ ID:5284, and is provided hereinbelow with reference to the sequence listing part.

[87027] VGAM2573 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2573 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87028] VGAM2573 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2573 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2573 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87029] The complementary binding of VGAM2573 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2573 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2573 host target RNA into VGAM2573 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87030] It is appreciated that VGAM2573 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2573 host target genes. The mRNA of each one of this plurality of VGAM2573 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2573 RNA, herein designated VGAM RNA, and which when bound by VGAM2573 RNA causes inhibition of translation of respective one or more VGAM2573 host target proteins.

[87031] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2573 gene, herein designated VGAM GENE, on one or more VGAM2573 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87032] It is yet further appreciated that a function of VGAM2573 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2573 correlate with, and may be deduced from, the identity of the host target genes which VGAM2573 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87033] Nucleotide sequences of the VGAM2573 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2573 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2573 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2573 are further described hereinbelow with reference to Table 1.

[87034] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2573 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2573 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87035] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2573 gene, herein designated VGAM is inhibition of expression of VGAM2573 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2573 correlate with, and may be deduced from, the identity of the target genes which VGAM2573 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87036] Contactin 3 (plasmacytoma associated) (CNTN3, Accession XM_039627) is a VGAM2573 host target gene. CNTN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNTN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNTN3 BINDING SITE, designated SEQ ID:33132, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87037] A function of VGAM2573 is therefore inhibition of Contactin 3 (plasmacytoma associated) (CNTN3, Accession

XM_039627), a gene which may play a role in the initial growth and guidance of axons. Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTN3. The function of CNTN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM420.C-reactive Protein, Pentraxin-related (CRP, Accession XM_049673) is another VGAM2573 host target gene. CRP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRP BINDING SITE, designated SEQ ID:35463, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87038] Another function of VGAM2573 is therefore inhibition of C-reactive Protein, Pentraxin-related (CRP, Accession XM_049673). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRP. Ectonucleoside Triphosphate Diphosphohydrolase 6 (putative function)

(ENTPD6, Accession NM_001247) is another VGAM2573 host target gene. ENTPD6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENTPD6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENTPD6 BINDING SITE, designated SEQ ID:6919, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87039] Another function of VGAM2573 is therefore inhibition of Ectonucleoside Triphosphate Diphosphohydrolase 6 (putative function) (ENTPD6, Accession NM_001247), a gene which might support glycosylation reactions in the golgi apparatus and, when released from cells, might catalyze the hydrolysis of extracellular nucleotides. Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENTPD6. The function of ENTPD6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM827.5-methyltetrahydrofolate-homocysteine

Methyltransferase (MTR, Accession NM_000254) is another VGAM2573 host target gene. MTR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTR BINDING SITE, designated SEQ ID:5795, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87040] Another function of VGAM2573 is therefore inhibition of 5-methyltetrahydrofolate-homocysteine Methyltransferase (MTR, Accession NM_000254). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTR. Protocadherin 11 X-linked (PCDH11X, Accession NM_032967) is another VGAM2573 host target gene. PCDH11X BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDH11X, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE, designated SEQ

ID:26780, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87041] Another function of VGAM2573 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032967), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Protocadherin 11 Y-linked (PCDH11Y, Accession NM_032971) is another VGAM2573 host target gene. PCDH11Y BINDING SITE1 and PCDH11Y BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDH11Y, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11Y BINDING SITE1 and PCDH11Y BINDING SITE2, designated SEQ

ID:26813 and SEQ ID:26815 respectively, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87042] Another function of VGAM2573 is therefore inhibition of Protocadherin 11 Y-linked (PCDH11Y, Accession NM_032971). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11Y. Ubiquitin-conjugating Enzyme E2 Variant 1 (UBE2V1, Accession NM_003349) is another VGAM2573 host target gene. UBE2V1 BINDING SITE1 through UBE2V1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by UBE2V1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2V1 BINDING SITE1 through UBE2V1 BINDING SITE3, designated SEQ ID:9366, SEQ ID:22518 and SEQ ID:6362 respectively, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87043] Another function of VGAM2573 is therefore inhibition of Ubiquitin-conjugating Enzyme E2 Variant 1 (UBE2V1, Accession NM_003349), a gene which may play a role in sig-

naling for DNA repair. Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2V1. The function of UBE2V1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM155.MGC12466 (Accession XM_086336) is another VGAM2573 host target gene. MGC12466 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC12466, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12466 BINDING SITE, designated SEQ ID:38609, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87044] Another function of VGAM2573 is therefore inhibition of MGC12466 (Accession XM_086336). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12466. Olfactory Receptor, Family 7, Subfamily C, Member 1 (OR7C1, Accession NM_017506) is another VGAM2573 host target gene. OR7C1 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OR7C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OR7C1 BINDING SITE, designated SEQ ID:18961, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87045] Another function of VGAM2573 is therefore inhibition of Olfactory Receptor, Family 7, Subfamily C, Member 1 (OR7C1, Accession NM_017506). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR7C1. Oxysterol Binding Protein-like 6 (OSBPL6, Accession NM_032523) is another VGAM2573 host target gene. OSBPL6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL6 BINDING SITE, designated SEQ ID:26269, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ

ID:5284.

[87046] Another function of VGAM2573 is therefore inhibition of Oxysterol Binding Protein-like 6 (OSBPL6, Accession NM_032523). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL6. PCCX2 (Accession XM_038352) is another VGAM2573 host target gene. PCCX2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCCX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCCX2 BINDING SITE, designated SEQ ID:32820, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87047] Another function of VGAM2573 is therefore inhibition of PCCX2 (Accession XM_038352). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCCX2. TUSP (Accession NM_020245) is another VGAM2573 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21521, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87048] Another function of VGAM2573 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. LOC118738 (Accession XM_061125) is another VGAM2573 host target gene. LOC118738 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC118738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118738 BINDING SITE, designated SEQ ID:37192, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87049] Another function of VGAM2573 is therefore inhibition of LOC118738 (Accession XM_061125). Accordingly, utilities

of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118738. LOC158056 (Accession XM_088463) is another VGAM2573 host target gene. LOC158056 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158056, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158056 BINDING SITE, designated SEQ ID:39712, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87050] Another function of VGAM2573 is therefore inhibition of LOC158056 (Accession XM_088463). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158056. LOC163231 (Accession XM_092094) is another VGAM2573 host target gene. LOC163231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC163231 BINDING SITE, designated SEQ ID:40092, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87051] Another function of VGAM2573 is therefore inhibition of LOC163231 (Accession XM_092094). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163231. LOC205669 (Accession XM_120309) is another VGAM2573 host target gene. LOC205669 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC205669, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC205669 BINDING SITE, designated SEQ ID:43607, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87052] Another function of VGAM2573 is therefore inhibition of LOC205669 (Accession XM_120309). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC205669. LOC219738 (Accession NM_145306) is another VGAM2573 host target gene. LOC219738 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219738 BINDING SITE, designated SEQ ID:29817, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87053] Another function of VGAM2573 is therefore inhibition of LOC219738 (Accession NM_145306). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219738. LOC253039 (Accession XM_171203) is another VGAM2573 host target gene. LOC253039 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253039, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253039 BINDING SITE, designated SEQ ID:45991, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87054] Another function of VGAM2573 is therefore inhibition of

LOC253039 (Accession XM_171203). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253039. LOC51337 (Accession NM_016647) is another VGAM2573 host target gene. LOC51337 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51337 BINDING SITE, designated SEQ ID:18761, to the nucleotide sequence of VGAM2573 RNA, herein designated VGAM RNA, also designated SEQ ID:5284.

[87055] Another function of VGAM2573 is therefore inhibition of LOC51337 (Accession NM_016647). Accordingly, utilities of VGAM2573 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51337. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2574 (VGAM2574) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[87056] VGAM2574 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2574 was detected is described hereinabove with reference to Figs. 1-8.

[87057] VGAM2574 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2574 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87058] VGAM2574 gene encodes a VGAM2574 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2574 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2574 precursor RNA is designated SEQ ID:2560, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2560 is located at position 2215 relative to the genome of Triatoma Virus.

[87059] VGAM2574 precursor RNA folds onto itself, forming VGAM2574 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87060] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2574 folded precursor RNA into VGAM2574 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2574 RNA is designated SEQ ID:5285, and is provided hereinbelow with reference to the sequence listing part.

[87061] VGAM2574 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2574 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87062] VGAM2574 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2574 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2574 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[87063] The complementary binding of VGAM2574 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2574 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2574 host target RNA into VGAM2574 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87064] It is appreciated that VGAM2574 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2574 host target genes. The mRNA of each one of this plurality of VGAM2574 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2574 RNA, herein designated VGAM RNA, and which when bound by VGAM2574 RNA causes inhibition of translation of respective one or more VGAM2574 host target proteins.

[87065] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2574 gene, herein designated VGAM GENE, on one

or more VGAM2574 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87066] It is yet further appreciated that a function of VGAM2574 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2574 correlate with, and may be deduced from, the identity of the host target genes which VGAM2574 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87067] Nucleotide sequences of the VGAM2574 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2574 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2574 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2574 are further described hereinbelow with reference to Table 1.

[87068] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2574 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2574 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87069] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2574 gene, herein designated VGAM is inhibition of expression of VGAM2574 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2574 correlate with, and may be deduced from, the identity of the target genes which VGAM2574 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87070] Amyotrophic Lateral Sclerosis 2 (juvenile) Chromosome

Region, Candidate 3 (ALS2CR3, Accession NM_015049) is a VGAM2574 host target gene. ALS2CR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALS2CR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALS2CR3 BINDING SITE, designated SEQ ID:17409, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87071] A function of VGAM2574 is therefore inhibition of Amyotrophic Lateral Sclerosis 2 (juvenile) Chromosome Region, Candidate 3 (ALS2CR3, Accession NM_015049). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALS2CR3. KIAA0555 (Accession NM_014790) is another VGAM2574 host target gene. KIAA0555 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ

ID:16681, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87072] Another function of VGAM2574 is therefore inhibition of KIAA0555 (Accession NM_014790). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555. KIAA0979 (Accession NM_015032) is another VGAM2574 host target gene. KIAA0979 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0979, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0979 BINDING SITE, designated SEQ ID:17388, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87073] Another function of VGAM2574 is therefore inhibition of KIAA0979 (Accession NM_015032). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0979. SBBI26 (Accession NM_018846) is another VGAM2574 host target gene. SBBI26 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by SBBI26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SBBI26 BINDING SITE, designated SEQ ID:20830, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87074] Another function of VGAM2574 is therefore inhibition of SBBI26 (Accession NM_018846). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBBI26. LOC120892 (Accession XM_058513) is another VGAM2574 host target gene. LOC120892 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120892, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120892 BINDING SITE, designated SEQ ID:36647, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87075] Another function of VGAM2574 is therefore inhibition of

LOC120892 (Accession XM_058513). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120892. LOC149734 (Accession XM_097713) is another VGAM2574 host target gene. LOC149734 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149734, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149734 BINDING SITE, designated SEQ ID:41055, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87076] Another function of VGAM2574 is therefore inhibition of LOC149734 (Accession XM_097713). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149734. LOC152687 (Accession XM_087503) is another VGAM2574 host target gene. LOC152687 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC152687 BINDING SITE, designated SEQ ID:39301, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87077] Another function of VGAM2574 is therefore inhibition of LOC152687 (Accession XM_087503). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152687. LOC166793 (Accession NM_145291) is another VGAM2574 host target gene. LOC166793 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC166793, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC166793 BINDING SITE, designated SEQ ID:29805, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87078] Another function of VGAM2574 is therefore inhibition of LOC166793 (Accession NM_145291). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC166793. LOC168391 (Accession XM_095061) is an-

other VGAM2574 host target gene. LOC168391 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC168391, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC168391 BINDING SITE, designated SEQ ID:40242, to the nucleotide sequence of VGAM2574 RNA, herein designated VGAM RNA, also designated SEQ ID:5285.

[87079] Another function of VGAM2574 is therefore inhibition of LOC168391 (Accession XM_095061). Accordingly, utilities of VGAM2574 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168391. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2575 (VGAM2575) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87080] VGAM2575 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2575 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[87081] VGAM2575 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2575 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87082] VGAM2575 gene encodes a VGAM2575 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2575 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2575 precursor RNA is designated SEQ ID:2561, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2561 is located at position 4661 relative to the genome of Triatoma Virus.

[87083] VGAM2575 precursor RNA folds onto itself, forming VGAM2575 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87084] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2575 folded precursor RNA into VGAM2575 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2575 RNA is designated SEQ ID:5286, and is provided hereinbelow with reference to the sequence listing part.

[87085] VGAM2575 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2575 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87086] VGAM2575 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2575 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2575 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2575 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87087] The complementary binding of VGAM2575 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2575 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2575 host target RNA into VGAM2575 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87088] It is appreciated that VGAM2575 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2575 host target genes. The mRNA of each one of this plurality of VGAM2575 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2575 RNA, herein designated VGAM RNA, and which when bound by VGAM2575 RNA causes inhibition of translation of respective one or more VGAM2575 host target proteins.

[87089] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2575 gene, herein designated VGAM GENE, on one or more VGAM2575 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87090] It is yet further appreciated that a function of VGAM2575 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2575 correlate with, and may be deduced from, the identity of the host target genes which VGAM2575 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87091] Nucleotide sequences of the VGAM2575 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2575 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2575 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2575 are further described hereinbelow with reference to Table 1.

[87092] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2575 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2575 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87093] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2575 gene, herein designated VGAM is inhibition of expression of VGAM2575 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2575 correlate with, and may be deduced from, the identity of the target genes which VGAM2575 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87094] Ellis Van Creveld Syndrome (EVC, Accession NM_014556) is a VGAM2575 host target gene. EVC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EVC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:15897, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87095] A function of VGAM2575 is therefore inhibition of Ellis Van Creveld Syndrome (EVC, Accession NM_014556). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC. High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483) is another VGAM2575 host target gene. HMGA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMGA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGA2 BINDING SITE, designated SEQ ID:9574, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87096] Another function of VGAM2575 is therefore inhibition of High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483), a gene which may affect transcription and

cell differentiation; shares common DNA-binding motif with other HMG HMG I/Y family members. Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGA2. The function of HMGA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.Integrin, Beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1, Accession NM_033666) is another VGAM2575 host target gene. ITGB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGB1 BINDING SITE, designated SEQ ID:27393, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87097] Another function of VGAM2575 is therefore inhibition of Integrin, Beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1, Accession NM_033666), a gene which acts as a fibronectin receptor.

Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGB1. The function of ITGB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM427.Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_139125) is another VGAM2575 host target gene. MASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MASP1 BINDING SITE, designated SEQ ID:29161, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87098] Another function of VGAM2575 is therefore inhibition of Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_139125), a gene which a complement-dependent bactericidal factor . Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with MASP1. The function of MASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM566.Myeloid Cell Leukemia Sequence 1 (BCL2-related) (MCL1, Accession NM_021960) is another VGAM2575 host target gene. MCL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCL1 BINDING SITE, designated SEQ ID:22491, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87099] Another function of VGAM2575 is therefore inhibition of Myeloid Cell Leukemia Sequence 1 (BCL2-related) (MCL1, Accession NM_021960), a gene which involved in programing of differentiation and concomitant maintenance of viability. Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCL1. The function of MCL1 and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM1083.Sp3 Transcription Factor (SP3, Accession XM_092672) is another VGAM2575 host target gene. SP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SP3 BINDING SITE, designated SEQ ID:40137, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87100] Another function of VGAM2575 is therefore inhibition of Sp3 Transcription Factor (SP3, Accession XM_092672), a gene which binds to gt and gc boxes promoters elements. Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP3. The function of SP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM861.Zinc Finger Protein 180 (HHZ168) (ZNF180, Accession NM_013256) is another VGAM2575 host target gene. ZNF180 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF180, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF180 BINDING SITE, designated SEQ ID:14925, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87101] Another function of VGAM2575 is therefore inhibition of Zinc Finger Protein 180 (HHZ168) (ZNF180, Accession NM_013256). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF180. Zinc Finger Protein 192 (ZNF192, Accession NM_006298) is another VGAM2575 host target gene. ZNF192 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF192, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF192 BINDING SITE, designated SEQ ID:12989, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87102] Another function of VGAM2575 is therefore inhibition of Zinc Finger Protein 192 (ZNF192, Accession NM_006298). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF192. Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769) is another VGAM2575 host target gene. C11orf11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf11 BINDING SITE, designated SEQ ID:44783, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87103] Another function of VGAM2575 is therefore inhibition of Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf11. C3IP1 (Accession NM_021633) is another VGAM2575 host target gene. C3IP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

C3IP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C3IP1 BINDING SITE, designated SEQ ID:22277, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87104] Another function of VGAM2575 is therefore inhibition of C3IP1 (Accession NM_021633). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C3IP1. Chromosome 6 Open Reading Frame 33 (C6orf33, Accession NM_133367) is another VGAM2575 host target gene. C6orf33 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf33, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6orf33 BINDING SITE, designated SEQ ID:28492, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87105] Another function of VGAM2575 is therefore inhibition of Chromosome 6 Open Reading Frame 33 (C6orf33, Acces-

sion NM_133367). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf33. CDC14 Cell Division Cycle 14 Homolog A (S. cerevisiae) (CDC14A, Accession NM_003672) is another VGAM2575 host target gene. CDC14A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDC14A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDC14A BINDING SITE, designated SEQ ID:9767, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87106] Another function of VGAM2575 is therefore inhibition of CDC14 Cell Division Cycle 14 Homolog A (S. cerevisiae) (CDC14A, Accession NM_003672). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14A. DKFZP434L187 (Accession XM_044070) is another VGAM2575 host target gene. DKFZP434L187 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434L187,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L187 BINDING SITE, designated SEQ ID:34126, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87107] Another function of VGAM2575 is therefore inhibition of DKFZP434L187 (Accession XM_044070). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434L187. FLJ00001 (Accession XM_088525) is another VGAM2575 host target gene. FLJ00001 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00001, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00001 BINDING SITE, designated SEQ ID:39786, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87108] Another function of VGAM2575 is therefore inhibition of FLJ00001 (Accession XM_088525). Accordingly, utilities of

VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00001. FLJ13081 (Accession NM_024834) is another VGAM2575 host target gene. FLJ13081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13081 BINDING SITE, designated SEQ ID:24239, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87109] Another function of VGAM2575 is therefore inhibition of FLJ13081 (Accession NM_024834). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13081. FLJ13614 (Accession NM_139076) is another VGAM2575 host target gene. FLJ13614 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13614, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13614

BINDING SITE, designated SEQ ID:29151, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87110] Another function of VGAM2575 is therefore inhibition of FLJ13614 (Accession NM_139076). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13614. FLJ13693 (Accession NM_024807) is another VGAM2575 host target gene. FLJ13693 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13693, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13693 BINDING SITE, designated SEQ ID:24187, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87111] Another function of VGAM2575 is therefore inhibition of FLJ13693 (Accession NM_024807). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13693. FLJ20232 (Accession NM_019008) is another VGAM2575 host target gene. FLJ20232 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20232, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20232 BINDING SITE, designated SEQ ID:21082, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87112] Another function of VGAM2575 is therefore inhibition of FLJ20232 (Accession NM_019008). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20232. HEMK (Accession NM_016173) is another VGAM2575 host target gene. HEMK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:18272, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87113] Another function of VGAM2575 is therefore inhibition of

HEMK (Accession NM_016173). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK. HSA249128 (Accession NM_017583) is another VGAM2575 host target gene. HSA249128 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSA249128, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSA249128 BINDING SITE, designated SEQ ID:19029, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87114] Another function of VGAM2575 is therefore inhibition of HSA249128 (Accession NM_017583). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSA249128. KIAA0172 (Accession XM_036295) is another VGAM2575 host target gene. KIAA0172 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0172, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0172 BINDING SITE, designated SEQ ID:32412, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87115] Another function of VGAM2575 is therefore inhibition of KIAA0172 (Accession XM_036295). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0172. KIAA0247 (Accession NM_014734) is another VGAM2575 host target gene. KIAA0247 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0247 BINDING SITE, designated SEQ ID:16381, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87116] Another function of VGAM2575 is therefore inhibition of KIAA0247 (Accession NM_014734). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0247. KIAA1034 (Accession XM_031223) is another

VGAM2575 host target gene. KIAA1034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1034 BINDING SITE, designated SEQ ID:31314, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87117] Another function of VGAM2575 is therefore inhibition of KIAA1034 (Accession XM_031223). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1034. KIAA1061 (Accession XM_048786) is another VGAM2575 host target gene. KIAA1061 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1061, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1061 BINDING SITE, designated SEQ ID:35270, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87118] Another function of VGAM2575 is therefore inhibition of KIAA1061 (Accession XM_048786). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1061. KIAA1877 (Accession XM_038616) is another VGAM2575 host target gene. KIAA1877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1877 BINDING SITE, designated SEQ ID:32881, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87119] Another function of VGAM2575 is therefore inhibition of KIAA1877 (Accession XM_038616). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1877. KIAA1946 (Accession XM_092459) is another VGAM2575 host target gene. KIAA1946 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1946, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1946 BINDING SITE, designated SEQ ID:40120, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87120] Another function of VGAM2575 is therefore inhibition of KIAA1946 (Accession XM_092459). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1946. LIN-28 (Accession NM_024674) is another VGAM2575 host target gene. LIN-28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIN-28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIN-28 BINDING SITE, designated SEQ ID:23983, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87121] Another function of VGAM2575 is therefore inhibition of LIN-28 (Accession NM_024674). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-28.

Mitochondrial Ribosomal Protein S35 (MRPS35, Accession NM_021821) is another VGAM2575 host target gene. MRPS35 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPS35, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPS35 BINDING SITE, designated SEQ ID:22399, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87122] Another function of VGAM2575 is therefore inhibition of Mitochondrial Ribosomal Protein S35 (MRPS35, Accession NM_021821). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS35. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840) is another VGAM2575 host target gene. PPP1R16B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R16B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of PPP1R16B BINDING SITE, designated SEQ ID:30779, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87123] Another function of VGAM2575 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R16B. PRO0097 (Accession NM_014114) is another VGAM2575 host target gene. PRO0097 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0097, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0097 BINDING SITE, designated SEQ ID:15366, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87124] Another function of VGAM2575 is therefore inhibition of PRO0097 (Accession NM_014114). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

PRO0097. LOC144871 (Accession XM_096698) is another VGAM2575 host target gene. LOC144871 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144871 BINDING SITE, designated SEQ ID:40473, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87125] Another function of VGAM2575 is therefore inhibition of LOC144871 (Accession XM_096698). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144871. LOC147495 (Accession XM_097240) is another VGAM2575 host target gene. LOC147495 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147495 BINDING SITE, designated SEQ ID:40841, to the nucleotide sequence of VGAM2575 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5286.

[87126] Another function of VGAM2575 is therefore inhibition of LOC147495 (Accession XM_097240). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147495. LOC149332 (Accession XM_097626) is another VGAM2575 host target gene. LOC149332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149332 BINDING SITE, designated SEQ ID:40982, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87127] Another function of VGAM2575 is therefore inhibition of LOC149332 (Accession XM_097626). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149332. LOC149837 (Accession XM_097747) is another VGAM2575 host target gene. LOC149837 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149837, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149837 BINDING SITE, designated SEQ ID:41101, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87128] Another function of VGAM2575 is therefore inhibition of LOC149837 (Accession XM_097747). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149837. LOC153027 (Accession XM_041221) is another VGAM2575 host target gene. LOC153027 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153027, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153027 BINDING SITE, designated SEQ ID:33490, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87129] Another function of VGAM2575 is therefore inhibition of LOC153027 (Accession XM_041221). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC153027. LOC255862 (Accession XM_170505) is another VGAM2575 host target gene. LOC255862 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255862, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255862 BINDING SITE, designated SEQ ID:45342, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87130] Another function of VGAM2575 is therefore inhibition of LOC255862 (Accession XM_170505). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255862. LOC257471 (Accession XM_171020) is another VGAM2575 host target gene. LOC257471 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257471, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257471 BINDING SITE, designated SEQ ID:45789, to

the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87131] Another function of VGAM2575 is therefore inhibition of LOC257471 (Accession XM_171020). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257471. LOC51097 (Accession NM_016002) is another VGAM2575 host target gene. LOC51097 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51097, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51097 BINDING SITE, designated SEQ ID:18090, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87132] Another function of VGAM2575 is therefore inhibition of LOC51097 (Accession NM_016002). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51097. LOC56965 (Accession NM_020213) is another VGAM2575 host target gene. LOC56965 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC56965, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56965 BINDING SITE, designated SEQ ID:21455, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87133] Another function of VGAM2575 is therefore inhibition of LOC56965 (Accession NM_020213). Accordingly, utilities of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56965. LOC91397 (Accession XM_038219) is another VGAM2575 host target gene. LOC91397 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91397 BINDING SITE, designated SEQ ID:32783, to the nucleotide sequence of VGAM2575 RNA, herein designated VGAM RNA, also designated SEQ ID:5286.

[87134] Another function of VGAM2575 is therefore inhibition of LOC91397 (Accession XM_038219). Accordingly, utilities

of VGAM2575 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91397. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2576 (VGAM2576) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87135] VGAM2576 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2576 was detected is described hereinabove with reference to Figs. 1-8.

[87136] VGAM2576 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2576 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87137] VGAM2576 gene encodes a VGAM2576 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2576 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2576 precursor RNA is designated SEQ ID:2562, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2562 is located at position 5068 relative to the genome of Triatoma Virus.

[87138] VGAM2576 precursor RNA folds onto itself, forming VGAM2576 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87139] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2576 folded precursor RNA into VGAM2576 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM2576 RNA is designated SEQ ID:5287, and

is provided hereinbelow with reference to the sequence listing part.

[87140] VGAM2576 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2576 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87141] VGAM2576 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2576 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2576 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87142] The complementary binding of VGAM2576 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2576 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2576 host target RNA into VGAM2576 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87143] It is appreciated that VGAM2576 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2576 host target genes. The mRNA of each one of this plurality of VGAM2576 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2576 RNA, herein designated VGAM RNA, and which when bound by VGAM2576 RNA causes inhibition of translation of respective one or more VGAM2576 host target proteins.

[87144] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2576 gene, herein designated VGAM GENE, on one or more VGAM2576 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87145] It is yet further appreciated that a function of VGAM2576 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2576 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2576 correlate with, and may be deduced from, the identity of the host target genes which VGAM2576 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87146] Nucleotide sequences of the VGAM2576 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2576 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2576 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2576 are further described hereinbelow with reference to Table 1.

[87147] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2576 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2576 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87148] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2576 gene, herein designated VGAM is inhibition of expression of VGAM2576 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2576 correlate with, and may be deduced from, the identity of the target genes which VGAM2576 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87149] Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858) is a VGAM2576 host target gene. COL19A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL19A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL19A1 BINDING SITE, designated SEQ ID:7595, to the nucleotide sequence of VGAM2576 RNA, herein designated VGAM RNA, also designated SEQ ID:5287.

[87150] A function of VGAM2576 is therefore inhibition of Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858), a gene which may act as a cross-bridge between fibrils and other extracellular matrix molecules. Accordingly, utilities of VGAM2576 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with COL19A1. The function of COL19A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM19.Eukaryotic Translation Initiation Factor 1A (EIF1A, Accession XM_114147) is another VGAM2576 host target gene. EIF1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF1A BINDING SITE, designated SEQ ID:42718, to the nucleotide sequence of VGAM2576 RNA, herein designated VGAM RNA, also designated SEQ ID:5287.

[87151] Another function of VGAM2576 is therefore inhibition of Eukaryotic Translation Initiation Factor 1A (EIF1A, Accession XM_114147), a gene which seems to be required for maximal rate of protein biosynthesis. Accordingly, utilities of VGAM2576 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF1A. The function of EIF1A and its association with various diseases and clinical conditions, has been established

by previous studies, as described hereinabove with reference to VGAM120.CRIPT (Accession XM_057669) is another VGAM2576 host target gene. CRIPT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRIPT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRIPT BINDING SITE, designated SEQ ID:36538, to the nucleotide sequence of VGAM2576 RNA, herein designated VGAM RNA, also designated SEQ ID:5287.

[87152] Another function of VGAM2576 is therefore inhibition of CRIPT (Accession XM_057669). Accordingly, utilities of VGAM2576 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRIPT. H_GS165L15.1 (Accession NM_004904) is another VGAM2576 host target gene. H_GS165L15.1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H_GS165L15.1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H_GS165L15.1 BINDING SITE, designated SEQ ID:11337, to

the nucleotide sequence of VGAM2576 RNA, herein designated VGAM RNA, also designated SEQ ID:5287.

[87153] Another function of VGAM2576 is therefore inhibition of H_GS165L15.1 (Accession NM_004904). Accordingly, utilities of VGAM2576 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H_GS165L15.1. NS1-BP (Accession XM_051877) is another VGAM2576 host target gene. NS1-BP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NS1-BP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NS1-BP BINDING SITE, designated SEQ ID:35912, to the nucleotide sequence of VGAM2576 RNA, herein designated VGAM RNA, also designated SEQ ID:5287.

[87154] Another function of VGAM2576 is therefore inhibition of NS1-BP (Accession XM_051877). Accordingly, utilities of VGAM2576 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NS1-BP. Splicing Factor, Arginine/serine-rich 12 (SFRS12, Accession NM_139168) is another VGAM2576 host target gene. SFRS12 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by SFRS12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS12 BINDING SITE, designated SEQ ID:29176, to the nucleotide sequence of VGAM2576 RNA, herein designated VGAM RNA, also designated SEQ ID:5287.

[87155] Another function of VGAM2576 is therefore inhibition of Splicing Factor, Arginine/serine-rich 12 (SFRS12, Accession NM_139168). Accordingly, utilities of VGAM2576 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS12. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2577 (VGAM2577) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87156] VGAM2577 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2577 was detected is described hereinabove with reference to Figs. 1-8.

[87157] VGAM2577 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2577 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87158] VGAM2577 gene encodes a VGAM2577 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2577 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2577 precursor RNA is designated SEQ ID:2563, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2563 is located at position 985 relative to the genome of Triatoma Virus.

[87159] VGAM2577 precursor RNA folds onto itself, forming VGAM2577 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[87160] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2577 folded precursor RNA into VGAM2577 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of VGAM2577 RNA is designated SEQ ID:5288, and is provided hereinbelow with reference to the sequence listing part.

[87161] VGAM2577 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2577 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87162] VGAM2577 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2577 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2577 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2577 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87163] The complementary binding of VGAM2577 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2577 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2577 host target RNA into VGAM2577 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87164] It is appreciated that VGAM2577 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2577 host target genes. The mRNA of each one of this plurality of VGAM2577 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2577 RNA, herein designated VGAM RNA, and which when bound by VGAM2577 RNA causes inhibition of translation of respective one or more VGAM2577 host target proteins.

[87165] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2577 gene, herein designated VGAM GENE, on one or more VGAM2577 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87166] It is yet further appreciated that a function of VGAM2577 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2577 correlate with, and may be deduced from, the identity of the host target genes which VGAM2577 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87167] Nucleotide sequences of the VGAM2577 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2577 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2577 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2577 are further described hereinbelow with reference to Table 1.

[87168] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2577 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2577 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87169] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2577 gene, herein designated VGAM is inhibition of expression of VGAM2577 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2577 correlate with, and may be deduced from, the identity of the target genes which VGAM2577 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87170] DQX1 (Accession NM_133637) is a VGAM2577 host target gene. DQX1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DQX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of DQX1 BINDING SITE, designated SEQ ID:28597, to the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, also designated SEQ ID:5288.

[87171] A function of VGAM2577 is therefore inhibition of DQX1 (Accession NM_133637). Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DQX1. FLJ11608 (Accession NM_024557) is another VGAM2577 host target gene. FLJ11608 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11608, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11608 BINDING SITE, designated SEQ ID:23777, to the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, also designated SEQ ID:5288.

[87172] Another function of VGAM2577 is therefore inhibition of FLJ11608 (Accession NM_024557). Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11608. FLJ13263 (Accession NM_025125) is another VGAM2577 host target gene. FLJ13263 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13263, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13263 BINDING SITE, designated SEQ ID:24769, to the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, also designated SEQ ID:5288.

[87173] Another function of VGAM2577 is therefore inhibition of FLJ13263 (Accession NM_025125). Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13263. ICB-1 (Accession NM_004848) is another VGAM2577 host target gene. ICB-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICB-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICB-1 BINDING SITE, designated SEQ ID:11259, to the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, also designated SEQ ID:5288.

[87174] Another function of VGAM2577 is therefore inhibition of

ICB-1 (Accession NM_004848). Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICB-1. Tumor Necrosis Factor, Alpha-induced Protein 3 (TNFAIP3, Accession NM_006290) is another VGAM2577 host target gene. TNFAIP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFAIP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFAIP3 BINDING SITE, designated SEQ ID:12978, to the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, also designated SEQ ID:5288.

[87175] Another function of VGAM2577 is therefore inhibition of Tumor Necrosis Factor, Alpha-induced Protein 3 (TNFAIP3, Accession NM_006290). Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TN-FAIP3. LOC130813 (Accession XM_065904) is another VGAM2577 host target gene. LOC130813 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130813, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:37307, to the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, also designated SEQ ID:5288.

[87176] Another function of VGAM2577 is therefore inhibition of LOC130813 (Accession XM_065904). Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813. LOC145828 (Accession XM_096879) is another VGAM2577 host target gene. LOC145828 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145828, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145828 BINDING SITE, designated SEQ ID:40611, to the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, also designated SEQ ID:5288.

[87177] Another function of VGAM2577 is therefore inhibition of LOC145828 (Accession XM_096879). Accordingly, utilities of VGAM2577 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145828. LOC151996 (Accession XM_098151) is another VGAM2577 host target gene. LOC151996 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151996, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151996 BINDING SITE, designated SEQ ID:41412, to the nucleotide sequence of VGAM2577 RNA, herein designated VGAM RNA, also designated SEQ ID:5288.

[87178] Another function of VGAM2577 is therefore inhibition of LOC151996 (Accession XM_098151). Accordingly, utilities of VGAM2577 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151996. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2578 (VGAM2578) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87179] VGAM2578 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2578 was detected is described hereinabove with reference to Figs. 1-8.

[87180] VGAM2578 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2578 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87181] VGAM2578 gene encodes a VGAM2578 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2578 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2578 precursor RNA is designated SEQ ID:2564, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2564 is located at position 849 relative to the genome of Triatoma Virus.

[87182] VGAM2578 precursor RNA folds onto itself, forming VGAM2578 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87183] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2578 folded precursor RNA into VGAM2578 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2578 RNA is designated SEQ ID:5289, and is provided hereinbelow with reference to the sequence listing part.

[87184] VGAM2578 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2578 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87185] VGAM2578 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2578 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2578 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87186] The complementary binding of VGAM2578 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2578 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2578 host target RNA into VGAM2578 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87187] It is appreciated that VGAM2578 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2578 host target genes. The mRNA of each one of this plurality of VGAM2578 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2578 RNA, herein designated VGAM RNA, and which when bound by VGAM2578 RNA causes inhibition of translation of respective one or more VGAM2578 host target proteins.

[87188] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2578 gene, herein designated VGAM GENE, on one or more VGAM2578 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87189] It is yet further appreciated that a function of VGAM2578 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2578 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2578 correlate with, and may be deduced from, the identity of the host target genes which VGAM2578 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87190] Nucleotide sequences of the VGAM2578 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2578 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2578 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2578 are further described hereinbelow with reference to Table 1.

[87191] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2578 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2578 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87192] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2578 gene, herein designated VGAM is inhibition of expression of VGAM2578 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2578 correlate with, and may be deduced from, the identity of the target genes which VGAM2578 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87193] Carbonic Anhydrase XII (CA12, Accession NM_001218) is a VGAM2578 host target gene. CA12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by CA12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CA12 BINDING SITE, designated SEQ ID:6878, to the nucleotide sequence of VGAM2578 RNA, herein designated VGAM RNA, also designated SEQ ID:5289.

[87194] A function of VGAM2578 is therefore inhibition of Carbonic Anhydrase XII (CA12, Accession NM_001218), a gene which functions in cellular transport and metabolic processes. Accordingly, utilities of VGAM2578 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CA12. The function of CA12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM508.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2579 (VGAM2579) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87195] VGAM2579 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2579 was detected is described hereinabove with reference to Figs. 1-8.

[87196] VGAM2579 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2579 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87197] VGAM2579 gene encodes a VGAM2579 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2579 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2579 precursor RNA is designated SEQ ID:2565, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2565 is located at position 7412 relative to the genome of Triatoma Virus.

[87198] VGAM2579 precursor RNA folds onto itself, forming VGAM2579 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87199] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2579 folded precursor RNA into VGAM2579 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2579 RNA is designated SEQ ID:5290, and is provided hereinbelow with reference to the sequence listing part.

[87200] VGAM2579 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2579 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87201] VGAM2579 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2579 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2579 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87202] The complementary binding of VGAM2579 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2579 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2579 host target RNA into VGAM2579 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87203] It is appreciated that VGAM2579 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2579 host target genes. The mRNA of each one of this plurality of VGAM2579 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2579 RNA, herein designated VGAM RNA, and which when bound by VGAM2579 RNA causes inhibition of translation of respective one or more VGAM2579 host target proteins.

[87204] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2579 gene, herein designated VGAM GENE, on one or more VGAM2579 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87205] It is yet further appreciated that a function of VGAM2579 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2579 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2579 correlate with, and may be deduced from, the identity of the host target genes which VGAM2579 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87206] Nucleotide sequences of the VGAM2579 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2579 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2579 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2579 are further described hereinbelow with reference to Table 1.

[87207] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2579 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2579 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87208] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2579 gene, herein designated VGAM is inhibition of expression of VGAM2579 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2579 correlate with, and may be deduced from, the identity of the target genes which VGAM2579 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87209] DXF68S1E (Accession XM_010289) is a VGAM2579 host target gene. DXF68S1E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by DXF68S1E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DXF68S1E BINDING SITE, designated SEQ ID:30152, to the nucleotide sequence of VGAM2579 RNA, herein designated VGAM RNA, also designated SEQ ID:5290.

[87210] A function of VGAM2579 is therefore inhibition of DXF68S1E (Accession XM_010289). Accordingly, utilities of VGAM2579 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DXF68S1E. Junctional Adhesion Molecule 1 (JAM1, Accession NM_016946) is another VGAM2579 host target gene. JAM1 BINDING SITE1 through JAM1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by JAM1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAM1 BINDING SITE1 through JAM1 BINDING SITE4, designated SEQ ID:18862, SEQ ID:29329, SEQ ID:29340 and SEQ ID:29350 respectively, to the nucleotide sequence of VGAM2579 RNA, herein designated VGAM RNA, also designated SEQ

ID:5290.

[87211] Another function of VGAM2579 is therefore inhibition of Junctional Adhesion Molecule 1 (JAM1, Accession NM_016946). Accordingly, utilities of VGAM2579 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAM1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2580 (VGAM2580) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87212] VGAM2580 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2580 was detected is described hereinabove with reference to Figs. 1-8.

[87213] VGAM2580 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2580 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87214] VGAM2580 gene encodes a VGAM2580 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2580 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2580 precursor RNA is designated SEQ ID:2566, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2566 is located at position 7916 relative to the genome of Triatoma Virus.

[87215] VGAM2580 precursor RNA folds onto itself, forming VGAM2580 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87216] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2580 folded precursor RNA into VGAM2580 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2580 RNA is designated SEQ ID:5291, and is provided hereinbelow with reference to the sequence listing part.

[87217] VGAM2580 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2580 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87218] VGAM2580 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2580 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2580 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87219] The complementary binding of VGAM2580 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2580 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2580 host target RNA into VGAM2580 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87220] It is appreciated that VGAM2580 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2580 host target genes. The mRNA of

each one of this plurality of VGAM2580 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2580 RNA, herein designated VGAM RNA, and which when bound by VGAM2580 RNA causes inhibition of translation of respective one or more VGAM2580 host target proteins.

[87221] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2580 gene, herein designated VGAM GENE, on one or more VGAM2580 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[87222] It is yet further appreciated that a function of VGAM2580 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2580 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2580 correlate with, and may be deduced from, the identity of the host target genes which VGAM2580 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87223] Nucleotide sequences of the VGAM2580 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2580 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2580 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2580 are further described hereinbelow with reference to Table 1.

[87224] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2580 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2580 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87225] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2580 gene, herein designated VGAM is inhibition of expression of VGAM2580 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2580 correlate with, and may be deduced from, the identity of the target genes which VGAM2580 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87226] Fibronectin Leucine Rich Transmembrane Protein 2 (FLRT2, Accession NM_013231) is a VGAM2580 host target gene. FLRT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLRT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLRT2 BINDING SITE, designated SEQ ID:14879, to the nucleotide sequence of VGAM2580 RNA, herein designated VGAM RNA, also designated SEQ ID:5291.

[87227] A function of VGAM2580 is therefore inhibition of Fibronectin Leucine Rich Transmembrane Protein 2 (FLRT2,

Accession NM_013231), a gene which may have a function in cell adhesion and/or receptor signaling. Accordingly, utilities of VGAM2580 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLRT2. The function of FLRT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.Steroid Sulfatase (microsomal), Arylsulfatase C, Isozyme S (STS, Accession NM_000351) is another VGAM2580 host target gene. STS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STS BINDING SITE, designated SEQ ID:5907, to the nucleotide sequence of VGAM2580 RNA, herein designated VGAM RNA, also designated SEQ ID:5291.

[87228] Another function of VGAM2580 is therefore inhibition of Steroid Sulfatase (microsomal), Arylsulfatase C, Isozyme S (STS, Accession NM_000351). Accordingly, utilities of VGAM2580 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STS.

Thyrotropin-releasing Hormone (TRH, Accession NM_007117) is another VGAM2580 host target gene. TRH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRH BINDING SITE, designated SEQ ID:13979, to the nucleotide sequence of VGAM2580 RNA, herein designated VGAM RNA, also designated SEQ ID:5291.

[87229] Another function of VGAM2580 is therefore inhibition of Thyrotropin-releasing Hormone (TRH, Accession NM_007117), a gene which functions as a regulator of the biosynthesis of tsh in the anterior pituitary gland and as a neurotransmitter/ neuromodulator in the central and peripheral nervous systems. Accordingly, utilities of VGAM2580 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRH. The function of TRH has been established by previous studies. Thyrotropin-releasing hormone (TRH), the major hypothalamic mediator of release of thyroid-stimulating hormone (TSHB; 188540), is a tripeptide (glu-his-pro) found in highest concentrations in the medial division of

the hypothalamic paraventricular nuclei and in the median eminence. TRH stimulates the release of prolactin as well as that of TSH. The prolactin response is enhanced in hypothyroidism and diminished in hyperthyroidism. Niimi et al. (1982) reported a girl with isolated TRH deficiency. The parents were unrelated. She was seen at age 4 years for short stature. The authors suggested that TRH-synthesizing enzyme in the hypothalamus (Mitnick and Reichlin, 1972) may be deficient. It is now known that TRH is a peptide synthesized as such. Katakami et al. (1984) described an 18-year-old girl with isolated TRH deficiency and suggested that hypothyroidism in this patient was due to dysfunction of hypothalamic TRH release. Foresti and Ferrari (1985) suggested that resistance of pituitary thyrotropes (TSH-producing pituitary cells) due to a receptor defect is a more likely explanation, and that direct serum determination of TRH is a valid way to diagnose TRH deficiency. Yamada et al. (1990) reported that the transcriptional unit of prepro-TRH is 3.3 kb long, with 3 exons interrupted by 2 introns of approximately 1,050 and 650 basepairs, respectively. The predicted human prepro-TRH has 242 amino acids.

[87230] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[87231] Niimi, H.; Inomata, H.; Sasaki, N.; Nakajima, H. : Congenital isolated thyrotrophin releasing hormone deficiency. Arch. Dis. Child. 57: 877-878, 1982. ; and

[87232] Foresti, V.; Ferrari, C. : Central hypothyroidism: isolated thyrotropin-releasing hormone deficiency or resistance of pituitary thyrotropes?. (Letter) J. Endocr. Invest. 8: 577 only, 19.

[87233] Further studies establishing the function and utilities of TRH are found in John Hopkins OMIM database record ID 275120, and in sited publications numbered 7236-7237, 658 and 7238-7242 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.LOC84549 (Accession NM_032509) is another VGAM2580 host target gene. LOC84549 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC84549, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC84549 BINDING SITE, designated SEQ ID:26258, to the nucleotide sequence of VGAM2580 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5291.

[87234] Another function of VGAM2580 is therefore inhibition of LOC84549 (Accession NM_032509). Accordingly, utilities of VGAM2580 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC84549. LOC90538 (Accession XM_032401) is another VGAM2580 host target gene. LOC90538 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90538 BINDING SITE, designated SEQ ID:31654, to the nucleotide sequence of VGAM2580 RNA, herein designated VGAM RNA, also designated SEQ ID:5291.

[87235] Another function of VGAM2580 is therefore inhibition of LOC90538 (Accession XM_032401). Accordingly, utilities of VGAM2580 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90538. LOC92935 (Accession XM_048197) is another VGAM2580 host target gene. LOC92935 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92935, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92935 BINDING SITE, designated SEQ ID:35131, to the nucleotide sequence of VGAM2580 RNA, herein designated VGAM RNA, also designated SEQ ID:5291.

[87236] Another function of VGAM2580 is therefore inhibition of LOC92935 (Accession XM_048197). Accordingly, utilities of VGAM2580 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92935. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2581 (VGAM2581) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87237] VGAM2581 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2581 was detected is described hereinabove with reference to Figs. 1-8.

[87238] VGAM2581 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus.

VGAM2581 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87239] VGAM2581 gene encodes a VGAM2581 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2581 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2581 precursor RNA is designated SEQ ID:2567, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2567 is located at position 6465 relative to the genome of Triatoma Virus.

[87240] VGAM2581 precursor RNA folds onto itself, forming VGAM2581 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87241] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2581 folded precursor RNA into VGAM2581 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2581 RNA is designated SEQ ID:5292, and is provided hereinbelow with reference to the sequence listing part.

[87242] VGAM2581 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2581 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87243] VGAM2581 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2581 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2581 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87244] The complementary binding of VGAM2581 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2581 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2581 host target RNA into VGAM2581 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87245] It is appreciated that VGAM2581 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2581 host target genes. The mRNA of each one of this plurality of VGAM2581 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2581 RNA, herein designated VGAM RNA, and which when bound by VGAM2581 RNA causes inhibition of translation of respective one or more VGAM2581 host target proteins.

[87246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2581 gene, herein designated VGAM GENE, on one or more VGAM2581 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87247] It is yet further appreciated that a function of VGAM2581 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2581 correlate with, and may be deduced from, the identity of the host target genes which VGAM2581 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87248] Nucleotide sequences of the VGAM2581 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2581 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2581 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2581 are further described hereinbelow with reference to Table 1.

[87249] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2581 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2581 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87250] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2581 gene, herein designated VGAM is inhibition of expression of VGAM2581 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2581 correlate with, and may be deduced from, the identity of the target genes which VGAM2581 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87251] Fatty-acid-Coenzyme A Ligase, Long-chain 4 (FACL4, Accession NM_004458) is a VGAM2581 host target gene. FACL4 BINDING SITE1 and FACL4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FACL4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FACL4 BINDING SITE1 and

FACL4 BINDING SITE2, designated SEQ ID:10760 and SEQ ID:23250 respectively, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87252] A function of VGAM2581 is therefore inhibition of Fatty-acid-Coenzyme A Ligase, Long-chain 4 (FACL4, Accession NM_004458). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FACL4. Ketohexokinase (fructokinase) (KHK, Accession NM_000221) is another VGAM2581 host target gene. KHK BINDING SITE1 and KHK BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KHK, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KHK BINDING SITE1 and KHK BINDING SITE2, designated SEQ ID:5730 and SEQ ID:37563 respectively, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87253] Another function of VGAM2581 is therefore inhibition of Ketohexokinase (fructokinase) (KHK, Accession NM_000221). Accordingly, utilities of VGAM2581 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with KHK. Phosphatidylinositol Glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA, Accession NM_020473) is another VGAM2581 host target gene. PIGA BINDING SITE1 and PIGA BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PIGA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIGA BINDING SITE1 and PIGA BINDING SITE2, designated SEQ ID:21716 and SEQ ID:8866 respectively, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87254] Another function of VGAM2581 is therefore inhibition of Phosphatidylinositol Glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA, Accession NM_020473). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGA. Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NM_003032) is another VGAM2581 host target gene. SIAT1 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by SIAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIAT1 BINDING SITE, designated SEQ ID:8975, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87255] Another function of VGAM2581 is therefore inhibition of Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NM_003032), a gene which transfers sialic acid from the donor of substrate cmp- sialic acid to galactose containing acceptor substrates. Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT1. The function of SIAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1224.Claudin 1 (CLDN1, Accession NM_021101) is another VGAM2581 host target gene. CLDN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLDN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLDN1 BINDING SITE, designated SEQ ID:22078, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87256] Another function of VGAM2581 is therefore inhibition of Claudin 1 (CLDN1, Accession NM_021101). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN1. KIAA0426 (Accession NM_014724) is another VGAM2581 host target gene. KIAA0426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0426 BINDING SITE, designated SEQ ID:16306, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87257] Another function of VGAM2581 is therefore inhibition of KIAA0426 (Accession NM_014724). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0426. KIAA1255 (Accession XM_040626) is another VGAM2581 host target gene. KIAA1255 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1255 BINDING SITE, designated SEQ ID:33345, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87258] Another function of VGAM2581 is therefore inhibition of KIAA1255 (Accession XM_040626). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1255. KIAA1712 (Accession XM_041497) is another VGAM2581 host target gene. KIAA1712 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE, designated SEQ ID:33537, to the nucleotide sequence of VGAM2581 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5292.

[87259] Another function of VGAM2581 is therefore inhibition of KIAA1712 (Accession XM_041497). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712. MEGF10 (Accession NM_032446) is another VGAM2581 host target gene. MEGF10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEGF10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEGF10 BINDING SITE, designated SEQ ID:26213, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87260] Another function of VGAM2581 is therefore inhibition of MEGF10 (Accession NM_032446). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEGF10. SCAN Domain Containing 2 (SCAND2, Accession NM_022050) is another VGAM2581 host target gene. SCAND2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

SCAND2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAND2 BINDING SITE, designated SEQ ID:22576, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87261] Another function of VGAM2581 is therefore inhibition of SCAN Domain Containing 2 (SCAND2, Accession NM_022050). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAND2. TAF9-like RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 31kDa (TAF9L, Accession NM_015975) is another VGAM2581 host target gene. TAF9L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAF9L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAF9L BINDING SITE, designated SEQ ID:18071, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87262] Another function of VGAM2581 is therefore inhibition of TAF9-like RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 31kDa (TAF9L, Accession NM_015975). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAF9L. Translocase of Outer Mitochondrial Membrane 70 Homolog A (yeast) (TOMM70A, Accession NM_014820) is another VGAM2581 host target gene. TOMM70A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOMM70A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOMM70A BINDING SITE, designated SEQ ID:16788, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87263] Another function of VGAM2581 is therefore inhibition of Translocase of Outer Mitochondrial Membrane 70 Homolog A (yeast) (TOMM70A, Accession NM_014820). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOMM70A. UQCR (Accession NM_006830)

is another VGAM2581 host target gene. UQCR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UQCR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UQCR BINDING SITE, designated SEQ ID:13708, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87264] Another function of VGAM2581 is therefore inhibition of UQCR (Accession NM_006830). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UQCR. LOC120939 (Accession XM_073688) is another VGAM2581 host target gene. LOC120939 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC120939, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120939 BINDING SITE, designated SEQ ID:37512, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87265] Another function of VGAM2581 is therefore inhibition of LOC120939 (Accession XM_073688). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120939. LOC128338 (Accession XM_059238) is another VGAM2581 host target gene. LOC128338 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128338, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128338 BINDING SITE, designated SEQ ID:36925, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87266] Another function of VGAM2581 is therefore inhibition of LOC128338 (Accession XM_059238). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128338. LOC144845 (Accession NM_138474) is another VGAM2581 host target gene. LOC144845 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144845, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144845 BINDING SITE, designated SEQ ID:28822, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87267] Another function of VGAM2581 is therefore inhibition of LOC144845 (Accession NM_138474). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144845. LOC146780 (Accession XM_097086) is another VGAM2581 host target gene. LOC146780 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146780, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146780 BINDING SITE, designated SEQ ID:40744, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87268] Another function of VGAM2581 is therefore inhibition of LOC146780 (Accession XM_097086). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC146780. LOC147804 (Accession XM_085901) is another VGAM2581 host target gene. LOC147804 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147804, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147804 BINDING SITE, designated SEQ ID:38381, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87269] Another function of VGAM2581 is therefore inhibition of LOC147804 (Accession XM_085901). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147804. LOC150998 (Accession XM_097990) is another VGAM2581 host target gene. LOC150998 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150998, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150998 BINDING SITE, designated SEQ ID:41285, to the nucleotide sequence of VGAM2581 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5292.

[87270] Another function of VGAM2581 is therefore inhibition of LOC150998 (Accession XM_097990). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150998. LOC151318 (Accession XM_087170) is another VGAM2581 host target gene. LOC151318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151318 BINDING SITE, designated SEQ ID:39104, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87271] Another function of VGAM2581 is therefore inhibition of LOC151318 (Accession XM_087170). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151318. LOC255481 (Accession XM_170489) is another VGAM2581 host target gene. LOC255481 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255481, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255481 BINDING SITE, designated SEQ ID:45329, to the nucleotide sequence of VGAM2581 RNA, herein designated VGAM RNA, also designated SEQ ID:5292.

[87272] Another function of VGAM2581 is therefore inhibition of LOC255481 (Accession XM_170489). Accordingly, utilities of VGAM2581 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255481. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2582 (VGAM2582) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87273] VGAM2582 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2582 was detected is described hereinabove with reference to Figs. 1-8.

[87274] VGAM2582 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus.

VGAM2582 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87275] VGAM2582 gene encodes a VGAM2582 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2582 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2582 precursor RNA is designated SEQ ID:2568, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2568 is located at position 8016 relative to the genome of Triatoma Virus.

[87276] VGAM2582 precursor RNA folds onto itself, forming VGAM2582 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87277] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2582 folded precursor RNA into VGAM2582 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2582 RNA is designated SEQ ID:5293, and is provided hereinbelow with reference to the sequence listing part.

[87278] VGAM2582 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2582 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87279] VGAM2582 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2582 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2582 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87280] The complementary binding of VGAM2582 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2582 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2582 host target RNA into VGAM2582 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87281] It is appreciated that VGAM2582 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2582 host target genes. The mRNA of each one of this plurality of VGAM2582 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2582 RNA, herein designated VGAM RNA, and which when bound by VGAM2582 RNA causes inhibition of translation of respective one or more VGAM2582 host target proteins.

[87282] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2582 gene, herein designated VGAM GENE, on one or more VGAM2582 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87283] It is yet further appreciated that a function of VGAM2582 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2582 correlate with, and may be deduced from, the identity of the host target genes which VGAM2582 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87284] Nucleotide sequences of the VGAM2582 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2582 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2582 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2582 are further described hereinbelow with reference to Table 1.

[87285] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2582 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2582 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87286] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2582 gene, herein designated VGAM is inhibition of expression of VGAM2582 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2582 correlate with, and may be deduced from, the identity of the target genes which VGAM2582 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87287] Dachshund Homolog (Drosophila) (DACH, Accession NM_080759) is a VGAM2582 host target gene. DACH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DACH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DACH BINDING SITE, designated SEQ ID:28040, to the nu-

cleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87288] A function of VGAM2582 is therefore inhibition of Dachshund Homolog (Drosophila) (DACH, Accession NM_080759), a gene which regulates early progenitor cell proliferation during retinogenesis and pituitary development . Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DACH. The function of DACH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM260.Eukaryotic Translation Initiation Factor 3, Subunit 10 Theta, 150/170kDa (EIF3S10, Accession XM_049795) is another VGAM2582 host target gene. EIF3S10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF3S10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF3S10 BINDING SITE, designated SEQ ID:35500, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ

ID:5293.

[87289] Another function of VGAM2582 is therefore inhibition of Eukaryotic Translation Initiation Factor 3, Subunit 10 Theta, 150/170kDa (EIF3S10, Accession XM_049795), a gene which binds to the 40s ribosome and promotes the binding of methionyl-trnai and mrna. Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF3S10. The function of EIF3S10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM882.Fucosyltransferase 9 (alpha (1,3) Fucosyltransferase) (FUT9, Accession XM_042167) is another VGAM2582 host target gene. FUT9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FUT9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FUT9 BINDING SITE, designated SEQ ID:33699, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87290] Another function of VGAM2582 is therefore inhibition of

Fucosyltransferase 9 (alpha (1,3) Fucosyltransferase) (FUT9, Accession XM_042167), a gene which catalyzes alpha-1,3 glycosidic linkages. Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT9. The function of FUT9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Loss of Heterozygosity, 11, Chromosomal Region 2, Gene A (LOH11CR2A, Accession NM_014622) is another VGAM2582 host target gene. LOH11CR2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOH11CR2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOH11CR2A BINDING SITE, designated SEQ ID:15985, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87291] Another function of VGAM2582 is therefore inhibition of Loss of Heterozygosity, 11, Chromosomal Region 2, Gene A (LOH11CR2A, Accession NM_014622). Accordingly, utilities of VGAM2582 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with LOH11CR2A. Optic Atrophy 1 (autosomal dominant) (OPA1, Accession NM_130834) is another VGAM2582 host target gene. OPA1 BINDING SITE1 through OPA1 BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OPA1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OPA1 BINDING SITE1 through OPA1 BINDING SITE5, designated SEQ ID:28331, SEQ ID:28355, SEQ ID:28339, SEQ ID:28323 and SEQ ID:28347 respectively, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87292] Another function of VGAM2582 is therefore inhibition of Optic Atrophy 1 (autosomal dominant) (OPA1, Accession NM_130834). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OPA1. Ubiquitination Factor E4A (UFD2 homolog, yeast) (UBE4A, Accession NM_004788) is another VGAM2582 host target gene. UBE4A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBE4A,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE4A BINDING SITE, designated SEQ ID:11196, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87293] Another function of VGAM2582 is therefore inhibition of Ubiquitination Factor E4A (UFD2 homolog, yeast) (UBE4A, Accession NM_004788), a gene which binds to the ubiquitin moieties of preformed conjugates and catalyzes ubiquitin chain assembly in conjunction with E1, E2, and E3. Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE4A. The function of UBE4A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM60.FLJ10803 (Accession NM_018224) is another VGAM2582 host target gene. FLJ10803 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10803, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10803 BINDING SITE, designated SEQ ID:20156, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87294] Another function of VGAM2582 is therefore inhibition of FLJ10803 (Accession NM_018224). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10803. KIAA0553 (Accession XM_045981) is another VGAM2582 host target gene. KIAA0553 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0553 BINDING SITE, designated SEQ ID:34633, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87295] Another function of VGAM2582 is therefore inhibition of KIAA0553 (Accession XM_045981). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0553. KIAA0924 (Accession NM_014897) is another VGAM2582 host target gene. KIAA0924 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0924, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0924 BINDING SITE, designated SEQ ID:17062, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87296] Another function of VGAM2582 is therefore inhibition of KIAA0924 (Accession NM_014897). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0924. KIAA1266 (Accession XM_038567) is another VGAM2582 host target gene. KIAA1266 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1266 BINDING SITE, designated SEQ ID:32867, to the nucleotide sequence of VGAM2582 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5293.

[87297] Another function of VGAM2582 is therefore inhibition of KIAA1266 (Accession XM_038567). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1266. KIAA1328 (Accession XM_029429) is another VGAM2582 host target gene. KIAA1328 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1328, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1328 BINDING SITE, designated SEQ ID:30889, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87298] Another function of VGAM2582 is therefore inhibition of KIAA1328 (Accession XM_029429). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1328. KIAA1554 (Accession XM_170834) is another VGAM2582 host target gene. KIAA1554 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1554, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1554 BINDING SITE, designated SEQ ID:45606, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87299] Another function of VGAM2582 is therefore inhibition of KIAA1554 (Accession XM_170834). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1554. SKIP (Accession NM_130766) is another VGAM2582 host target gene. SKIP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SKIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SKIP BINDING SITE, designated SEQ ID:28263, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87300] Another function of VGAM2582 is therefore inhibition of SKIP (Accession NM_130766). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SKIP. LOC118668 (Accession XM_061081) is another VGAM2582 host target gene. LOC118668 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC118668, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118668 BINDING SITE, designated SEQ ID:37190, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87301] Another function of VGAM2582 is therefore inhibition of LOC118668 (Accession XM_061081). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118668. LOC151318 (Accession XM_087170) is another VGAM2582 host target gene. LOC151318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151318 BINDING SITE, designated SEQ ID:39106, to

the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87302] Another function of VGAM2582 is therefore inhibition of LOC151318 (Accession XM_087170). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151318. LOC91115 (Accession XM_036218) is another VGAM2582 host target gene. LOC91115 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91115, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE, designated SEQ ID:32401, to the nucleotide sequence of VGAM2582 RNA, herein designated VGAM RNA, also designated SEQ ID:5293.

[87303] Another function of VGAM2582 is therefore inhibition of LOC91115 (Accession XM_036218). Accordingly, utilities of VGAM2582 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91115. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2583 (VGAM2583) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87304] VGAM2583 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2583 was detected is described hereinabove with reference to Figs. 1-8.

[87305] VGAM2583 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Triatoma Virus. VGAM2583 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87306] VGAM2583 gene encodes a VGAM2583 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2583 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2583 precursor RNA is designated SEQ ID:2569, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2569 is located at position 7137 relative to the genome of Triatoma Virus.

[87307] VGAM2583 precursor RNA folds onto itself, forming VGAM2583 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87308] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2583 folded precursor RNA into VGAM2583 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2583 RNA is designated SEQ ID:5294, and is provided hereinbelow with reference to the sequence listing part.

[87309] VGAM2583 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2583 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2583 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87310] VGAM2583 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2583 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2583 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2583 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2583 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87311] The complementary binding of VGAM2583 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2583 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2583 host target RNA into VGAM2583 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87312] It is appreciated that VGAM2583 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2583 host target genes. The mRNA of each one of this plurality of VGAM2583 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2583 RNA, herein designated VGAM RNA, and which when bound by VGAM2583 RNA causes inhibition of translation of respective one or more VGAM2583 host target proteins.

[87313] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2583 gene, herein designated VGAM GENE, on one or more VGAM2583 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87314] It is yet further appreciated that a function of VGAM2583 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGAM2583 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2583 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87315] Nucleotide sequences of the VGAM2583 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2583 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2583 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2583 are further described hereinbelow with reference to Table 1.

[87316] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2583 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2583 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87317] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2583 gene, herein designated VGAM is inhibition of expression of VGAM2583 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2583 correlate with, and may be deduced from, the identity of the target genes which VGAM2583

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87318] Cystic Fibrosis Transmembrane Conductance Regulator, ATP-binding Cassette (sub-family C, member 7) (CFTR, Accession NM_000492) is a VGAM2583 host target gene. CFTR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CFTR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CFTR BINDING SITE, designated SEQ ID:6100, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87319] A function of VGAM2583 is therefore inhibition of Cystic Fibrosis Transmembrane Conductance Regulator, ATP-binding Cassette (sub-family C, member 7) (CFTR, Accession NM_000492). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CFTR. Leucine Zipper, Down-regulated In Cancer 1 (LDOC1, Accession NM_012317) is another VGAM2583 host target gene. LDOC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

LDOC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LDOC1 BINDING SITE, designated SEQ ID:14694, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87320] Another function of VGAM2583 is therefore inhibition of Leucine Zipper, Down-regulated In Cancer 1 (LDOC1, Accession NM_012317). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LDOC1. POU Domain, Class 4, Transcription Factor 1 (POU4F1, Accession NM_006237) is another VGAM2583 host target gene. POU4F1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU4F1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU4F1 BINDING SITE, designated SEQ ID:12902, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87321] Another function of VGAM2583 is therefore inhibition of POU Domain, Class 4, Transcription Factor 1 (POU4F1, Accession NM_006237), a gene which plays a role in the regulation of specific gene expression within a subset of neuronal lineages. Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU4F1. The function of POU4F1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1026.Solute Carrier Family 21 (prostaglandin transporter), Member 2 (SLC21A2, Accession NM_005630) is another VGAM2583 host target gene. SLC21A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC21A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC21A2 BINDING SITE, designated SEQ ID:12157, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87322] Another function of VGAM2583 is therefore inhibition of Solute Carrier Family 21 (prostaglandin transporter),

Member 2 (SLC21A2, Accession NM_005630), a gene which is a Prostaglandin transporter. Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC21A2. The function of SLC21A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM83.BICD2 (Accession XM_046863) is another VGAM2583 host target gene. BICD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BICD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BICD2 BINDING SITE, designated SEQ ID:34853, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87323] Another function of VGAM2583 is therefore inhibition of BICD2 (Accession XM_046863). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BICD2. FLJ11117 (Accession NM_018329) is another VGAM2583 host target gene. FLJ11117 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by FLJ11117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11117 BINDING SITE, designated SEQ ID:20328, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87324] Another function of VGAM2583 is therefore inhibition of FLJ11117 (Accession NM_018329). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11117. FLJ20209 (Accession XM_098142) is another VGAM2583 host target gene. FLJ20209 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20209, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20209 BINDING SITE, designated SEQ ID:41406, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87325] Another function of VGAM2583 is therefore inhibition of

FLJ20209 (Accession XM_098142). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20209. KIAA0172 (Accession XM_036295) is another VGAM2583 host target gene. KIAA0172 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0172, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0172 BINDING SITE, designated SEQ ID:32413, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87326] Another function of VGAM2583 is therefore inhibition of KIAA0172 (Accession XM_036295). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0172. KIAA0564 (Accession XM_038664) is another VGAM2583 host target gene. KIAA0564 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0564, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0564 BINDING SITE, designated SEQ ID:32901, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87327] Another function of VGAM2583 is therefore inhibition of KIAA0564 (Accession XM_038664). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0564. Paternally Expressed 10 (PEG10, Accession NM_015068) is another VGAM2583 host target gene. PEG10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PEG10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEG10 BINDING SITE, designated SEQ ID:17435, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87328] Another function of VGAM2583 is therefore inhibition of Paternally Expressed 10 (PEG10, Accession NM_015068). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with PEG10. XPO5 (Accession XM_166042) is another VGAM2583 host target gene. XPO5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XPO5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XPO5 BINDING SITE, designated SEQ ID:43842, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87329] Another function of VGAM2583 is therefore inhibition of XPO5 (Accession XM_166042). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XPO5. LOC144558 (Accession XM_096629) is another VGAM2583 host target gene. LOC144558 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144558, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144558 BINDING SITE, designated SEQ ID:40439, to the nucleotide sequence of VGAM2583 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5294.

[87330] Another function of VGAM2583 is therefore inhibition of LOC144558 (Accession XM_096629). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144558. LOC151623 (Accession XM_098096) is another VGAM2583 host target gene. LOC151623 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151623, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151623 BINDING SITE, designated SEQ ID:41379, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87331] Another function of VGAM2583 is therefore inhibition of LOC151623 (Accession XM_098096). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151623. LOC221962 (Accession XM_166554) is another VGAM2583 host target gene. LOC221962 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221962, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221962 BINDING SITE, designated SEQ ID:44529, to the nucleotide sequence of VGAM2583 RNA, herein designated VGAM RNA, also designated SEQ ID:5294.

[87332] Another function of VGAM2583 is therefore inhibition of LOC221962 (Accession XM_166554). Accordingly, utilities of VGAM2583 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221962. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2584 (VGAM2584) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87333] VGAM2584 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2584 was detected is described hereinabove with reference to Figs. 1-8.

[87334] VGAM2584 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Satsuma Dwarf Virus.

VGAM2584 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87335] VGAM2584 gene encodes a VGAM2584 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2584 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2584 precursor RNA is designated SEQ ID:2570, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2570 is located at position 2340 relative to the genome of Satsuma Dwarf Virus.

[87336] VGAM2584 precursor RNA folds onto itself, forming VGAM2584 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87337] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2584 folded precursor RNA into VGAM2584 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2584 RNA is designated SEQ ID:5295, and is provided hereinbelow with reference to the sequence listing part.

[87338] VGAM2584 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2584 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87339] VGAM2584 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2584 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2584 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87340] The complementary binding of VGAM2584 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2584 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2584 host target RNA into VGAM2584 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87341] It is appreciated that VGAM2584 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2584 host target genes. The mRNA of each one of this plurality of VGAM2584 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2584 RNA, herein designated VGAM RNA, and which when bound by VGAM2584 RNA causes inhibition of translation of respective one or more VGAM2584 host target proteins.

[87342] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2584 gene, herein designated VGAM GENE, on one or more VGAM2584 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87343] It is yet further appreciated that a function of VGAM2584 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2584 include diagnosis, prevention and treatment of viral infection by Satsuma Dwarf Virus. Specific functions, and accordingly utilities, of VGAM2584 correlate with, and may be deduced from, the identity of the host target genes which VGAM2584 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87344] Nucleotide sequences of the VGAM2584 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2584 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2584 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2584 are further described hereinbelow with reference to Table 1.

[87345] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2584 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2584 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87346] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2584 gene, herein designated VGAM is inhibition of expression of VGAM2584 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2584 correlate with, and may be deduced from, the identity of the target genes which VGAM2584 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87347] KIAA0471 (Accession NM_014857) is a VGAM2584 host target gene. KIAA0471 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0471, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0471 BINDING SITE, designated SEQ ID:16909, to the nucleotide sequence of

VGAM2584 RNA, herein designated VGAM RNA, also designated SEQ ID:5295.

[87348] A function of VGAM2584 is therefore inhibition of KIAA0471 (Accession NM_014857). Accordingly, utilities of VGAM2584 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0471. Ubiquitin-conjugating Enzyme E2N (UBC13 homolog, yeast) (UBE2N, Accession NM_003348) is another VGAM2584 host target gene. UBE2N BINDING SITE1 and UBE2N BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by UBE2N, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2N BINDING SITE1 and UBE2N BINDING SITE2, designated SEQ ID:9363 and SEQ ID:45358 respectively, to the nucleotide sequence of VGAM2584 RNA, herein designated VGAM RNA, also designated SEQ ID:5295.

[87349] Another function of VGAM2584 is therefore inhibition of Ubiquitin-conjugating Enzyme E2N (UBC13 homolog, yeast) (UBE2N, Accession NM_003348). Accordingly, utilities of VGAM2584 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with UBE2N. Chromosome 22 Open Reading Frame 19 (C22orf19, Accession NM_003678) is another VGAM2585 host target gene. C22orf19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C22orf19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C22orf19 BINDING SITE, designated SEQ ID:9773, to the nucleotide sequence of VGAM2585 RNA, herein designated VGAM RNA, also designated SEQ ID:5296.

[87350] Another function of VGAM2585 is therefore inhibition of Chromosome 22 Open Reading Frame 19 (C22orf19, Accession NM_003678). Accordingly, utilities of VGAM2585 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf19. KIAA1040 (Accession XM_051091) is another VGAM2585 host target gene. KIAA1040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of KIAA1040 BINDING SITE, designated SEQ ID:35743, to the nucleotide sequence of VGAM2585 RNA, herein designated VGAM RNA, also designated SEQ ID:5296.

[87351] Another function of VGAM2585 is therefore inhibition of KIAA1040 (Accession XM_051091). Accordingly, utilities of VGAM2585 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1040. KIAA1204 (Accession XM_045011) is another VGAM2585 host target gene. KIAA1204 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1204, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1204 BINDING SITE, designated SEQ ID:34312, to the nucleotide sequence of VGAM2585 RNA, herein designated VGAM RNA, also designated SEQ ID:5296.

[87352] Another function of VGAM2585 is therefore inhibition of KIAA1204 (Accession XM_045011). Accordingly, utilities of VGAM2585 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1204. LOC144871 (Accession XM_096698) is another

VGAM2585 host target gene. LOC144871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144871 BINDING SITE, designated SEQ ID:40472, to the nucleotide sequence of VGAM2585 RNA, herein designated VGAM RNA, also designated SEQ ID:5296.

[87353] Another function of VGAM2585 is therefore inhibition of LOC144871 (Accession XM_096698). Accordingly, utilities of VGAM2585 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144871. LOC145921 (Accession XM_071845) is another VGAM2585 host target gene. LOC145921 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145921, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145921 BINDING SITE, designated SEQ ID:37426, to the nucleotide sequence of VGAM2585 RNA, herein designated VGAM RNA, also designated SEQ ID:5296.

[87354] Another function of VGAM2585 is therefore inhibition of LOC145921 (Accession XM_071845). Accordingly, utilities of VGAM2585 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145921. LOC150333 (Accession XM_097874) is another VGAM2585 host target gene. LOC150333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150333 BINDING SITE, designated SEQ ID:41196, to the nucleotide sequence of VGAM2585 RNA, herein designated VGAM RNA, also designated SEQ ID:5296.

[87355] Another function of VGAM2585 is therefore inhibition of LOC150333 (Accession XM_097874). Accordingly, utilities of VGAM2585 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150333. LOC152190 (Accession XM_045692) is another VGAM2585 host target gene. LOC152190 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152190, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152190 BINDING SITE, designated SEQ ID:34525, to the nucleotide sequence of VGAM2585 RNA, herein designated VGAM RNA, also designated SEQ ID:5296.

[87356] Another function of VGAM2585 is therefore inhibition of LOC152190 (Accession XM_045692). Accordingly, utilities of VGAM2585 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152190. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2586 (VGAM2586) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87357] VGAM2586 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2586 was detected is described hereinabove with reference to Figs. 1-8.

[87358] VGAM2586 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Satsuma Dwarf Virus. VGAM2586 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[87359] VGAM2586 gene encodes a VGAM2586 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2586 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2586 precursor RNA is designated SEQ ID:2572, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2572 is located at position 5834 relative to the genome of Satsuma Dwarf Virus.

[87360] VGAM2586 precursor RNA folds onto itself, forming VGAM2586 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87361] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2586 folded precursor RNA into VGAM2586

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2586 RNA is designated SEQ ID:5297, and is provided hereinbelow with reference to the sequence listing part.

[87362] VGAM2586 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2586 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87363] VGAM2586 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2586 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2586 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87364] The complementary binding of VGAM2586 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2586 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2586 host target RNA into VGAM2586 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[87365] It is appreciated that VGAM2586 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2586 host target genes. The mRNA of each one of this plurality of VGAM2586 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2586 RNA, herein designated VGAM RNA, and which when bound by VGAM2586 RNA causes inhibition of translation of respective one or more VGAM2586 host target proteins.

[87366] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2586 gene, herein designated VGAM GENE, on one or more VGAM2586 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87367] It is yet further appreciated that a function of VGAM2586 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment of viral infection by Satsuma Dwarf Virus. Specific functions, and accordingly utilities, of VGAM2586 correlate with, and may be deduced from, the identity of the host target genes which VGAM2586 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87368] Nucleotide sequences of the VGAM2586 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2586 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2586 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2586 are further described hereinbelow with reference to Table 1.

[87369] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2586 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2586 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87370] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2586 gene, herein designated VGAM is inhibition of expression of VGAM2586 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2586 correlate with, and may be deduced from, the identity of the target genes which VGAM2586 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87371] Glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK, Accession NM_033508) is a VGAM2586 host target gene. GCK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GCK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GCK BINDING SITE, designated SEQ ID:27286, to the nucleotide sequence of VGAM2586

RNA, herein designated VGAM RNA, also designated SEQ ID:5297.

[87372] A function of VGAM2586 is therefore inhibition of Glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK, Accession NM_033508), a gene which catalyzes the initial step in utilization of glucose by the beta-cell and liver at physiological glucose concentration. Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GCK. The function of GCK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1781.Interleukin 1 Receptor Accessory Protein-like 2 (IL1RAPL2, Accession NM_017416) is another VGAM2586 host target gene. IL1RAPL2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IL1RAPL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1RAPL2 BINDING SITE, designated SEQ ID:18873, to the nucleotide sequence of VGAM2586 RNA, herein designated VGAM RNA, also designated SEQ ID:5297.

[87373] Another function of VGAM2586 is therefore inhibition of Interleukin 1 Receptor Accessory Protein-like 2 (IL1RAPL2, Accession NM_017416), a gene which may act in the development or function of the central nervous system. Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RAPL2. The function of IL1RAPL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1965.FLJ10751 (Accession NM_018239) is another VGAM2586 host target gene. FLJ10751 BINDING SITE1 and FLJ10751 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ10751, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10751 BINDING SITE1 and FLJ10751 BINDING SITE2, designated SEQ ID:20190 and SEQ ID:20091 respectively, to the nucleotide sequence of VGAM2586 RNA, herein designated VGAM RNA, also designated SEQ ID:5297.

[87374] Another function of VGAM2586 is therefore inhibition of

FLJ10751 (Accession NM_018239). Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10751. KIAA0062 (Accession XM_046677) is another VGAM2586 host target gene. KIAA0062 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0062, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0062 BINDING SITE, designated SEQ ID:34793, to the nucleotide sequence of VGAM2586 RNA, herein designated VGAM RNA, also designated SEQ ID:5297.

[87375] Another function of VGAM2586 is therefore inhibition of KIAA0062 (Accession XM_046677). Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0062. KIAA0237 (Accession NM_014747) is another VGAM2586 host target gene. KIAA0237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0237 BINDING SITE, designated SEQ ID:16436, to the nucleotide sequence of VGAM2586 RNA, herein designated VGAM RNA, also designated SEQ ID:5297.

[87376] Another function of VGAM2586 is therefore inhibition of KIAA0237 (Accession NM_014747). Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237. Lectin, Galactoside-binding, Soluble, 8 (galectin 8) (LGALS8, Accession NM_006499) is another VGAM2586 host target gene. LGALS8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LGALS8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LGALS8 BINDING SITE, designated SEQ ID:13244, to the nucleotide sequence of VGAM2586 RNA, herein designated VGAM RNA, also designated SEQ ID:5297.

[87377] Another function of VGAM2586 is therefore inhibition of Lectin, Galactoside-binding, Soluble, 8 (galectin 8) (LGALS8, Accession NM_006499). Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with LGALS8. LOC158156 (Accession XM_088496) is another VGAM2586 host target gene. LOC158156 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158156, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158156 BINDING SITE, designated SEQ ID:39735, to the nucleotide sequence of VGAM2586 RNA, herein designated VGAM RNA, also designated SEQ ID:5297.

[87378] Another function of VGAM2586 is therefore inhibition of LOC158156 (Accession XM_088496). Accordingly, utilities of VGAM2586 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158156. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2587 (VGAM2587) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87379] VGAM2587 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2587 was detected is described hereinabove with reference to Figs. 1-8.

[87380] VGAM2587 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Satsuma Dwarf Virus. VGAM2587 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87381] VGAM2587 gene encodes a VGAM2587 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2587 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2587 precursor RNA is designated SEQ ID:2573, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2573 is located at position 4499 relative to the genome of Satsuma Dwarf Virus.

[87382] VGAM2587 precursor RNA folds onto itself, forming VGAM2587 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87383] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2587 folded precursor RNA into VGAM2587 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2587 RNA is designated SEQ ID:5298, and is provided hereinbelow with reference to the sequence listing part.

[87384] VGAM2587 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2587 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87385] VGAM2587 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2587 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2587 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87386] The complementary binding of VGAM2587 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2587 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2587 host target RNA into VGAM2587 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87387] It is appreciated that VGAM2587 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2587 host target genes. The mRNA of each one of this plurality of VGAM2587 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2587 RNA, herein designated VGAM RNA, and which when bound by VGAM2587 RNA causes inhibition of translation of respective one or more VGAM2587 host target proteins.

[87388] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2587 gene, herein designated VGAM GENE, on one or more VGAM2587 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87389] It is yet further appreciated that a function of VGAM2587 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of viral infection by Satsuma Dwarf Virus. Specific functions, and accordingly utilities, of VGAM2587 correlate with, and may be deduced from, the identity of the host target genes which VGAM2587 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87390] Nucleotide sequences of the VGAM2587 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2587 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2587 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2587 are further described hereinbelow with reference to Table 1.

[87391] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2587 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2587 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87392] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2587 gene, herein designated VGAM is inhibition of expression of VGAM2587 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2587 correlate with, and may be deduced from, the identity of the target genes which VGAM2587 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87393] Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858) is a VGAM2587 host target gene. COL19A1 BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by COL19A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL19A1 BINDING SITE, designated SEQ ID:7600, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87394] A function of VGAM2587 is therefore inhibition of Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858), a gene which may act as a cross-bridge between fibrils and other extracellular matrix molecules. Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL19A1. The function of COL19A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM19.HTRA3 (Accession XM_114416) is another VGAM2587 host target gene. HTRA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HTRA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of HTRA3 BINDING SITE, designated SEQ ID:42939, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87395] Another function of VGAM2587 is therefore inhibition of HTRA3 (Accession XM_114416). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTRA3. Isovaleryl Coenzyme A Dehydrogenase (IVD, Accession NM_002225) is another VGAM2587 host target gene. IVD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IVD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IVD BINDING SITE, designated SEQ ID:8003, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87396] Another function of VGAM2587 is therefore inhibition of Isovaleryl Coenzyme A Dehydrogenase (IVD, Accession NM_002225). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with IVD. Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NM_003679) is another VGAM2587 host target gene. KMO BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KMO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KMO BINDING SITE, designated SEQ ID:9781, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87397] Another function of VGAM2587 is therefore inhibition of Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NM_003679), a gene which may play a role in encephalic photoreception. Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KMO. The function of KMO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM162.SMURF1 (Accession XM_166483) is another VGAM2587 host target gene. SMURF1 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by SMURF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMURF1 BINDING SITE, designated SEQ ID:44416, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87398] Another function of VGAM2587 is therefore inhibition of SMURF1 (Accession XM_166483). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMURF1. SPS2 (Accession NM_012248) is another VGAM2587 host target gene. SPS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPS2 BINDING SITE, designated SEQ ID:14556, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87399] Another function of VGAM2587 is therefore inhibition of

SPS2 (Accession NM_012248), a gene which synthesizes selenophosphate from selenide and ATP. Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPS2. The function of SPS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1754.VAMP (vesicle-associated membrane protein)-associated Protein A, 33kDa (VAPA, Accession NM_003574) is another VGAM2587 host target gene. VAPA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VAPA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VAPA BINDING SITE, designated SEQ ID:9626, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87400] Another function of VGAM2587 is therefore inhibition of VAMP (vesicle-associated membrane protein)-associated Protein A, 33kDa (VAPA, Accession NM_003574), a gene which may have a role in vesicle trafficking. Accordingly, utilities of VGAM2587 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with VAPA. The function of VAPA has been established by previous studies. By searching an EST database for human homologs of the Aplysia 33-kD VAMP-associated protein (Vap33), Weir et al. (1998) identified a cDNA encoding VAPA, which they termed VAP33. Sequence analysis predicted that the 242-amino acid protein, which is 50% identical to the molluscan sequence, contains 8 potential phosphorylation sites, an alpha-helical coiled-coil domain, and a C-terminal transmembrane domain. Northern blot analysis of mouse tissues detected a major 1.9-kb transcript and minor 3.9- and 7.1-kb transcripts in all tissues tested, with highest expression in brain, testis, ovary, kidney and skeletal muscle. In contrast, Vap33 expression is neuron specific in Aplysia. Western blot analysis showed that VAPA interacts with VAMP1 (OMIM Ref. No. 185880) and VAMP2 (OMIM Ref. No. 185881) but not with SNAP25 (OMIM Ref. No. 600322). Nishimura et al. (1999) identified cDNAs encoding VAPA and the 60% homologous VAPB (OMIM Ref. No. 605704). Northern blot analysis detected a 1.7-kb VAPA transcript in all human tissues tested. SDS-PAGE analysis demonstrated that the transmembrane domain of recombinant VAPA interacted

with VAPA and VAPB fusion proteins.

[87401] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[87402] Weir, M. L.; Klip, A.; Trimble, W. S. : Identification of a human homologue of the vesicle-associated membrane protein (VAMP)-associated protein of 33 kDa (VAP-33): a broadly expressed protein that binds to VAMP. Biochem. J. 333: 247-251, 1998. ; and

[87403] Nishimura, Y.; Hayashi, M.; Inada, H.; Tanaka, T. : Molecular cloning and characterization of mammalian homologues of vesicle-associated membrane protein-associated (VAMP-associated) prote.

[87404] Further studies establishing the function and utilities of VAPA are found in John Hopkins OMIM database record ID 605703, and in sited publications numbered 6617-6618 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Complement Component 1, Q Subcomponent, Receptor 1 (C1QR1, Accession NM_012072) is another VGAM2587 host target gene. C1QR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1QR1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1QR1 BINDING SITE, designated SEQ ID:14334, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87405] Another function of VGAM2587 is therefore inhibition of Complement Component 1, Q Subcomponent, Receptor 1 (C1QR1, Accession NM_012072). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QR1. DKFZP434F091 (Accession NM_015453) is another VGAM2587 host target gene. DKFZP434F091 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F091, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434F091 BINDING SITE, designated SEQ ID:17737, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87406] Another function of VGAM2587 is therefore inhibition of

DKFZP434F091 (Accession NM_015453). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F091. FLJ11413 (Accession NM_024554) is another VGAM2587 host target gene. FLJ11413 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11413, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11413 BINDING SITE, designated SEQ ID:23773, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87407] Another function of VGAM2587 is therefore inhibition of FLJ11413 (Accession NM_024554). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11413. KIAA1271 (Accession XM_045472) is another VGAM2587 host target gene. KIAA1271 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1271 BINDING SITE, designated SEQ ID:34468, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87408] Another function of VGAM2587 is therefore inhibition of KIAA1271 (Accession XM_045472). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1271. Ligand of Numb-protein X (LNX, Accession NM_032622) is another VGAM2587 host target gene. LNX BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LNX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LNX BINDING SITE, designated SEQ ID:26339, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87409] Another function of VGAM2587 is therefore inhibition of Ligand of Numb-protein X (LNX, Accession NM_032622). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNX. PRO0246 (Accession

NM_014123) is another VGAM2587 host target gene. PRO0246 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0246, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0246 BINDING SITE, designated SEQ ID:15379, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87410] Another function of VGAM2587 is therefore inhibition of PRO0246 (Accession NM_014123). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0246. LOC143154 (Accession XM_084441) is another VGAM2587 host target gene. LOC143154 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143154, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143154 BINDING SITE, designated SEQ ID:37589, to the nucleotide sequence of VGAM2587 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5298.

[87411] Another function of VGAM2587 is therefore inhibition of LOC143154 (Accession XM_084441). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143154. LOC204970 (Accession XM_114795) is another VGAM2587 host target gene. LOC204970 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC204970, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC204970 BINDING SITE, designated SEQ ID:43075, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87412] Another function of VGAM2587 is therefore inhibition of LOC204970 (Accession XM_114795). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC204970. LOC219294 (Accession XM_167566) is another VGAM2587 host target gene. LOC219294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219294, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219294 BINDING SITE, designated SEQ ID:44687, to the nucleotide sequence of VGAM2587 RNA, herein designated VGAM RNA, also designated SEQ ID:5298.

[87413] Another function of VGAM2587 is therefore inhibition of LOC219294 (Accession XM_167566). Accordingly, utilities of VGAM2587 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219294. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2588 (VGAM2588) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87414] VGAM2588 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2588 was detected is described hereinabove with reference to Figs. 1-8.

[87415] VGAM2588 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Satsuma Dwarf Virus.

VGAM2588 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87416] VGAM2588 gene encodes a VGAM2588 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2588 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2588 precursor RNA is designated SEQ ID:2574, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2574 is located at position 1651 relative to the genome of Satsuma Dwarf Virus.

[87417] VGAM2588 precursor RNA folds onto itself, forming VGAM2588 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87418] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2588 folded precursor RNA into VGAM2588 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2588 RNA is designated SEQ ID:5299, and is provided hereinbelow with reference to the sequence listing part.

[87419] VGAM2588 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2588 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87420] VGAM2588 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2588 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2588 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87421] The complementary binding of VGAM2588 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2588 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2588 host target RNA into VGAM2588 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87422] It is appreciated that VGAM2588 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2588 host target genes. The mRNA of each one of this plurality of VGAM2588 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2588 RNA, herein designated VGAM RNA, and which when bound by VGAM2588 RNA causes inhibition of translation of respective one or more VGAM2588 host target proteins.

[87423] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2588 gene, herein designated VGAM GENE, on one or more VGAM2588 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87424] It is yet further appreciated that a function of VGAM2588 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of viral infection by Satsuma Dwarf Virus. Specific functions, and accordingly utilities, of VGAM2588 correlate with, and may be deduced from, the identity of the host target genes which VGAM2588 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87425] Nucleotide sequences of the VGAM2588 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2588 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2588 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2588 are further described hereinbelow with reference to Table 1.

[87426] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2588 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2588 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87427] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2588 gene, herein designated VGAM is inhibition of expression of VGAM2588 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2588 correlate with, and may be deduced from, the identity of the target genes which VGAM2588 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87428] Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105) is a VGAM2588 host target gene. CLASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLASP1 BINDING SITE, designated SEQ

ID:32539, to the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87429] A function of VGAM2588 is therefore inhibition of Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105), a gene which plays a role in the local regulation of microtubule dynamics . Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLASP1. The function of CLASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM298.FLJ21817 (Accession NM_022448) is another VGAM2588 host target gene. FLJ21817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21817 BINDING SITE, designated SEQ ID:22784, to the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87430] Another function of VGAM2588 is therefore inhibition of

FLJ21817 (Accession NM_022448). Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21817. KIAA1069 (Accession XM_042635) is another VGAM2588 host target gene. KIAA1069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1069 BINDING SITE, designated SEQ ID:33722, to the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87431] Another function of VGAM2588 is therefore inhibition of KIAA1069 (Accession XM_042635). Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1069. PHRET1 (Accession NM_021200) is another VGAM2588 host target gene. PHRET1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PHRET1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PHRET1 BINDING SITE, designated SEQ ID:22176, to the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87432] Another function of VGAM2588 is therefore inhibition of PHRET1 (Accession NM_021200). Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHRET1. PRO1600 (Accession NM_014095) is another VGAM2588 host target gene. PRO1600 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO1600, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1600 BINDING SITE, designated SEQ ID:15313, to the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87433] Another function of VGAM2588 is therefore inhibition of PRO1600 (Accession NM_014095). Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1600. SMT3 Suppressor of Mif Two 3 Homolog 2

(yeast) (SMT3H2, Accession NM_006937) is another VGAM2588 host target gene. SMT3H2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMT3H2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMT3H2 BINDING SITE, designated SEQ ID:13819, to the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87434] Another function of VGAM2588 is therefore inhibition of SMT3 Suppressor of Mif Two 3 Homolog 2 (yeast) (SMT3H2, Accession NM_006937). Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMT3H2. LOC143888 (Accession XM_084669) is another VGAM2588 host target gene. LOC143888 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143888, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143888 BINDING SITE, designated SEQ ID:37672, to

the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87435] Another function of VGAM2588 is therefore inhibition of LOC143888 (Accession XM_084669). Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143888. LOC157695 (Accession XM_098811) is another VGAM2588 host target gene. LOC157695 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157695, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157695 BINDING SITE, designated SEQ ID:41832, to the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87436] Another function of VGAM2588 is therefore inhibition of LOC157695 (Accession XM_098811). Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157695. LOC158997 (Accession XM_088736) is another VGAM2588 host target gene. LOC158997 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC158997, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158997 BINDING SITE, designated SEQ ID:39933, to the nucleotide sequence of VGAM2588 RNA, herein designated VGAM RNA, also designated SEQ ID:5299.

[87437] Another function of VGAM2588 is therefore inhibition of LOC158997 (Accession XM_088736). Accordingly, utilities of VGAM2588 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158997. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2589 (VGAM2589) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87438] VGAM2589 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2589 was detected is described hereinabove with reference to Figs. 1-8.

[87439] VGAM2589 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Apple Latent Spherical Virus. VGAM2589 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87440] VGAM2589 gene encodes a VGAM2589 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2589 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2589 precursor RNA is designated SEQ ID:2575, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2575 is located at position 1180 relative to the genome of Apple Latent Spherical Virus.

[87441] VGAM2589 precursor RNA folds onto itself, forming VGAM2589 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87442] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2589 folded precursor RNA into VGAM2589 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2589 RNA is designated SEQ ID:5300, and is provided hereinbelow with reference to the sequence listing part.

[87443] VGAM2589 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2589 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87444] VGAM2589 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2589 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2589 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87445] The complementary binding of VGAM2589 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2589 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2589

host target RNA into VGAM2589 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87446] It is appreciated that VGAM2589 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2589 host target genes. The mRNA of each one of this plurality of VGAM2589 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2589 RNA, herein designated VGAM RNA, and which when bound by VGAM2589 RNA causes inhibition of translation of respective one or more VGAM2589 host target proteins.

[87447] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2589 gene, herein designated VGAM GENE, on one or more VGAM2589 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87448] It is yet further appreciated that a function of VGAM2589 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2589 include diagnosis, prevention and treatment of viral infection by Apple Latent Spherical Virus. Specific functions, and accordingly utilities, of VGAM2589 correlate with, and may be deduced from, the identity of the host target genes which VGAM2589 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87449] Nucleotide sequences of the VGAM2589 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2589 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2589 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2589 are further

described hereinbelow with reference to Table 1.

[87450] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2589 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2589 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87451] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2589 gene, herein designated VGAM is inhibition of expression of VGAM2589 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2589 correlate with, and may be deduced from, the identity of the target genes which VGAM2589 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87452] ATP-binding Cassette, Sub-family D (ALD), Member 3 (ABCD3, Accession NM_002858) is a VGAM2589 host target gene. ABCD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of ABCD3 BINDING SITE, designated SEQ ID:8752, to the nucleotide sequence of VGAM2589 RNA, herein designated VGAM RNA, also designated SEQ ID:5300.

[87453] A function of VGAM2589 is therefore inhibition of ATP-binding Cassette, Sub-family D (ALD), Member 3 (ABCD3, Accession NM_002858), a gene which a probable transporter. Accordingly, utilities of VGAM2589 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCD3. The function of ABCD3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1775.Endothelial Cell-specific Molecule 1 (ESM1, Accession NM_007036) is another VGAM2589 host target gene. ESM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESM1 BINDING SITE, designated SEQ ID:13912, to the nucleotide sequence of VGAM2589 RNA, herein designated VGAM RNA, also designated SEQ ID:5300.

[87454] Another function of VGAM2589 is therefore inhibition of Endothelial Cell-specific Molecule 1 (ESM1, Accession NM_007036). Accordingly, utilities of VGAM2589 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESM1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2590 (VGAM2590) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87455] VGAM2590 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2590 was detected is described hereinabove with reference to Figs. 1-8.

[87456] VGAM2590 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple Latent Spherical Virus. VGAM2590 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87457] VGAM2590 gene encodes a VGAM2590 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2590 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2590 precursor RNA is designated SEQ ID:2576, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2576 is located at position 2408 relative to the genome of Apple Latent Spherical Virus.

[87458] VGAM2590 precursor RNA folds onto itself, forming VGAM2590 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87459] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2590 folded precursor RNA into VGAM2590 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2590 RNA is designated SEQ ID:5301, and is provided hereinbelow with reference to the sequence listing part.

[87460] VGAM2590 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2590 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87461] VGAM2590 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2590 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2590 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87462] The complementary binding of VGAM2590 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2590 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2590 host target RNA into VGAM2590 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87463] It is appreciated that VGAM2590 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2590 host target genes. The mRNA of each one of this plurality of VGAM2590 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2590 RNA, herein designated VGAM RNA, and which when bound by VGAM2590 RNA causes inhibition of translation of respective one or more VGAM2590 host target proteins.

[87464] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2590 gene, herein designated VGAM GENE, on one or more VGAM2590 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87465] It is yet further appreciated that a function of VGAM2590 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of viral infection by Apple Latent Spherical Virus. Specific functions, and accordingly utilities, of VGAM2590 correlate with, and may be deduced from, the identity of the host target genes which VGAM2590 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87466] Nucleotide sequences of the VGAM2590 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2590 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2590 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2590 are further described hereinbelow with reference to Table 1.

[87467] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2590 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2590 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[87468] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2590 gene, herein designated VGAM is inhibition of expression of VGAM2590 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2590 correlate with, and may be deduced from, the identity of the target genes which VGAM2590 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87469] Ankyrin-like with Transmembrane Domains 1 (ANKTM1, Accession NM_007332) is a VGAM2590 host target gene. ANKTM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANKTM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANKTM1 BINDING SITE, designated SEQ ID:14260, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87470] A function of VGAM2590 is therefore inhibition of Ankyrin-like with Transmembrane Domains 1 (ANKTM1, Accession NM_007332), a gene which attaches integral

membrane proteins to cytoskeletal elements. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKTM1. The function of ANKTM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM644.Calcium Channel, Voltage-dependent, Alpha 2/delta 3 Subunit (CACNA2D3, Accession NM_018398) is another VGAM2590 host target gene. CACNA2D3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CACNA2D3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CACNA2D3 BINDING SITE, designated SEQ ID:20435, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87471] Another function of VGAM2590 is therefore inhibition of Calcium Channel, Voltage-dependent, Alpha 2/delta 3 Subunit (CACNA2D3, Accession NM_018398). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with CACNA2D3. Cadherin, EGF LAG Seven-pass G-type Receptor 1 (flamingo homolog, Drosophila) (CELSR1, Accession NM_014246) is another VGAM2590 host target gene. CELSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CELSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CELSR1 BINDING SITE, designated SEQ ID:15513, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87472] Another function of VGAM2590 is therefore inhibition of Cadherin, EGF LAG Seven-pass G-type Receptor 1 (flamingo homolog, Drosophila) (CELSR1, Accession NM_014246), a gene which is involved in contact-mediated communication. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CELSR1. The function of CELSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM459.7-dehydrocholesterol Reductase (DHCR7, Ac-

cession NM_001360) is another VGAM2590 host target gene. DHCR7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DHCR7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DHCR7 BINDING SITE, designated SEQ ID:7039, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87473] Another function of VGAM2590 is therefore inhibition of 7-dehydrocholesterol Reductase (DHCR7, Accession NM_001360). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHCR7. V-myb Myeloblastosis Viral Oncogene Homolog (avian)-like 1 (MYBL1, Accession XM_034274) is another VGAM2590 host target gene. MYBL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYBL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYBL1 BINDING SITE, designated SEQ

ID:32045, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87474] Another function of VGAM2590 is therefore inhibition of V-myb Myeloblastosis Viral Oncogene Homolog (avian)-like 1 (MYBL1, Accession XM_034274), a gene which could have a role in the proliferation and/or differentiation of neurogenic, spermatogenic and b-lymphoid cells. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYBL1. The function of MYBL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM184.Phosphodiesterase 4C, CAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila) (PDE4C, Accession NM_000923) is another VGAM2590 host target gene. PDE4C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4C BINDING SITE, des-

ignated SEQ ID:6634, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87475] Another function of VGAM2590 is therefore inhibition of Phosphodiesterase 4C, CAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila) (PDE4C, Accession NM_000923), a gene which is a cAMP-specific phosphodiesterase and may be a protein involved in learning and memory. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4C. The function of PDE4C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1965.Polymyositis/scleroderma Autoantigen 1, 75kDa (PMSCL1, Accession NM_005033) is another VGAM2590 host target gene. PMSCL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PMSCL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMSCL1 BINDING SITE, designated SEQ ID:11474, to the nucleotide

sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87476] Another function of VGAM2590 is therefore inhibition of Polymyositis/scleroderma Autoantigen 1, 75kDa (PMSCL1, Accession NM_005033). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMSCL1. POU Domain, Class 4, Transcription Factor 1 (POU4F1, Accession NM_006237) is another VGAM2590 host target gene. POU4F1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU4F1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU4F1 BINDING SITE, designated SEQ ID:12903, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87477] Another function of VGAM2590 is therefore inhibition of POU Domain, Class 4, Transcription Factor 1 (POU4F1, Accession NM_006237), a gene which plays a role in the regulation of specific gene expression within a subset of neuronal lineages. Accordingly, utilities of VGAM2590 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with POU4F1. The function of POU4F1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1026.Protein Kinase C, Beta 1 (PRKCB1, Accession XM_047187) is another VGAM2590 host target gene. PRKCB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKCB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKCB1 BINDING SITE, designated SEQ ID:34904, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87478] Another function of VGAM2590 is therefore inhibition of Protein Kinase C, Beta 1 (PRKCB1, Accession XM_047187), a gene which is a calcium-activated, phospholipid-dependent, serine- and threonine-specific enzyme. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKCB1. The function of PRKCB1 and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2065.SH3-domain Binding Protein 2 (SH3BP2, Accession NM_003023) is another VGAM2590 host target gene. SH3BP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3BP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3BP2 BINDING SITE, designated SEQ ID:8953, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87479] Another function of VGAM2590 is therefore inhibition of SH3-domain Binding Protein 2 (SH3BP2, Accession NM_003023). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP2. SRY (sex determining region Y)-box 13 (SOX13, Accession NM_005686) is another VGAM2590 host target gene. SOX13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX13 BINDING SITE, designated SEQ ID:12243, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87480] Another function of VGAM2590 is therefore inhibition of SRY (sex determining region Y)-box 13 (SOX13, Accession NM_005686). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX13. Sp3 Transcription Factor (SP3, Accession XM_092672) is another VGAM2590 host target gene. SP3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SP3 BINDING SITE, designated SEQ ID:40134, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87481] Another function of VGAM2590 is therefore inhibition of Sp3 Transcription Factor (SP3, Accession XM_092672), a gene which binds to gt and gc boxes promoters elements.

Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP3. The function of SP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM861.TIA1 Cytotoxic Granule-associated RNA Binding Protein-like 1 (TIAL1, Accession NM_022333) is another VGAM2590 host target gene. TIAL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIAL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIAL1 BINDING SITE, designated SEQ ID:22743, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87482] Another function of VGAM2590 is therefore inhibition of TIA1 Cytotoxic Granule-associated RNA Binding Protein-like 1 (TIAL1, Accession NM_022333), a gene which possesses nucleolytic activity against cytotoxic lymphocyte target cells. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIAL1. The function of

TIAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM350.Transmembrane, Cochlear Expressed, 1 (TMC1, Accession NM_138691) is another VGAM2590 host target gene. TMC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TMC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMC1 BINDING SITE, designated SEQ ID:28932, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87483] Another function of VGAM2590 is therefore inhibition of Transmembrane, Cochlear Expressed, 1 (TMC1, Accession NM_138691), a gene which is required for normal function of cochlear hair cells. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMC1. The function of TMC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM554.Thioredoxin Reductase 1 (TXNRD1, Accession

NM_003330) is another VGAM2590 host target gene. TXNRD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TXNRD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TXNRD1 BINDING SITE, designated SEQ ID:9337, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87484] Another function of VGAM2590 is therefore inhibition of Thioredoxin Reductase 1 (TXNRD1, Accession NM_003330), a gene which acts as an antioxidant enzyme and is involved in maintaining redox balance. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXNRD1. The function of TXNRD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695) is another VGAM2590 host target gene. VANGL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by VANGL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VANGL2 BINDING SITE, designated SEQ ID:35486, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87485] Another function of VGAM2590 is therefore inhibition of Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695), a gene which may take part in defining the lateral boundary of floorplate differentiation. Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VANGL2. The function of VANGL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.ABLIM (Accession NM_002313) is another VGAM2590 host target gene. ABLIM BINDING SITE1 and ABLIM BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ABLIM, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of ABLIM BINDING SITE1 and ABLIM BINDING SITE2, designated SEQ ID:8121 and SEQ ID:13554 respectively, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87486] Another function of VGAM2590 is therefore inhibition of ABLIM (Accession NM_002313). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM. BPES (Accession NM_023067) is another VGAM2590 host target gene. BPES BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BPES, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BPES BINDING SITE, designated SEQ ID:23326, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87487] Another function of VGAM2590 is therefore inhibition of BPES (Accession NM_023067). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BPES.

Chromosome 11 Open Reading Frame 23 (C11orf23, Accession NM_018312) is another VGAM2590 host target gene. C11orf23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf23 BINDING SITE, designated SEQ ID:20305, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87488] Another function of VGAM2590 is therefore inhibition of Chromosome 11 Open Reading Frame 23 (C11orf23, Accession NM_018312). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf23. Chromosome 20 Open Reading Frame 108 (C20orf108, Accession NM_080821) is another VGAM2590 host target gene. C20orf108 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf108, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of C20orf108 BINDING SITE, designated SEQ ID:28083, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87489] Another function of VGAM2590 is therefore inhibition of Chromosome 20 Open Reading Frame 108 (C20orf108, Accession NM_080821). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf108. Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259) is another VGAM2590 host target gene. DOCK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DOCK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DOCK3 BINDING SITE, designated SEQ ID:33041, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87490] Another function of VGAM2590 is therefore inhibition of Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259). Accordingly, utilities of VGAM2590 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with DOCK3. FLJ10702 (Accession NM_018184) is another VGAM2590 host target gene. FLJ10702 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10702, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10702 BINDING SITE, designated SEQ ID:20029, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87491] Another function of VGAM2590 is therefore inhibition of FLJ10702 (Accession NM_018184). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10702. FLJ21438 (Accession XM_029084) is another VGAM2590 host target gene. FLJ21438 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ21438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21438

BINDING SITE, designated SEQ ID:30846, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87492] Another function of VGAM2590 is therefore inhibition of FLJ21438 (Accession XM_029084). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21438. Heterogeneous Nuclear Ribonucleoprotein A3 (HNRPA3, Accession NM_005758) is another VGAM2590 host target gene. HNRPA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HNRPA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPA3 BINDING SITE, designated SEQ ID:12325, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87493] Another function of VGAM2590 is therefore inhibition of Heterogeneous Nuclear Ribonucleoprotein A3 (HNRPA3, Accession NM_005758). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HN-

RPA3. KIAA0133 (Accession NM_014777) is another VGAM2590 host target gene. KIAA0133 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0133, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0133 BINDING SITE, designated SEQ ID:16610, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87494] Another function of VGAM2590 is therefore inhibition of KIAA0133 (Accession NM_014777). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0133. KIAA0469 (Accession NM_014851) is another VGAM2590 host target gene. KIAA0469 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0469, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE, designated SEQ ID:16897, to the nucleotide sequence of VGAM2590 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5301.

[87495] Another function of VGAM2590 is therefore inhibition of KIAA0469 (Accession NM_014851). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469. KIAA1023 (Accession NM_017604) is another VGAM2590 host target gene. KIAA1023 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1023, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1023 BINDING SITE, designated SEQ ID:19094, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87496] Another function of VGAM2590 is therefore inhibition of KIAA1023 (Accession NM_017604). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1023. KIAA1069 (Accession XM_042635) is another VGAM2590 host target gene. KIAA1069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1069, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1069 BINDING SITE, designated SEQ ID:33726, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87497] Another function of VGAM2590 is therefore inhibition of KIAA1069 (Accession XM_042635). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1069. KIAA1203 (Accession XM_049683) is another VGAM2590 host target gene. KIAA1203 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1203, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1203 BINDING SITE, designated SEQ ID:35472, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87498] Another function of VGAM2590 is therefore inhibition of KIAA1203 (Accession XM_049683). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1203. KIAA1872 (Accession XM_031917) is another VGAM2590 host target gene. KIAA1872 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1872, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1872 BINDING SITE, designated SEQ ID:31525, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87499] Another function of VGAM2590 is therefore inhibition of KIAA1872 (Accession XM_031917). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1872. LHX6 (Accession NM_014368) is another VGAM2590 host target gene. LHX6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LHX6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHX6 BINDING SITE, designated SEQ ID:15701, to the nucleotide sequence of

VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87500] Another function of VGAM2590 is therefore inhibition of LHX6 (Accession NM_014368). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHX6. Lipase, Endothelial (LIPG, Accession NM_006033) is another VGAM2590 host target gene. LIPG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIPG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIPG BINDING SITE, designated SEQ ID:12656, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87501] Another function of VGAM2590 is therefore inhibition of Lipase, Endothelial (LIPG, Accession NM_006033). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIPG. MGC15634 (Accession NM_032755) is another VGAM2590 host target gene. MGC15634 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by MGC15634, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15634 BINDING SITE, designated SEQ ID:26497, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87502] Another function of VGAM2590 is therefore inhibition of MGC15634 (Accession NM_032755). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15634. MGC26684 (Accession NM_144568) is another VGAM2590 host target gene. MGC26684 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC26684, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC26684 BINDING SITE, designated SEQ ID:29374, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87503] Another function of VGAM2590 is therefore inhibition of MGC26684 (Accession NM_144568). Accordingly, utilities

of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26684. NCUBE1 (Accession NM_016021) is another VGAM2590 host target gene. NCUBE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NCUBE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCUBE1 BINDING SITE, designated SEQ ID:18095, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87504] Another function of VGAM2590 is therefore inhibition of NCUBE1 (Accession NM_016021). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCUBE1. N-myristoyltransferase 1 (NMT1, Accession NM_021079) is another VGAM2590 host target gene. NMT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NMT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of NMT1 BINDING SITE, designated SEQ ID:22052, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87505] Another function of VGAM2590 is therefore inhibition of N-myristoyltransferase 1 (NMT1, Accession NM_021079). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NMT1. NYD-SP11 (Accession NM_031951) is another VGAM2590 host target gene. NYD-SP11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NYD-SP11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NYD-SP11 BINDING SITE, designated SEQ ID:25689, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87506] Another function of VGAM2590 is therefore inhibition of NYD-SP11 (Accession NM_031951). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NYD-SP11. Oxysterol Binding Protein-like 3 (OSBPL3, Ac-

cession NM_015550) is another VGAM2590 host target gene. OSBPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:17817, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87507] Another function of VGAM2590 is therefore inhibition of Oxysterol Binding Protein-like 3 (OSBPL3, Accession NM_015550). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3. POU Domain, Class 4, Transcription Factor 2 (POU4F2, Accession NM_004575) is another VGAM2590 host target gene. POU4F2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU4F2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU4F2 BINDING SITE, designated SEQ ID:10920, to the

nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87508] Another function of VGAM2590 is therefore inhibition of POU Domain, Class 4, Transcription Factor 2 (POU4F2, Accession NM_004575). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU4F2. PP1665 (Accession NM_030792) is another VGAM2590 host target gene. PP1665 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PP1665, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP1665 BINDING SITE, designated SEQ ID:25093, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87509] Another function of VGAM2590 is therefore inhibition of PP1665 (Accession NM_030792). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1665. Syntaphilin (SNPH, Accession NM_014723) is another VGAM2590 host target gene. SNPH BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNPH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE, designated SEQ ID:16301, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87510] Another function of VGAM2590 is therefore inhibition of Syntaphilin (SNPH, Accession NM_014723). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH. Stomatin (EPB72)-like 1 (STOML1, Accession NM_004809) is another VGAM2590 host target gene. STOML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STOML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STOML1 BINDING SITE, designated SEQ ID:11233, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87511] Another function of VGAM2590 is therefore inhibition of Stomatin (EPB72)-like 1 (STOML1, Accession NM_004809). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STOML1. LOC124216 (Accession XM_058783) is another VGAM2590 host target gene. LOC124216 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124216, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124216 BINDING SITE, designated SEQ ID:36738, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87512] Another function of VGAM2590 is therefore inhibition of LOC124216 (Accession XM_058783). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124216. LOC126302 (Accession XM_059020) is another VGAM2590 host target gene. LOC126302 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126302, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126302 BINDING SITE, designated SEQ ID:36826, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87513] Another function of VGAM2590 is therefore inhibition of LOC126302 (Accession XM_059020). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126302. LOC131870 (Accession XM_059544) is another VGAM2590 host target gene. LOC131870 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC131870, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC131870 BINDING SITE, designated SEQ ID:37015, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87514] Another function of VGAM2590 is therefore inhibition of LOC131870 (Accession XM_059544). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC131870. LOC138399 (Accession XM_059971) is another VGAM2590 host target gene. LOC138399 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC138399, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138399 BINDING SITE, designated SEQ ID:37130, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87515] Another function of VGAM2590 is therefore inhibition of LOC138399 (Accession XM_059971). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138399. LOC145955 (Accession XM_096912) is another VGAM2590 host target gene. LOC145955 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145955 BINDING SITE, designated SEQ ID:40647, to

the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87516] Another function of VGAM2590 is therefore inhibition of LOC145955 (Accession XM_096912). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145955. LOC149464 (Accession XM_097645) is another VGAM2590 host target gene. LOC149464 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149464 BINDING SITE, designated SEQ ID:40997, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87517] Another function of VGAM2590 is therefore inhibition of LOC149464 (Accession XM_097645). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149464. LOC150468 (Accession XM_086926) is another VGAM2590 host target gene. LOC150468 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC150468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150468 BINDING SITE, designated SEQ ID:38977, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87518] Another function of VGAM2590 is therefore inhibition of LOC150468 (Accession XM_086926). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150468. LOC155066 (Accession XM_088142) is another VGAM2590 host target gene. LOC155066 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155066, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155066 BINDING SITE, designated SEQ ID:39541, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87519] Another function of VGAM2590 is therefore inhibition of LOC155066 (Accession XM_088142). Accordingly, utilities

of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155066. LOC155179 (Accession XM_088169) is another VGAM2590 host target gene. LOC155179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155179 BINDING SITE, designated SEQ ID:39560, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87520] Another function of VGAM2590 is therefore inhibition of LOC155179 (Accession XM_088169). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155179. LOC159053 (Accession XM_099021) is another VGAM2590 host target gene. LOC159053 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC159053, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC159053 BINDING SITE, designated SEQ ID:42061, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87521] Another function of VGAM2590 is therefore inhibition of LOC159053 (Accession XM_099021). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159053. LOC201562 (Accession XM_114343) is another VGAM2590 host target gene. LOC201562 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:42885, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87522] Another function of VGAM2590 is therefore inhibition of LOC201562 (Accession XM_114343). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562. LOC201771 (Accession XM_046083) is another VGAM2590 host target gene. LOC201771 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201771, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201771 BINDING SITE, designated SEQ ID:34678, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87523] Another function of VGAM2590 is therefore inhibition of LOC201771 (Accession XM_046083). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201771. LOC203378 (Accession XM_117541) is another VGAM2590 host target gene. LOC203378 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203378, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203378 BINDING SITE, designated SEQ ID:43562, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87524] Another function of VGAM2590 is therefore inhibition of

LOC203378 (Accession XM_117541). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203378. LOC219918 (Accession XM_166197) is another VGAM2590 host target gene. LOC219918 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219918 BINDING SITE, designated SEQ ID:44003, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87525] Another function of VGAM2590 is therefore inhibition of LOC219918 (Accession XM_166197). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219918. LOC220071 (Accession XM_167848) is another VGAM2590 host target gene. LOC220071 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220071, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC220071 BINDING SITE, designated SEQ ID:44878, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87526] Another function of VGAM2590 is therefore inhibition of LOC220071 (Accession XM_167848). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220071. LOC220988 (Accession XM_165561) is another VGAM2590 host target gene. LOC220988 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220988 BINDING SITE, designated SEQ ID:43685, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87527] Another function of VGAM2590 is therefore inhibition of LOC220988 (Accession XM_165561). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220988. LOC221747 (Accession XM_166460) is an-

other VGAM2590 host target gene. LOC221747 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221747, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221747 BINDING SITE, designated SEQ ID:44366, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87528] Another function of VGAM2590 is therefore inhibition of LOC221747 (Accession XM_166460). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221747. LOC254085 (Accession XM_171189) is another VGAM2590 host target gene. LOC254085 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254085, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254085 BINDING SITE, designated SEQ ID:45974, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87529] Another function of VGAM2590 is therefore inhibition of LOC254085 (Accession XM_171189). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254085. LOC256940 (Accession XM_172879) is another VGAM2590 host target gene. LOC256940 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256940 BINDING SITE, designated SEQ ID:46157, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87530] Another function of VGAM2590 is therefore inhibition of LOC256940 (Accession XM_172879). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256940. LOC257471 (Accession XM_171020) is another VGAM2590 host target gene. LOC257471 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257471, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257471 BINDING SITE, designated SEQ ID:45786, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87531] Another function of VGAM2590 is therefore inhibition of LOC257471 (Accession XM_171020). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257471. LOC92228 (Accession XM_043731) is another VGAM2590 host target gene. LOC92228 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92228 BINDING SITE, designated SEQ ID:34004, to the nucleotide sequence of VGAM2590 RNA, herein designated VGAM RNA, also designated SEQ ID:5301.

[87532] Another function of VGAM2590 is therefore inhibition of LOC92228 (Accession XM_043731). Accordingly, utilities of VGAM2590 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC92228. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2591 (VGAM2591) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87533] VGAM2591 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2591 was detected is described hereinabove with reference to Figs. 1-8.

[87534] VGAM2591 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple Latent Spherical Virus. VGAM2591 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87535] VGAM2591 gene encodes a VGAM2591 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2591 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2591 precursor RNA is designated SEQ ID:2577, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2577 is located at position 6309 relative to the genome of Apple Latent Spherical Virus.

[87536] VGAM2591 precursor RNA folds onto itself, forming VGAM2591 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87537] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2591 folded precursor RNA into VGAM2591 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of VGAM2591 RNA is designated SEQ ID:5302, and is provided hereinbelow with reference to the sequence listing part.

[87538] VGAM2591 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2591 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87539] VGAM2591 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2591 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2591 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87540] The complementary binding of VGAM2591 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2591 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2591 host target RNA into VGAM2591 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87541] It is appreciated that VGAM2591 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2591 host target genes. The mRNA of each one of this plurality of VGAM2591 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2591 RNA, herein designated VGAM RNA, and which when bound by VGAM2591 RNA causes

inhibition of translation of respective one or more VGAM2591 host target proteins.

[87542] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2591 gene, herein designated VGAM GENE, on one or more VGAM2591 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87543] It is yet further appreciated that a function of VGAM2591 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2591 include diagnosis, prevention and

treatment of viral infection by Apple Latent Spherical Virus. Specific functions, and accordingly utilities, of VGAM2591 correlate with, and may be deduced from, the identity of the host target genes which VGAM2591 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87544] Nucleotide sequences of the VGAM2591 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2591 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2591 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2591 are further described hereinbelow with reference to Table 1.

[87545] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2591 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2591 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87546] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2591 gene, herein designated VGAM is inhibition of expression of VGAM2591 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2591 correlate with, and may be deduced from, the identity of the target genes which VGAM2591 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87547] Sorting Nexin 6 (SNX6, Accession NM_021249) is a VGAM2591 host target gene. SNX6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNX6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNX6 BINDING SITE, designated SEQ ID:22217, to the nucleotide sequence of VGAM2591 RNA, herein designated VGAM RNA, also designated SEQ ID:5302.

[87548] A function of VGAM2591 is therefore inhibition of Sorting Nexin 6 (SNX6, Accession NM_021249). Accordingly, utilities of VGAM2591 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX6. FLJ12287 (Accession NM_022367) is another VGAM2591 host target gene. FLJ12287 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12287, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12287 BINDING SITE, designated SEQ ID:22752, to the nucleotide sequence of VGAM2591 RNA, herein designated VGAM RNA, also designated SEQ ID:5302.

[87549] Another function of VGAM2591 is therefore inhibition of FLJ12287 (Accession NM_022367). Accordingly, utilities of VGAM2591 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12287. Wingless-type MMTV Integration Site Family, Member 2B (WNT2B, Accession NM_004185) is another VGAM2591 host target gene. WNT2B BINDING SITE1 and WNT2B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WNT2B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT2B BINDING SITE1 and WNT2B BINDING SITE2, designated SEQ ID:10391 and SEQ ID:23692 respectively, to the nucleotide sequence of VGAM2591 RNA, herein designated VGAM RNA, also designated SEQ ID:5302.

[87550] Another function of VGAM2591 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 2B (WNT2B, Accession NM_004185). Accordingly, utilities of VGAM2591 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT2B. LOC220776 (Accession XM_043388) is another VGAM2591 host target gene. LOC220776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220776 BINDING SITE, designated SEQ ID:33927, to the nucleotide sequence of VGAM2591 RNA, herein designated VGAM RNA, also designated SEQ ID:5302.

[87551] Another function of VGAM2591 is therefore inhibition of LOC220776 (Accession XM_043388). Accordingly, utilities of VGAM2591 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220776. LOC253936 (Accession XM_170637) is another VGAM2591 host target gene. LOC253936 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253936, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253936 BINDING SITE, designated SEQ ID:45407, to the nucleotide sequence of VGAM2591 RNA, herein designated VGAM RNA, also designated SEQ ID:5302.

[87552] Another function of VGAM2591 is therefore inhibition of LOC253936 (Accession XM_170637). Accordingly, utilities of VGAM2591 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253936. LOC91138 (Accession XM_036406) is another VGAM2591 host target gene. LOC91138 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91138, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91138 BINDING SITE, designated SEQ ID:32438, to the nucleotide sequence of VGAM2591 RNA, herein designated VGAM RNA, also designated SEQ ID:5302.

[87553] Another function of VGAM2591 is therefore inhibition of LOC91138 (Accession XM_036406). Accordingly, utilities of VGAM2591 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC91138. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2592 (VGAM2592) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87554] VGAM2592 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2592 was detected is described hereinabove with reference to Figs. 1-8.

[87555] VGAM2592 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple Latent Spherical Virus. VGAM2592 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87556] VGAM2592 gene encodes a VGAM2592 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2592 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2592 precursor RNA is desig-

nated SEQ ID:2578, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2578 is located at position 1588 relative to the genome of Apple Latent Spherical Virus.

[87557] VGAM2592 precursor RNA folds onto itself, forming VGAM2592 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87558] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2592 folded precursor RNA into VGAM2592 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2592 RNA is designated SEQ ID:5303, and is provided hereinbelow with reference to the sequence

listing part.

[87559] VGAM2592 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2592 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87560] VGAM2592 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2592 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2592 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87561] The complementary binding of VGAM2592 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2592 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2592 host target RNA into VGAM2592 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87562] It is appreciated that VGAM2592 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2592 host target genes. The mRNA of each one of this plurality of VGAM2592 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2592 RNA, herein designated VGAM

RNA, and which when bound by VGAM2592 RNA causes inhibition of translation of respective one or more VGAM2592 host target proteins.

[87563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2592 gene, herein designated VGAM GENE, on one or more VGAM2592 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87564] It is yet further appreciated that a function of VGAM2592 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2592 include diagnosis, prevention and treatment of viral infection by Apple Latent Spherical Virus. Specific functions, and accordingly utilities, of VGAM2592 correlate with, and may be deduced from, the identity of the host target genes which VGAM2592 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87565] Nucleotide sequences of the VGAM2592 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2592 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2592 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2592 are further described hereinbelow with reference to Table 1.

[87566] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2592 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2592 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87567] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2592 gene, herein designated VGAM is

inhibition of expression of VGAM2592 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2592 correlate with, and may be deduced from, the identity of the target genes which VGAM2592 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87568] MIG (Accession NM_002416) is a VGAM2592 host target gene. MIG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MIG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MIG BINDING SITE, designated SEQ ID:8243, to the nucleotide sequence of VGAM2592 RNA, herein designated VGAM RNA, also designated SEQ ID:5303.

[87569] A function of VGAM2592 is therefore inhibition of MIG (Accession NM_002416). Accordingly, utilities of VGAM2592 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIG. PRO1596 (Accession NM_031270) is another VGAM2592 host target gene. PRO1596 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO1596, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1596 BINDING SITE, designated SEQ ID:25294, to the nucleotide sequence of VGAM2592 RNA, herein designated VGAM RNA, also designated SEQ ID:5303.

[87570] Another function of VGAM2592 is therefore inhibition of PRO1596 (Accession NM_031270). Accordingly, utilities of VGAM2592 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1596. LOC256073 (Accession XM_172972) is another VGAM2592 host target gene. LOC256073 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256073 BINDING SITE, designated SEQ ID:46229, to the nucleotide sequence of VGAM2592 RNA, herein designated VGAM RNA, also designated SEQ ID:5303.

[87571] Another function of VGAM2592 is therefore inhibition of LOC256073 (Accession XM_172972). Accordingly, utilities of VGAM2592 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC256073. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2593 (VGAM2593) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87572] VGAM2593 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2593 was detected is described hereinabove with reference to Figs. 1-8.

[87573] VGAM2593 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple Latent Spherical Virus. VGAM2593 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87574] VGAM2593 gene encodes a VGAM2593 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2593 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2593 precursor RNA is desig-

nated SEQ ID:2579, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2579 is located at position 5091 relative to the genome of Apple Latent Spherical Virus.

[87575] VGAM2593 precursor RNA folds onto itself, forming VGAM2593 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87576] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2593 folded precursor RNA into VGAM2593 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2593 RNA is designated SEQ ID:5304, and is provided hereinbelow with reference to the sequence

listing part.

[87577] VGAM2593 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2593 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87578] VGAM2593 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2593 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2593 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87579] The complementary binding of VGAM2593 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2593 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2593 host target RNA into VGAM2593 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87580] It is appreciated that VGAM2593 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2593 host target genes. The mRNA of each one of this plurality of VGAM2593 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2593 RNA, herein designated VGAM

RNA, and which when bound by VGAM2593 RNA causes inhibition of translation of respective one or more VGAM2593 host target proteins.

[87581] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2593 gene, herein designated VGAM GENE, on one or more VGAM2593 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87582] It is yet further appreciated that a function of VGAM2593 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2593 include diagnosis, prevention and treatment of viral infection by Apple Latent Spherical Virus. Specific functions, and accordingly utilities, of VGAM2593 correlate with, and may be deduced from, the identity of the host target genes which VGAM2593 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87583] Nucleotide sequences of the VGAM2593 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2593 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2593 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2593 are further described hereinbelow with reference to Table 1.

[87584] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2593 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2593 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87585] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2593 gene, herein designated VGAM is

inhibition of expression of VGAM2593 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2593 correlate with, and may be deduced from, the identity of the target genes which VGAM2593 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87586] Sirtuin Silent Mating Type Information Regulation 2 Homolog 1 (S. cerevisiae) (SIRT1, Accession NM_012238) is a VGAM2593 host target gene. SIRT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIRT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIRT1 BINDING SITE, designated SEQ ID:14542, to the nucleotide sequence of VGAM2593 RNA, herein designated VGAM RNA, also designated SEQ ID:5304.

[87587] A function of VGAM2593 is therefore inhibition of Sirtuin Silent Mating Type Information Regulation 2 Homolog 1 (S. cerevisiae) (SIRT1, Accession NM_012238), a gene which may function as intracellular regulatory protein with mono-ADP-ribosyltransferase activity. Accordingly, utilities of VGAM2593 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with SIRT1. The function of SIRT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM244.FLJ20725 (Accession NM_017943) is another VGAM2593 host target gene. FLJ20725 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20725, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20725 BINDING SITE, designated SEQ ID:19636, to the nucleotide sequence of VGAM2593 RNA, herein designated VGAM RNA, also designated SEQ ID:5304.

[87588] Another function of VGAM2593 is therefore inhibition of FLJ20725 (Accession NM_017943). Accordingly, utilities of VGAM2593 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20725. LOC122773 (Accession XM_058665) is another VGAM2593 host target gene. LOC122773 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122773, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122773 BINDING SITE, designated SEQ ID:36710, to the nucleotide sequence of VGAM2593 RNA, herein designated VGAM RNA, also designated SEQ ID:5304.

[87589] Another function of VGAM2593 is therefore inhibition of LOC122773 (Accession XM_058665). Accordingly, utilities of VGAM2593 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122773. LOC152200 (Accession XM_098174) is another VGAM2593 host target gene. LOC152200 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152200, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152200 BINDING SITE, designated SEQ ID:41437, to the nucleotide sequence of VGAM2593 RNA, herein designated VGAM RNA, also designated SEQ ID:5304.

[87590] Another function of VGAM2593 is therefore inhibition of LOC152200 (Accession XM_098174). Accordingly, utilities of VGAM2593 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC152200. LOC221931 (Accession XM_168348) is another VGAM2593 host target gene. LOC221931 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221931, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221931 BINDING SITE, designated SEQ ID:45118, to the nucleotide sequence of VGAM2593 RNA, herein designated VGAM RNA, also designated SEQ ID:5304.

[87591] Another function of VGAM2593 is therefore inhibition of LOC221931 (Accession XM_168348). Accordingly, utilities of VGAM2593 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221931. LOC91947 (Accession XM_041721) is another VGAM2593 host target gene. LOC91947 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91947, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91947 BINDING SITE, designated SEQ ID:33568, to the nucleotide sequence of VGAM2593 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5304.

[87592] Another function of VGAM2593 is therefore inhibition of LOC91947 (Accession XM_041721). Accordingly, utilities of VGAM2593 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91947. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2594 (VGAM2594) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87593] VGAM2594 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2594 was detected is described hereinabove with reference to Figs. 1-8.

[87594] VGAM2594 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple Latent Spherical Virus. VGAM2594 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87595] VGAM2594 gene encodes a VGAM2594 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2594 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2594 precursor RNA is designated SEQ ID:2580, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2580 is located at position 1452 relative to the genome of Apple Latent Spherical Virus.

[87596] VGAM2594 precursor RNA folds onto itself, forming VGAM2594 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87597] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2594 folded precursor RNA into VGAM2594 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2594 RNA is designated SEQ ID:5305, and is provided hereinbelow with reference to the sequence listing part.

[87598] VGAM2594 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2594 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87599] VGAM2594 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2594 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2594 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87600] The complementary binding of VGAM2594 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2594 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2594 host target RNA into VGAM2594 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87601] It is appreciated that VGAM2594 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2594 host target genes. The mRNA of

each one of this plurality of VGAM2594 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2594 RNA, herein designated VGAM RNA, and which when bound by VGAM2594 RNA causes inhibition of translation of respective one or more VGAM2594 host target proteins.

[87602] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2594 gene, herein designated VGAM GENE, on one or more VGAM2594 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[87603] It is yet further appreciated that a function of VGAM2594 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2594 include diagnosis, prevention and treatment of viral infection by Apple Latent Spherical Virus. Specific functions, and accordingly utilities, of VGAM2594 correlate with, and may be deduced from, the identity of the host target genes which VGAM2594 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87604] Nucleotide sequences of the VGAM2594 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2594 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2594 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2594 are further described hereinbelow with reference to Table 1.

[87605] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2594 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2594 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87606] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2594 gene, herein designated VGAM is inhibition of expression of VGAM2594 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2594 correlate with, and may be deduced from, the identity of the target genes which VGAM2594 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87607] Diphtheria Toxin Receptor (heparin-binding epidermal growth factor-like growth factor) (DTR, Accession NM_001945) is a VGAM2594 host target gene. DTR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DTR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DTR BINDING SITE, designated SEQ ID:7658, to the nucleotide sequence of VGAM2594 RNA, herein designated VGAM RNA, also designated SEQ ID:5305.

[87608] A function of VGAM2594 is therefore inhibition of Diphtheria Toxin Receptor (heparin-binding epidermal growth

factor-like growth factor) (DTR, Accession NM_001945), a gene which may be involved in macrophage-mediated cellular proliferation. Accordingly, utilities of VGAM2594 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DTR. The function of DTR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM242.Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411) is another VGAM2594 host target gene. HLCS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HLCS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:5994, to the nucleotide sequence of VGAM2594 RNA, herein designated VGAM RNA, also designated SEQ ID:5305.

[87609] Another function of VGAM2594 is therefore inhibition of Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase

(ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411). Accordingly, utilities of VGAM2594 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS. NORE1 (Accession NM_031437) is another VGAM2594 host target gene. NORE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NORE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NORE1 BINDING SITE, designated SEQ ID:25440, to the nucleotide sequence of VGAM2594 RNA, herein designated VGAM RNA, also designated SEQ ID:5305.

[87610] Another function of VGAM2594 is therefore inhibition of NORE1 (Accession NM_031437), a gene which may modulate intracellular signal transduction pathways. Accordingly, utilities of VGAM2594 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NORE1. The function of NORE1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM276.AUT-like 1, Cysteine

Endopeptidase (S. cerevisiae) (AUTL1, Accession NM_032852) is another VGAM2594 host target gene. AUTL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AUTL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AUTL1 BINDING SITE, designated SEQ ID:26646, to the nucleotide sequence of VGAM2594 RNA, herein designated VGAM RNA, also designated SEQ ID:5305.

[87611] Another function of VGAM2594 is therefore inhibition of AUT-like 1, Cysteine Endopeptidase (S. cerevisiae) (AUTL1, Accession NM_032852). Accordingly, utilities of VGAM2594 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AUTL1. KIAA1143 (Accession XM_044014) is another VGAM2594 host target gene. KIAA1143 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1143, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1143 BINDING SITE,

designated SEQ ID:34068, to the nucleotide sequence of VGAM2594 RNA, herein designated VGAM RNA, also designated SEQ ID:5305.

[87612] Another function of VGAM2594 is therefore inhibition of KIAA1143 (Accession XM_044014). Accordingly, utilities of VGAM2594 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1143. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2595 (VGAM2595) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87613] VGAM2595 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2595 was detected is described hereinabove with reference to Figs. 1-8.

[87614] VGAM2595 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Apple Latent Spherical Virus. VGAM2595 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87615] VGAM2595 gene encodes a VGAM2595 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2595 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2595 precursor RNA is designated SEQ ID:2581, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2581 is located at position 6486 relative to the genome of Apple Latent Spherical Virus.

[87616] VGAM2595 precursor RNA folds onto itself, forming VGAM2595 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87617] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2595 folded precursor RNA into VGAM2595 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2595 RNA is designated SEQ ID:5306, and is provided hereinbelow with reference to the sequence listing part.

[87618] VGAM2595 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2595 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87619] VGAM2595 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2595 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2595 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87620] The complementary binding of VGAM2595 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2595 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2595 host target RNA into VGAM2595 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87621] It is appreciated that VGAM2595 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2595 host target genes. The mRNA of each one of this plurality of VGAM2595 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2595 RNA, herein designated VGAM RNA, and which when bound by VGAM2595 RNA causes inhibition of translation of respective one or more VGAM2595 host target proteins.

[87622] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2595 gene, herein designated VGAM GENE, on one or more VGAM2595 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87623] It is yet further appreciated that a function of VGAM2595 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of viral infection by Apple Latent Spherical Virus. Specific functions, and accordingly utilities, of VGAM2595 correlate with, and may be deduced from, the identity of the host target genes which VGAM2595 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87624] Nucleotide sequences of the VGAM2595 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2595 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2595 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2595 are further described hereinbelow with reference to Table 1.

[87625] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2595 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2595 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87626] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2595 gene, herein designated VGAM is inhibition of expression of VGAM2595 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2595 correlate with, and may be deduced from, the identity of the target genes which VGAM2595 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87627] Mastermind-like 1 (Drosophila) (MAML1, Accession NM_014757) is a VGAM2595 host target gene. MAML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAML1 BINDING SITE, designated SEQ ID:16495, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87628] A function of VGAM2595 is therefore inhibition of Master-

mind-like 1 (Drosophila) (MAML1, Accession NM_014757), a gene which MAML1 functions as a transcriptional coactivator for Notch signaling. Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAML1. The function of MAML1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM556.AWP1 (Accession NM_019006) is another VGAM2595 host target gene. AWP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AWP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AWP1 BINDING SITE, designated SEQ ID:21079, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87629] Another function of VGAM2595 is therefore inhibition of AWP1 (Accession NM_019006). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AWP1. Baculoviral IAP Repeat-containing 1 (BIRC1, Accession

NM_004536) is another VGAM2595 host target gene. BIRC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIRC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIRC1 BINDING SITE, designated SEQ ID:10883, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87630] Another function of VGAM2595 is therefore inhibition of Baculoviral IAP Repeat-containing 1 (BIRC1, Accession NM_004536). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC1. FLJ10159 (Accession NM_018013) is another VGAM2595 host target gene. FLJ10159 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10159, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10159 BINDING SITE, designated SEQ ID:19749, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ

ID:5306.

[87631] Another function of VGAM2595 is therefore inhibition of FLJ10159 (Accession NM_018013). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10159. KIAA0419 (Accession NM_014711) is another VGAM2595 host target gene. KIAA0419 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0419, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0419 BINDING SITE, designated SEQ ID:16260, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87632] Another function of VGAM2595 is therefore inhibition of KIAA0419 (Accession NM_014711). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0419. KIAA0970 (Accession NM_014923) is another VGAM2595 host target gene. KIAA0970 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0970, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0970 BINDING SITE, designated SEQ ID:17205, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87633] Another function of VGAM2595 is therefore inhibition of KIAA0970 (Accession NM_014923). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0970. KIAA1546 (Accession XM_042301) is another VGAM2595 host target gene. KIAA1546 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1546, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1546 BINDING SITE, designated SEQ ID:33716, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87634] Another function of VGAM2595 is therefore inhibition of KIAA1546 (Accession XM_042301). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1546. KIAA1673 (Accession XM_047672) is another VGAM2595 host target gene. KIAA1673 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1673, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1673 BINDING SITE, designated SEQ ID:35025, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87635] Another function of VGAM2595 is therefore inhibition of KIAA1673 (Accession XM_047672). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1673. TRAD (Accession NM_007064) is another VGAM2595 host target gene. TRAD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRAD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAD BINDING SITE, designated SEQ ID:13929, to the nucleotide sequence of

VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87636] Another function of VGAM2595 is therefore inhibition of TRAD (Accession NM_007064). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAD. LOC158381 (Accession XM_048461) is another VGAM2595 host target gene. LOC158381 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158381, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158381 BINDING SITE, designated SEQ ID:35175, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87637] Another function of VGAM2595 is therefore inhibition of LOC158381 (Accession XM_048461). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158381. LOC196283 (Accession XM_113684) is another VGAM2595 host target gene. LOC196283 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC196283, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196283 BINDING SITE, designated SEQ ID:42342, to the nucleotide sequence of VGAM2595 RNA, herein designated VGAM RNA, also designated SEQ ID:5306.

[87638] Another function of VGAM2595 is therefore inhibition of LOC196283 (Accession XM_113684). Accordingly, utilities of VGAM2595 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196283. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2596 (VGAM2596) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87639] VGAM2596 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2596 was detected is described hereinabove with reference to Figs. 1-8.

[87640] VGAM2596 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Tobacco Rattle Virus. VGAM2596 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87641] VGAM2596 gene encodes a VGAM2596 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2596 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2596 precursor RNA is designated SEQ ID:2582, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2582 is located at position 3368 relative to the genome of Tobacco Rattle Virus.

[87642] VGAM2596 precursor RNA folds onto itself, forming VGAM2596 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87643] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2596 folded precursor RNA into VGAM2596 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2596 RNA is designated SEQ ID:5307, and is provided hereinbelow with reference to the sequence listing part.

[87644] VGAM2596 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2596 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87645] VGAM2596 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2596 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2596 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87646] The complementary binding of VGAM2596 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2596 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2596

host target RNA into VGAM2596 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87647] It is appreciated that VGAM2596 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2596 host target genes. The mRNA of each one of this plurality of VGAM2596 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2596 RNA, herein designated VGAM RNA, and which when bound by VGAM2596 RNA causes inhibition of translation of respective one or more VGAM2596 host target proteins.

[87648] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2596 gene, herein designated VGAM GENE, on one or more VGAM2596 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87649] It is yet further appreciated that a function of VGAM2596 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of viral infection by Tobacco Rattle Virus. Specific functions, and accordingly utilities, of VGAM2596 correlate with, and may be deduced from, the identity of the host target genes which VGAM2596 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87650] Nucleotide sequences of the VGAM2596 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2596 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2596 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2596 are further described hereinbelow with reference to Table 1.

[87651] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2596 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2596 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87652] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2596 gene, herein designated VGAM is inhibition of expression of VGAM2596 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2596 correlate with, and may be deduced from, the identity of the target genes which VGAM2596 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87653] Cysteine-rich Motor Neuron 1 (CRIM1, Accession

NM_016441) is a VGAM2596 host target gene. CRIM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRIM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRIM1 BINDING SITE, designated SEQ ID:18559, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87654] A function of VGAM2596 is therefore inhibition of Cysteine-rich Motor Neuron 1 (CRIM1, Accession NM_016441). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRIM1. Deafness, Autosomal Dominant 5 (DFNA5, Accession NM_004403) is another VGAM2596 host target gene. DFNA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DFNA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DFNA5 BINDING SITE, designated SEQ ID:10656, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA,

also designated SEQ ID:5307.

[87655] Another function of VGAM2596 is therefore inhibition of Deafness, Autosomal Dominant 5 (DFNA5, Accession NM_004403). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFNA5. G Protein-coupled Receptor 4 (GPR4, Accession XM_009140) is another VGAM2596 host target gene. GPR4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPR4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR4 BINDING SITE, designated SEQ ID:30101, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87656] Another function of VGAM2596 is therefore inhibition of G Protein-coupled Receptor 4 (GPR4, Accession XM_009140), a gene which stimulates to produce increased calcium by both SPC and LPC . Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR4. The function of GPR4 and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2087.S100 Calcium Binding Protein, Beta (neural) (S100B, Accession NM_006272) is another VGAM2596 host target gene. S100B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of S100B BINDING SITE, designated SEQ ID:12956, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87657] Another function of VGAM2596 is therefore inhibition of S100 Calcium Binding Protein, Beta (neural) (S100B, Accession NM_006272), a gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with S100B. The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described here-

inabove with reference to VGAM1078.1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) (AGPAT1, Accession NM_032741) is another VGAM2596 host target gene. AGPAT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AGPAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AGPAT1 BINDING SITE, designated SEQ ID:26474, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87658] Another function of VGAM2596 is therefore inhibition of 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) (AGPAT1, Accession NM_032741). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AG-PAT1. Adaptor-related Protein Complex 3, Mu 1 Subunit (AP3M1, Accession NM_012095) is another VGAM2596 host target gene. AP3M1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by AP3M1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP3M1 BINDING SITE, designated SEQ ID:14398, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87659] Another function of VGAM2596 is therefore inhibition of Adaptor-related Protein Complex 3, Mu 1 Subunit (AP3M1, Accession NM_012095). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3M1. Chromosome 9 Open Reading Frame 7 (C9orf7, Accession NM_017586) is another VGAM2596 host target gene. C9orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf7 BINDING SITE, designated SEQ ID:19036, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87660] Another function of VGAM2596 is therefore inhibition of Chromosome 9 Open Reading Frame 7 (C9orf7, Accession NM_017586). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf7. DKFZP434F0318 (Accession NM_030817) is another VGAM2596 host target gene. DKFZP434F0318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F0318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE, designated SEQ ID:25146, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87661] Another function of VGAM2596 is therefore inhibition of DKFZP434F0318 (Accession NM_030817). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F0318. DKFZP434H132 (Accession XM_057020) is another VGAM2596 host target gene. DKFZP434H132 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

DKFZP434H132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434H132 BINDING SITE, designated SEQ ID:36443, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87662] Another function of VGAM2596 is therefore inhibition of DKFZP434H132 (Accession XM_057020). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H132. DKFZP566K1924 (Accession XM_057469) is another VGAM2596 host target gene. DKFZP566K1924 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP566K1924, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566K1924 BINDING SITE, designated SEQ ID:36522, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87663] Another function of VGAM2596 is therefore inhibition of

DKFZP566K1924 (Accession XM_057469). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566K1924. HSU79252 (Accession NM_013298) is another VGAM2596 host target gene. HSU79252 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSU79252, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSU79252 BINDING SITE, designated SEQ ID:14958, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87664] Another function of VGAM2596 is therefore inhibition of HSU79252 (Accession NM_013298). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSU79252. KIAA0064 (Accession NM_014748) is another VGAM2596 host target gene. KIAA0064 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0064, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0064 BINDING SITE, designated SEQ ID:16460, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87665] Another function of VGAM2596 is therefore inhibition of KIAA0064 (Accession NM_014748). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0064. KIAA0410 (Accession NM_014778) is another VGAM2596 host target gene. KIAA0410 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0410, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0410 BINDING SITE, designated SEQ ID:16623, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87666] Another function of VGAM2596 is therefore inhibition of KIAA0410 (Accession NM_014778). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0410. KIAA1710 (Accession XM_031283) is another

VGAM2596 host target gene. KIAA1710 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1710, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1710 BINDING SITE, designated SEQ ID:31331, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87667] Another function of VGAM2596 is therefore inhibition of KIAA1710 (Accession XM_031283). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1710. KIAA1853 (Accession XM_045184) is another VGAM2596 host target gene. KIAA1853 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1853, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1853 BINDING SITE, designated SEQ ID:34390, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87668] Another function of VGAM2596 is therefore inhibition of KIAA1853 (Accession XM_045184). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1853. MGC5338 (Accession NM_024062) is another VGAM2596 host target gene. MGC5338 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC5338, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5338 BINDING SITE, designated SEQ ID:23498, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87669] Another function of VGAM2596 is therefore inhibition of MGC5338 (Accession NM_024062). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5338. Oxysterol Binding Protein-like 3 (OSBPL3, Accession NM_015550) is another VGAM2596 host target gene. OSBPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL3, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:17819, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87670] Another function of VGAM2596 is therefore inhibition of Oxysterol Binding Protein-like 3 (OSBPL3, Accession NM_015550). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3. P37NB (Accession NM_005824) is another VGAM2596 host target gene. P37NB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by P37NB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P37NB BINDING SITE, designated SEQ ID:12436, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87671] Another function of VGAM2596 is therefore inhibition of P37NB (Accession NM_005824). Accordingly, utilities of

VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P37NB. Protocadherin 19 (PCDH19, Accession XM_033173) is another VGAM2596 host target gene. PCDH19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDH19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH19 BINDING SITE, designated SEQ ID:31865, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87672] Another function of VGAM2596 is therefore inhibition of Protocadherin 19 (PCDH19, Accession XM_033173). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH19. PI4KII (Accession NM_018425) is another VGAM2596 host target gene. PI4KII BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PI4KII, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PI4KII BIND-

ING SITE, designated SEQ ID:20482, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87673] Another function of VGAM2596 is therefore inhibition of PI4KII (Accession NM_018425). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PI4KII. Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737) is another VGAM2596 host target gene. RASSF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASSF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:16400, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87674] Another function of VGAM2596 is therefore inhibition of Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

RASSF2. LOC115286 (Accession XM_055644) is another VGAM2596 host target gene. LOC115286 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115286 BINDING SITE, designated SEQ ID:36314, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87675] Another function of VGAM2596 is therefore inhibition of LOC115286 (Accession XM_055644). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115286. LOC152195 (Accession XM_098172) is another VGAM2596 host target gene. LOC152195 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152195 BINDING SITE, designated SEQ ID:41433, to the nucleotide sequence of VGAM2596 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5307.

[87676] Another function of VGAM2596 is therefore inhibition of LOC152195 (Accession XM_098172). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152195. LOC54516 (Accession NM_019041) is another VGAM2596 host target gene. LOC54516 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC54516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC54516 BINDING SITE, designated SEQ ID:21124, to the nucleotide sequence of VGAM2596 RNA, herein designated VGAM RNA, also designated SEQ ID:5307.

[87677] Another function of VGAM2596 is therefore inhibition of LOC54516 (Accession NM_019041). Accordingly, utilities of VGAM2596 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC54516. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2597 (VGAM2597) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87678] VGAM2597 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2597 was detected is described hereinabove with reference to Figs. 1-8.

[87679] VGAM2597 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tobacco Rattle Virus. VGAM2597 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87680] VGAM2597 gene encodes a VGAM2597 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2597 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2597 precursor RNA is designated SEQ ID:2583, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2583 is located at position 1854 relative to the genome of Tobacco Rattle Virus.

[87681] VGAM2597 precursor RNA folds onto itself, forming

VGAM2597 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87682] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2597 folded precursor RNA into VGAM2597 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2597 RNA is designated SEQ ID:5308, and is provided hereinbelow with reference to the sequence listing part.

[87683] VGAM2597 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2597 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87684] VGAM2597 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2597 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2597 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87685] The complementary binding of VGAM2597 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2597 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2597 host target RNA into VGAM2597 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87686] It is appreciated that VGAM2597 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2597 host target genes. The mRNA of each one of this plurality of VGAM2597 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2597 RNA, herein designated VGAM RNA, and which when bound by VGAM2597 RNA causes inhibition of translation of respective one or more VGAM2597 host target proteins.

[87687] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2597 gene, herein designated VGAM GENE, on one or more VGAM2597 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87688] It is yet further appreciated that a function of VGAM2597 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2597 include diagnosis, prevention and treatment of viral infection by Tobacco Rattle Virus. Specific functions, and accordingly utilities, of VGAM2597 correlate with, and may be deduced from, the identity of the host target genes which VGAM2597 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[87689] Nucleotide sequences of the VGAM2597 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2597 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2597 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2597 are further described hereinbelow with reference to Table 1.

[87690] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2597 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2597 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87691] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2597 gene, herein designated VGAM is inhibition of expression of VGAM2597 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2597 correlate with, and may be deduced from, the identity of the target genes which VGAM2597 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[87692] Toll-like Receptor 1 (TLR1, Accession NM_003263) is a VGAM2597 host target gene. TLR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TLR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TLR1 BINDING SITE, designated SEQ ID:9275, to the nucleotide sequence of VGAM2597 RNA, herein designated VGAM RNA, also designated SEQ ID:5308.

[87693] A function of VGAM2597 is therefore inhibition of Toll-like Receptor 1 (TLR1, Accession NM_003263), a gene which is a critical for antibody responses to OspA. Accordingly, utilities of VGAM2597 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLR1. The function of TLR1 has been established by previous studies. TLRs and IL1Rs share a conserved cytoplasmic TIR domain. Mutations in this domain disrupt responses to LPS and to gram-positive bacteria, mediated by TLR4 and TLR2 (OMIM Ref. No. 603028), respectively. By structural analysis, Xu et al. (2000) determined that the TIR domains of human TLR2

and TLR1, which are 50% identical at the amino acid level, contain a central 5-stranded parallel beta-sheet surrounded by 5 alpha helices on both sides. The structures have a large conserved surface patch, and mutational and functional analyses indicated that residues in the surface patch are crucial for receptor signaling. The authors concluded that instead of disturbing the structure of the TIR domain, mutations may abolish signaling by disrupting the recruitment of the MYD88 (OMIM Ref. No. 602170) adaptor molecule. Alexopoulou et al. (2002) reported that a small percentage of individuals who receive a vaccination series with the OspA antigen of Borrelia burgdorferi, the causative spirochete agent of Lyme disease, have very low antibody responses to the vaccine. They studied 7 of these 'low responders.' Macrophages from the low responders produced lower levels of the proinflammatory cytokines tumor necrosis factor (TNF; 191160) and IL6 (OMIM Ref. No. 147620), while production of the antiinflammatory cytokine IL10 (OMIM Ref. No. 124092) was similar to that of normal responders. Mutation analysis did not identify any defects in the TLR2 gene in the low responders. The human low antibody responders had no mutations in the TLR1 gene. However, flow cytometric

analysis demonstrated undetectable cell-surface expression of TLR1, but not of TLR2, in all but 1 of the low responders. Animal model experiments lend further support to the function of TLR1. Tlr2-deficient mice produced lower levels of antibody and IL6 in response to OspA in the absence of complete Freund adjuvant (CFA), but not to intact B. burgdorferi. Apart from a higher spirochete burden early in the course of the disease, Tlr2 -/- mice resolved the infection in a manner similar to wildtype mice. Tlr1-deficient mice had a similar pattern of responses, except that these mice were capable of producing IL6 in response to peptidoglycan and were also capable of making IL10 in response to OspA. Alexopoulou et al. (2002) concluded that although TLR1 expression is critical for antibody responses to OspA, the presence of other TLRs in the host that presumably recognize other B. burgdorferi antigens results in no greater susceptibility to infection and disease in these hosts.

[87694] It is appreciated that the abovementioned animal model for TLR1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[87695] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[87696] Xu, Y.; Tao, X.; Shen, B.; Horng, T.; Medzhitov, R.; Manley, J. L.; Tong, L. : Structural basis for signal transduction by the Toll/interleukin-1 receptor domains. Nature 408: 111-115, 2000. ; and

[87697] Alexopoulou, L.; Thomas, V.; Schnare, M.; Lobet, Y.; Anguita, J.; Schoen, R. T.; Medzhitov, R.; Fikrig, E.; Flavell, R. A. : Hyporesponsiveness to vaccination with Borrelia burgdorferi.

[87698] Further studies establishing the function and utilities of TLR1 are found in John Hopkins OMIM database record ID 601194, and in sited publications numbered 9835-9836, 6736, 983 and 10819-9840 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.FLJ14440 (Accession NM_032784) is another VGAM2597 host target gene. FLJ14440 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14440, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14440 BINDING SITE, designated SEQ ID:26529, to the nucleotide

sequence of VGAM2597 RNA, herein designated VGAM RNA, also designated SEQ ID:5308.

[87699] Another function of VGAM2597 is therefore inhibition of FLJ14440 (Accession NM_032784). Accordingly, utilities of VGAM2597 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14440. P450RAI-2 (Accession NM_019885) is another VGAM2597 host target gene. P450RAI-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P450RAI-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P450RAI-2 BINDING SITE, designated SEQ ID:21265, to the nucleotide sequence of VGAM2597 RNA, herein designated VGAM RNA, also designated SEQ ID:5308.

[87700] Another function of VGAM2597 is therefore inhibition of P450RAI-2 (Accession NM_019885). Accordingly, utilities of VGAM2597 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P450RAI-2. LOC200347 (Accession XM_114219) is another VGAM2597 host target gene. LOC200347 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC200347, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200347 BINDING SITE, designated SEQ ID:42806, to the nucleotide sequence of VGAM2597 RNA, herein designated VGAM RNA, also designated SEQ ID:5308.

[87701] Another function of VGAM2597 is therefore inhibition of LOC200347 (Accession XM_114219). Accordingly, utilities of VGAM2597 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200347. LOC51716 (Accession NM_016280) is another VGAM2597 host target gene. LOC51716 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51716, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51716 BINDING SITE, designated SEQ ID:18404, to the nucleotide sequence of VGAM2597 RNA, herein designated VGAM RNA, also designated SEQ ID:5308.

[87702] Another function of VGAM2597 is therefore inhibition of LOC51716 (Accession NM_016280). Accordingly, utilities

of VGAM2597 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51716. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2598 (VGAM2598) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87703] VGAM2598 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2598 was detected is described hereinabove with reference to Figs. 1-8.

[87704] VGAM2598 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tobacco Rattle Virus. VGAM2598 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87705] VGAM2598 gene encodes a VGAM2598 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2598 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2598 precursor RNA is designated SEQ ID:2584, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2584 is located at position 1327 relative to the genome of Tobacco Rattle Virus.

[87706] VGAM2598 precursor RNA folds onto itself, forming VGAM2598 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87707] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2598 folded precursor RNA into VGAM2598 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2598 RNA is designated SEQ ID:5309, and

is provided hereinbelow with reference to the sequence listing part.

[87708] VGAM2598 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2598 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87709] VGAM2598 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2598 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2598 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87710] The complementary binding of VGAM2598 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2598 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2598 host target RNA into VGAM2598 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87711] It is appreciated that VGAM2598 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2598 host target genes. The mRNA of each one of this plurality of VGAM2598 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2598 RNA, herein designated VGAM RNA, and which when bound by VGAM2598 RNA causes inhibition of translation of respective one or more VGAM2598 host target proteins.

[87712] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2598 gene, herein designated VGAM GENE, on one or more VGAM2598 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87713] It is yet further appreciated that a function of VGAM2598 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2598 include diagnosis, prevention and treatment of viral infection by Tobacco Rattle Virus. Specific functions, and accordingly utilities, of VGAM2598 correlate with, and may be deduced from, the identity of the host target genes which VGAM2598 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87714] Nucleotide sequences of the VGAM2598 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2598 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2598 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2598 are further described hereinbelow with reference to Table 1.

[87715] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2598 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2598 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87716] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2598 gene, herein designated VGAM is inhibition of expression of VGAM2598 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2598 correlate with, and may be deduced from, the identity of the target genes which VGAM2598 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87717] Formyl Peptide Receptor-like 1 (FPRL1, Accession NM_001462) is a VGAM2598 host target gene. FPRL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FPRL1 BINDING SITE, designated SEQ ID:7196, to the nucleotide sequence of VGAM2598 RNA, herein designated VGAM RNA, also designated SEQ ID:5309.

[87718] A function of VGAM2598 is therefore inhibition of Formyl Peptide Receptor-like 1 (FPRL1, Accession NM_001462). Accordingly, utilities of VGAM2598 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FPRL1. Interleukin 1 Receptor Accessory Protein (IL1RAP, Accession NM_002182) is another

VGAM2598 host target gene. IL1RAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL1RAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1RAP BINDING SITE, designated SEQ ID:7939, to the nucleotide sequence of VGAM2598 RNA, herein designated VGAM RNA, also designated SEQ ID:5309.

[87719] Another function of VGAM2598 is therefore inhibition of Interleukin 1 Receptor Accessory Protein (IL1RAP, Accession NM_002182), a gene which may function as a membrane receptor. promotes heterophilic cellular adhesion. Accordingly, utilities of VGAM2598 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RAP. The function of IL1RAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM142.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2599 (VGAM2599) viral gene, which modulates expression

of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87720] VGAM2599 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2599 was detected is described hereinabove with reference to Figs. 1-8.

[87721] VGAM2599 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Obuda Pepper Virus. VGAM2599 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87722] VGAM2599 gene encodes a VGAM2599 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2599 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2599 precursor RNA is designated SEQ ID:2585, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2585 is located at position 2974 relative to the genome of Obuda Pepper Virus.

[87723] VGAM2599 precursor RNA folds onto itself, forming VGAM2599 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87724] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2599 folded precursor RNA into VGAM2599 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2599 RNA is designated SEQ ID:5310, and is provided hereinbelow with reference to the sequence listing part.

[87725] VGAM2599 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2599 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87726] VGAM2599 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2599 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2599 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87727] The complementary binding of VGAM2599 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2599 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2599 host target RNA into VGAM2599 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87728] It is appreciated that VGAM2599 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2599 host target genes. The mRNA of each one of this plurality of VGAM2599 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2599 RNA, herein designated VGAM RNA, and which when bound by VGAM2599 RNA causes inhibition of translation of respective one or more VGAM2599 host target proteins.

[87729] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2599 gene, herein designated VGAM GENE, on one or more VGAM2599 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87730] It is yet further appreciated that a function of VGAM2599 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of viral infection by Obuda Pepper Virus. Specific functions, and accordingly utilities, of VGAM2599 correlate with, and may be deduced from, the identity of the host target genes which VGAM2599 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[87731] Nucleotide sequences of the VGAM2599 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2599 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2599 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2599 are further described hereinbelow with reference to Table 1.

[87732] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2599 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2599 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87733] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2599 gene, herein designated VGAM is inhibition of expression of VGAM2599 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2599 correlate with, and may be deduced from, the identity of the target genes which VGAM2599 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87734] Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein) (RSN, Accession NM_002956) is a VGAM2599 host target gene. RSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RSN BINDING SITE, designated SEQ ID:8865, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87735] A function of VGAM2599 is therefore inhibition of Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein) (RSN, Accession NM_002956), a gene which seems to be a intermediate filament associated protein that links endocytic vesicles to microtubules. Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RSN. The function of RSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1086.BY55 (Accession XM_001667) is another VGAM2599 host target gene. BY55

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BY55, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BY55 BINDING SITE, designated SEQ ID:29846, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87736] Another function of VGAM2599 is therefore inhibition of BY55 (Accession XM_001667). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BY55. FLJ13340 (Accession NM_057175) is another VGAM2599 host target gene. FLJ13340 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13340, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13340 BINDING SITE, designated SEQ ID:27707, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87737] Another function of VGAM2599 is therefore inhibition of

FLJ13340 (Accession NM_057175). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13340. KIAA0092 (Accession NM_014679) is another VGAM2599 host target gene. KIAA0092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0092 BINDING SITE, designated SEQ ID:16154, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87738] Another function of VGAM2599 is therefore inhibition of KIAA0092 (Accession NM_014679). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0092. KIAA1361 (Accession XM_030845) is another VGAM2599 host target gene. KIAA1361 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1361, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1361 BINDING SITE, designated SEQ ID:31167, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87739] Another function of VGAM2599 is therefore inhibition of KIAA1361 (Accession XM_030845). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1361. Karyopherin (importin) Beta 3 (KPNB3, Accession NM_002271) is another VGAM2599 host target gene. KPNB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KPNB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KPNB3 BINDING SITE, designated SEQ ID:8062, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87740] Another function of VGAM2599 is therefore inhibition of Karyopherin (importin) Beta 3 (KPNB3, Accession NM_002271). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KPNB3. OSF-2 (Accession

NM_006475) is another VGAM2599 host target gene. OSF-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSF-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSF-2 BINDING SITE, designated SEQ ID:13198, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87741] Another function of VGAM2599 is therefore inhibition of OSF-2 (Accession NM_006475). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSF-2. TBDN100 (Accession NM_025085) is another VGAM2599 host target gene. TBDN100 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBDN100, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBDN100 BINDING SITE, designated SEQ ID:24698, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5310.

[87742] Another function of VGAM2599 is therefore inhibition of TBDN100 (Accession NM_025085). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBDN100. Thioesterase, Adipose Associated (THEA, Accession XM_038922) is another VGAM2599 host target gene. THEA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by THEA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of THEA BINDING SITE, designated SEQ ID:32953, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87743] Another function of VGAM2599 is therefore inhibition of Thioesterase, Adipose Associated (THEA, Accession XM_038922). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THEA. LOC221431 (Accession XM_166380) is another VGAM2599 host target gene. LOC221431 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by LOC221431, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221431 BINDING SITE, designated SEQ ID:44223, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87744] Another function of VGAM2599 is therefore inhibition of LOC221431 (Accession XM_166380). Accordingly, utilities of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221431. LOC255326 (Accession XM_172832) is another VGAM2599 host target gene. LOC255326 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255326, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255326 BINDING SITE, designated SEQ ID:46107, to the nucleotide sequence of VGAM2599 RNA, herein designated VGAM RNA, also designated SEQ ID:5310.

[87745] Another function of VGAM2599 is therefore inhibition of LOC255326 (Accession XM_172832). Accordingly, utilities

of VGAM2599 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255326. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2600 (VGAM2600) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87746] VGAM2600 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2600 was detected is described hereinabove with reference to Figs. 1-8.

[87747] VGAM2600 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Obuda Pepper Virus. VGAM2600 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87748] VGAM2600 gene encodes a VGAM2600 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2600 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2600 precursor RNA is designated SEQ ID:2586, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2586 is located at position 1275 relative to the genome of Obuda Pepper Virus.

[87749] VGAM2600 precursor RNA folds onto itself, forming VGAM2600 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87750] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2600 folded precursor RNA into VGAM2600 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2600 RNA is designated SEQ ID:5311, and

is provided hereinbelow with reference to the sequence listing part.

[87751] VGAM2600 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2600 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87752] VGAM2600 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2600 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2600 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87753] The complementary binding of VGAM2600 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2600 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2600 host target RNA into VGAM2600 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87754] It is appreciated that VGAM2600 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2600 host target genes. The mRNA of each one of this plurality of VGAM2600 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2600 RNA, herein designated VGAM RNA, and which when bound by VGAM2600 RNA causes inhibition of translation of respective one or more VGAM2600 host target proteins.

[87755] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2600 gene, herein designated VGAM GENE, on one or more VGAM2600 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87756] It is yet further appreciated that a function of VGAM2600 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2600 include diagnosis, prevention and treatment of viral infection by Obuda Pepper Virus. Specific functions, and accordingly utilities, of VGAM2600 correlate with, and may be deduced from, the identity of the host target genes which VGAM2600 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87757] Nucleotide sequences of the VGAM2600 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2600 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2600 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2600 are further described hereinbelow with reference to Table 1.

[87758] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2600 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2600 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87759] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2600 gene, herein designated VGAM is inhibition of expression of VGAM2600 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2600 correlate with, and may be deduced from, the identity of the target genes which VGAM2600 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87760] Discs, Large (Drosophila) Homolog 5 (DLG5, Accession XM_096398) is a VGAM2600 host target gene. DLG5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DLG5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLG5 BINDING SITE, designated SEQ ID:40333, to the nucleotide sequence of VGAM2600 RNA, herein designated VGAM RNA, also designated SEQ ID:5311.

[87761] A function of VGAM2600 is therefore inhibition of Discs, Large (Drosophila) Homolog 5 (DLG5, Accession XM_096398), a gene which may transmit extracellular signals to inhibit cell proliferation. Accordingly, utilities of VGAM2600 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLG5.

The function of DLG5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM444.Interleukin 2 Receptor, Beta (IL2RB, Accession NM_000878) is another VGAM2600 host target gene. IL2RB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL2RB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL2RB BINDING SITE, designated SEQ ID:6569, to the nucleotide sequence of VGAM2600 RNA, herein designated VGAM RNA, also designated SEQ ID:5311.

[87762] Another function of VGAM2600 is therefore inhibition of Interleukin 2 Receptor, Beta (IL2RB, Accession NM_000878), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il-2. Accordingly, utilities of VGAM2600 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL2RB. The function of IL2RB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM450.FLJ14075

(Accession NM_024894) is another VGAM2600 host target gene. FLJ14075 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14075, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14075 BINDING SITE, designated SEQ ID:24372, to the nucleotide sequence of VGAM2600 RNA, herein designated VGAM RNA, also designated SEQ ID:5311.

[87763] Another function of VGAM2600 is therefore inhibition of FLJ14075 (Accession NM_024894). Accordingly, utilities of VGAM2600 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14075. MGC4707 (Accession NM_024113) is another VGAM2600 host target gene. MGC4707 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4707, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4707 BINDING SITE, designated SEQ ID:23562, to the nucleotide sequence of VGAM2600 RNA, herein designated VGAM

RNA, also designated SEQ ID:5311.

[87764] Another function of VGAM2600 is therefore inhibition of MGC4707 (Accession NM_024113). Accordingly, utilities of VGAM2600 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4707. Netrin 4 (NTN4, Accession XM_031896) is another VGAM2600 host target gene. NTN4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTN4 BINDING SITE, designated SEQ ID:31510, to the nucleotide sequence of VGAM2600 RNA, herein designated VGAM RNA, also designated SEQ ID:5311.

[87765] Another function of VGAM2600 is therefore inhibition of Netrin 4 (NTN4, Accession XM_031896). Accordingly, utilities of VGAM2600 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTN4. LOC138429 (Accession XM_059973) is another VGAM2600 host target gene. LOC138429 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC138429, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138429 BINDING SITE, designated SEQ ID:37134, to the nucleotide sequence of VGAM2600 RNA, herein designated VGAM RNA, also designated SEQ ID:5311.

[87766] Another function of VGAM2600 is therefore inhibition of LOC138429 (Accession XM_059973). Accordingly, utilities of VGAM2600 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138429. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2601 (VGAM2601) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87767] VGAM2601 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2601 was detected is described hereinabove with reference to Figs. 1-8.

[87768] VGAM2601 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Obuda Pepper Virus.

VGAM2601 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87769] VGAM2601 gene encodes a VGAM2601 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2601 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2601 precursor RNA is designated SEQ ID:2587, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2587 is located at position 589 relative to the genome of Obuda Pepper Virus.

[87770] VGAM2601 precursor RNA folds onto itself, forming VGAM2601 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87771] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2601 folded precursor RNA into VGAM2601 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of VGAM2601 RNA is designated SEQ ID:5312, and is provided hereinbelow with reference to the sequence listing part.

[87772] VGAM2601 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2601 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87773] VGAM2601 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2601 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2601 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87774] The complementary binding of VGAM2601 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2601 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2601 host target RNA into VGAM2601 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87775] It is appreciated that VGAM2601 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2601 host target genes. The mRNA of each one of this plurality of VGAM2601 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2601 RNA, herein designated VGAM RNA, and which when bound by VGAM2601 RNA causes inhibition of translation of respective one or more VGAM2601 host target proteins.

[87776] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2601 gene, herein designated VGAM GENE, on one or more VGAM2601 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87777] It is yet further appreciated that a function of VGAM2601 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2601 include diagnosis, prevention and treatment of viral infection by Obuda Pepper Virus. Specific functions, and accordingly utilities, of VGAM2601 correlate with, and may be deduced from, the identity of the host target genes which VGAM2601 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87778] Nucleotide sequences of the VGAM2601 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2601 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2601 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2601 are further described hereinbelow with reference to Table 1.

[87779] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2601 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2601 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87780] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2601 gene, herein designated VGAM is inhibition of expression of VGAM2601 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2601 correlate with, and may be deduced from, the identity of the target genes which VGAM2601 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87781] DKFZp761N1114 (Accession XM_086327) is a VGAM2601 host target gene. DKFZp761N1114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761N1114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761N1114 BINDING SITE, designated SEQ ID:38602, to

the nucleotide sequence of VGAM2601 RNA, herein designated VGAM RNA, also designated SEQ ID:5312.

[87782] A function of VGAM2601 is therefore inhibition of DKFZp761N1114 (Accession XM_086327). Accordingly, utilities of VGAM2601 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761N1114. PRO2949 (Accession NM_018544) is another VGAM2601 host target gene. PRO2949 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2949, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2949 BINDING SITE, designated SEQ ID:20618, to the nucleotide sequence of VGAM2601 RNA, herein designated VGAM RNA, also designated SEQ ID:5312.

[87783] Another function of VGAM2601 is therefore inhibition of PRO2949 (Accession NM_018544). Accordingly, utilities of VGAM2601 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2949. LOC147991 (Accession XM_085993) is another VGAM2601 host target gene. LOC147991 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC147991, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147991 BINDING SITE, designated SEQ ID:38433, to the nucleotide sequence of VGAM2601 RNA, herein designated VGAM RNA, also designated SEQ ID:5312.

[87784] Another function of VGAM2601 is therefore inhibition of LOC147991 (Accession XM_085993). Accordingly, utilities of VGAM2601 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147991. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2602 (VGAM2602) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87785] VGAM2602 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2602 was detected is described hereinabove with reference to Figs. 1-8.

[87786] VGAM2602 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Obuda Pepper Virus. VGAM2602 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87787] VGAM2602 gene encodes a VGAM2602 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2602 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2602 precursor RNA is designated SEQ ID:2588, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2588 is located at position 2115 relative to the genome of Obuda Pepper Virus.

[87788] VGAM2602 precursor RNA folds onto itself, forming VGAM2602 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87789] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2602 folded precursor RNA into VGAM2602 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2602 RNA is designated SEQ ID:5313, and is provided hereinbelow with reference to the sequence listing part.

[87790] VGAM2602 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2602 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87791] VGAM2602 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2602 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2602 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87792] The complementary binding of VGAM2602 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2602 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2602

host target RNA into VGAM2602 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87793] It is appreciated that VGAM2602 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2602 host target genes. The mRNA of each one of this plurality of VGAM2602 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2602 RNA, herein designated VGAM RNA, and which when bound by VGAM2602 RNA causes inhibition of translation of respective one or more VGAM2602 host target proteins.

[87794] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2602 gene, herein designated VGAM GENE, on one or more VGAM2602 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87795] It is yet further appreciated that a function of VGAM2602 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2602 include diagnosis, prevention and treatment of viral infection by Obuda Pepper Virus. Specific functions, and accordingly utilities, of VGAM2602 correlate with, and may be deduced from, the identity of the host target genes which VGAM2602 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87796] Nucleotide sequences of the VGAM2602 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2602 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2602 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2602 are further

described hereinbelow with reference to Table 1.

[87797] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2602 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2602 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87798] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2602 gene, herein designated VGAM is inhibition of expression of VGAM2602 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2602 correlate with, and may be deduced from, the identity of the target genes which VGAM2602 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87799] Replication Factor C (activator 1) 1, 145kDa (RFC1, Accession NM_002913) is a VGAM2602 host target gene. RFC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RFC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

RFC1 BINDING SITE, designated SEQ ID:8819, to the nucleotide sequence of VGAM2602 RNA, herein designated VGAM RNA, also designated SEQ ID:5313.

[87800] A function of VGAM2602 is therefore inhibition of Replication Factor C (activator 1) 1, 145kDa (RFC1, Accession NM_002913), a gene which plays a role in dna transcription, replication and/or repair. Accordingly, utilities of VGAM2602 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFC1. The function of RFC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.LOC90917 (Accession XM_034861) is another VGAM2602 host target gene. LOC90917 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90917, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90917 BINDING SITE, designated SEQ ID:32172, to the nucleotide sequence of VGAM2602 RNA, herein designated VGAM RNA, also designated SEQ ID:5313.

[87801] Another function of VGAM2602 is therefore inhibition of

LOC90917 (Accession XM_034861). Accordingly, utilities of VGAM2602 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90917. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2603 (VGAM2603) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87802] VGAM2603 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2603 was detected is described hereinabove with reference to Figs. 1-8.

[87803] VGAM2603 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sugarcane Striate Mosaic Associated Virus. VGAM2603 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87804] VGAM2603 gene encodes a VGAM2603 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2603 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2603 precursor RNA is designated SEQ ID:2589, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2589 is located at position 5796 relative to the genome of Sugarcane Striate Mosaic Associated Virus.

[87805] VGAM2603 precursor RNA folds onto itself, forming VGAM2603 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87806] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2603 folded precursor RNA into VGAM2603 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide se-

quence of VGAM2603 RNA is designated SEQ ID:5314, and is provided hereinbelow with reference to the sequence listing part.

[87807] VGAM2603 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2603 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87808] VGAM2603 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2603 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2603 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87809] The complementary binding of VGAM2603 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2603 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2603 host target RNA into VGAM2603 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87810] It is appreciated that VGAM2603 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2603 host target genes. The mRNA of each one of this plurality of VGAM2603 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2603 RNA, herein designated VGAM RNA, and which when bound by VGAM2603 RNA causes inhibition of translation of respective one or more VGAM2603 host target proteins.

[87811] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2603 gene, herein designated VGAM GENE, on one or more VGAM2603 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87812] It is yet further appreciated that a function of VGAM2603

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of viral infection by Sugarcane Striate Mosaic Associated Virus. Specific functions, and accordingly utilities, of VGAM2603 correlate with, and may be deduced from, the identity of the host target genes which VGAM2603 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87813] Nucleotide sequences of the VGAM2603 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2603 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2603 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2603 are further described hereinbelow with reference to Table 1.

[87814] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2603 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2603 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87815] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2603 gene, herein designated VGAM is inhibition of expression of VGAM2603 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2603 correlate with, and may be deduced from, the identity of the target genes which VGAM2603 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87816] Alcohol Dehydrogenase 5 (class III), Chi Polypeptide (ADH5, Accession NM_000671) is a VGAM2603 host target gene. ADH5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADH5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADH5 BINDING SITE, designated SEQ ID:6325, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87817] A function of VGAM2603 is therefore inhibition of Alcohol Dehydrogenase 5 (class III), Chi Polypeptide (ADH5, Accession NM_000671), a gene which oxidizes ethanol and activated by fatty acids.It oxidizes ethanol very poorly. Accordingly, utilities of VGAM2603 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with ADH5. The function of ADH5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM438.Formyl Peptide Receptor-like 1 (FPRL1, Accession NM_001462) is another VGAM2603 host target gene. FPRL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FPRL1 BINDING SITE, designated SEQ ID:7197, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87818] Another function of VGAM2603 is therefore inhibition of Formyl Peptide Receptor-like 1 (FPRL1, Accession NM_001462). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FPRL1. Peptidylprolyl Isomerase F (cyclophilin F) (PPIF, Accession NM_005729) is another VGAM2603 host target gene. PPIF BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by PPIF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPIF BINDING SITE, designated SEQ ID:12285, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87819] Another function of VGAM2603 is therefore inhibition of Peptidylprolyl Isomerase F (cyclophilin F) (PPIF, Accession NM_005729), a gene which catalyzes the cis to trans isomerization of certain proline imidic peptide bonds in oligopeptides. Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPIF. The function of PPIF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM251.Protein Tyrosine Phosphatase Type IVA, Member 2 (PTP4A2, Accession NM_003479) is another VGAM2603 host target gene. PTP4A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTP4A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of PTP4A2 BINDING SITE, designated SEQ ID:9556, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87820] Another function of VGAM2603 is therefore inhibition of Protein Tyrosine Phosphatase Type IVA, Member 2 (PTP4A2, Accession NM_003479), a gene which is a protein tyrosine phosphatase which has a C-terminal prenylation site. Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTP4A2. The function of PTP4A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.KIAA0565 (Accession XM_039912) is another VGAM2603 host target gene. KIAA0565 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0565 BINDING SITE, designated SEQ ID:33223, to the

nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87821] Another function of VGAM2603 is therefore inhibition of KIAA0565 (Accession XM_039912). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0565. NIMA (never in mitosis gene a)-related Kinase 1 (NEK1, Accession XM_171077) is another VGAM2603 host target gene. NEK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NEK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NEK1 BINDING SITE, designated SEQ ID:45885, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87822] Another function of VGAM2603 is therefore inhibition of NIMA (never in mitosis gene a)-related Kinase 1 (NEK1, Accession XM_171077). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEK1. RAB40C, Member RAS Oncogene Family (RAB40C, Acces-

sion NM_021168) is another VGAM2603 host target gene. RAB40C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB40C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB40C BINDING SITE, designated SEQ ID:22148, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87823] Another function of VGAM2603 is therefore inhibition of RAB40C, Member RAS Oncogene Family (RAB40C, Accession NM_021168). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB40C. SH3 Domain Binding Glutamic Acid-rich Protein Like 2 (SH3BGRL2, Accession NM_031469) is another VGAM2603 host target gene. SH3BGRL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3BGRL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3BGRL2 BINDING SITE, designated

SEQ ID:25534, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87824] Another function of VGAM2603 is therefore inhibition of SH3 Domain Binding Glutamic Acid-rich Protein Like 2 (SH3BGRL2, Accession NM_031469). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BGRL2. Syntaxin 12 (STX12, Accession XM_039018) is another VGAM2603 host target gene. STX12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STX12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STX12 BINDING SITE, designated SEQ ID:32985, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87825] Another function of VGAM2603 is therefore inhibition of Syntaxin 12 (STX12, Accession XM_039018). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX12. TRIP-Br2 (Accession NM_014755) is another

VGAM2603 host target gene. TRIP-Br2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP-Br2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:16481, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87826] Another function of VGAM2603 is therefore inhibition of TRIP-Br2 (Accession NM_014755). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP-Br2. LOC256207 (Accession XM_170837) is another VGAM2603 host target gene. LOC256207 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256207, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256207 BINDING SITE, designated SEQ ID:45623, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87827] Another function of VGAM2603 is therefore inhibition of LOC256207 (Accession XM_170837). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256207. LOC92597 (Accession XM_046066) is another VGAM2603 host target gene. LOC92597 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92597, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92597 BINDING SITE, designated SEQ ID:34676, to the nucleotide sequence of VGAM2603 RNA, herein designated VGAM RNA, also designated SEQ ID:5314.

[87828] Another function of VGAM2603 is therefore inhibition of LOC92597 (Accession XM_046066). Accordingly, utilities of VGAM2603 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92597. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2604 (VGAM2604) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[87829] VGAM2604 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2604 was detected is described hereinabove with reference to Figs. 1-8.

[87830] VGAM2604 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sugarcane Striate Mosaic Associated Virus. VGAM2604 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87831] VGAM2604 gene encodes a VGAM2604 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2604 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2604 precursor RNA is designated SEQ ID:2590, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2590 is located at position 3074 relative to the genome of Sugarcane Striate Mosaic Associated Virus.

[87832] VGAM2604 precursor RNA folds onto itself, forming VGAM2604 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87833] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2604 folded precursor RNA into VGAM2604 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2604 RNA is designated SEQ ID:5315, and is provided hereinbelow with reference to the sequence listing part.

[87834] VGAM2604 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2604 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87835] VGAM2604 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2604 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2604 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87836] The complementary binding of VGAM2604 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2604 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2604 host target RNA into VGAM2604 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87837] It is appreciated that VGAM2604 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2604 host target genes. The mRNA of each one of this plurality of VGAM2604 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2604 RNA, herein designated VGAM RNA, and which when bound by VGAM2604 RNA causes inhibition of translation of respective one or more VGAM2604 host target proteins.

[87838] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2604 gene, herein designated VGAM GENE, on one or more VGAM2604 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87839] It is yet further appreciated that a function of VGAM2604 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of viral infection by Sugarcane Striate Mosaic Associated Virus. Specific functions, and accordingly utilities, of VGAM2604 correlate with, and may be deduced from, the identity of the host target genes which VGAM2604 binds and inhibits, and the function of these

host target genes, as elaborated hereinbelow.

[87840] Nucleotide sequences of the VGAM2604 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2604 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2604 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2604 are further described hereinbelow with reference to Table 1.

[87841] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2604 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2604 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87842] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2604 gene, herein designated VGAM is inhibition of expression of VGAM2604 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2604 correlate with, and may be deduced from, the identity of the target genes which VGAM2604 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87843] A Kinase (PRKA) Anchor Protein 1 (AKAP1, Accession NM_003488) is a VGAM2604 host target gene. AKAP1 BINDING SITE1 and AKAP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AKAP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP1 BINDING SITE1 and AKAP1 BINDING SITE2, designated SEQ ID:9582 and SEQ ID:29268 respectively, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87844] A function of VGAM2604 is therefore inhibition of A Kinase (PRKA) Anchor Protein 1 (AKAP1, Accession NM_003488), a gene which binds to type i and ii regulatory subunits of protein kinase a . Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP1. The function of AKAP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1392.Collagen, Type VI, Alpha 3 (COL6A3, Accession NM_057167) is another VGAM2604 host target gene.

COL6A3 BINDING SITE1 and COL6A3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COL6A3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL6A3 BINDING SITE1 and COL6A3 BINDING SITE2, designated SEQ ID:27670 and SEQ ID:10586 respectively, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87845] Another function of VGAM2604 is therefore inhibition of Collagen, Type VI, Alpha 3 (COL6A3, Accession NM_057167). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A3. Cytochrome P450, Subfamily VIIIB (sterol 12-alpha-hydroxylase), Polypeptide 1 (CYP8B1, Accession NM_004391) is another VGAM2604 host target gene. CYP8B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP8B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP8B1 BINDING SITE,

designated SEQ ID:10627, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87846] Another function of VGAM2604 is therefore inhibition of Cytochrome P450, Subfamily VIIIB (sterol 12-alpha-hydroxylase), Polypeptide 1 (CYP8B1, Accession NM_004391), a gene which functions in bile acid biosynthesis. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP8B1. The function of CYP8B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM923.Disrupted In Schizophrenia 1 (DISC1, Accession NM_018662) is another VGAM2604 host target gene. DISC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DISC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE, designated SEQ ID:20739, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ

ID:5315.

[87847] Another function of VGAM2604 is therefore inhibition of Disrupted In Schizophrenia 1 (DISC1, Accession NM_018662), a gene which has globular N-terminal domain(s) and a helical C-terminal domain. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DISC1. The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Espin (ESPN, Accession NM_031475) is another VGAM2604 host target gene. ESPN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESPN BINDING SITE, designated SEQ ID:25550, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87848] Another function of VGAM2604 is therefore inhibition of Espin (ESPN, Accession NM_031475), a gene which a membrane-cytoskeletal assemblages . Accordingly, utili-

ties of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESPN. The function of ESPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1006.Fatty Acid Binding Protein 2, Intestinal (FABP2, Accession NM_000134) is another VGAM2604 host target gene. FABP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FABP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FABP2 BINDING SITE, designated SEQ ID:5627, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87849] Another function of VGAM2604 is therefore inhibition of Fatty Acid Binding Protein 2, Intestinal (FABP2, Accession NM_000134), a gene which may have a role in dietary fat uptake or processing. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FABP2. The function of FABP2 and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM951.Fanconi Anemia, Complementation Group C (FANCC, Accession XM_047190) is another VGAM2604 host target gene. FANCC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FANCC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FANCC BINDING SITE, designated SEQ ID:34908, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87850] Another function of VGAM2604 is therefore inhibition of Fanconi Anemia, Complementation Group C (FANCC, Accession XM_047190). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCC. Fer (fps/fes related) Tyrosine Kinase (phosphoprotein NCP94) (FER, Accession NM_005246) is another VGAM2604 host target gene. FER BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FER, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FER BINDING SITE, designated SEQ ID:11756, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87851] Another function of VGAM2604 is therefore inhibition of Fer (fps/fes related) Tyrosine Kinase (phosphoprotein NCP94) (FER, Accession NM_005246), a gene which Non-receptor protein tyrosine kinase; member of the Src family. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER. The function of FER and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM224.Forkhead Box E3 (FOXE3, Accession NM_012186) is another VGAM2604 host target gene. FOXE3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FOXE3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXE3 BINDING SITE, designated SEQ ID:14473, to the nucleotide sequence of

VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87852] Another function of VGAM2604 is therefore inhibition of Forkhead Box E3 (FOXE3, Accession NM_012186), a gene which regulates embryonic development. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXE3. The function of FOXE3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM632.Inositol 1,4,5-trisphosphate 3-kinase B (ITPKB, Accession NM_002221) is another VGAM2604 host target gene. ITPKB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITPKB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPKB BINDING SITE, designated SEQ ID:7983, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87853] Another function of VGAM2604 is therefore inhibition of Inositol 1,4,5-trisphosphate 3-kinase B (ITPKB, Accession

NM_002221), a gene which is a type B inositol 1,4,5-triphosphate 3 kinase. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPKB. The function of ITPKB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1252.LFG (Accession XM_084780) is another VGAM2604 host target gene. LFG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LFG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LFG BINDING SITE, designated SEQ ID:37699, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87854] Another function of VGAM2604 is therefore inhibition of LFG (Accession XM_084780). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LFG. MHC Class II Transactivator (MHC2TA, Accession NM_000246) is another VGAM2604 host target gene.

MHC2TA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MHC2TA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE, designated SEQ ID:5785, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87855] Another function of VGAM2604 is therefore inhibition of MHC Class II Transactivator (MHC2TA, Accession NM_000246). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA. Nebulin-related Anchoring Protein (Nrap, Accession NM_139235) is another VGAM2604 host target gene. Nrap BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Nrap, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Nrap BINDING SITE, designated SEQ ID:29238, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA,

also designated SEQ ID:5315.

[87856] Another function of VGAM2604 is therefore inhibition of Nebulin-related Anchoring Protein (Nrap, Accession NM_139235), a gene which performs an anchoring function to link the terminal actin filaments of myofibrils to protein complexes located beneath the sarcolemma. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nrap. The function of Nrap and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM649.Parathyroid Hormone Receptor 2 (PTHR2, Accession NM_005048) is another VGAM2604 host target gene. PTHR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTHR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTHR2 BINDING SITE, designated SEQ ID:11482, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87857] Another function of VGAM2604 is therefore inhibition of

Parathyroid Hormone Receptor 2 (PTHR2, Accession NM_005048), a gene which is a G protein-coupled receptor selective for parathyroid hormone binding. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTHR2. The function of PTHR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM607.Protein Tyrosine Phosphatase, Receptor Type, O (PTPRO, Accession NM_030668) is another VGAM2604 host target gene. PTPRO BINDING SITE1 through PTPRO BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPRO, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRO BINDING SITE1 through PTPRO BINDING SITE3, designated SEQ ID:25015, SEQ ID:25024 and SEQ ID:25035 respectively, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87858] Another function of VGAM2604 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, O (PTPRO,

Accession NM_030668), a gene which may function as a cell contact receptor that mediates and controls cell-cell signals. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRO. The function of PTPRO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM140.Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155) is another VGAM2604 host target gene. SERPINB9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINB9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE, designated SEQ ID:10369, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87859] Another function of VGAM2604 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155), a gene which may be a serpin serine pro-

tease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB9. The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM60.Src-like-adaptor 2 (SLA2, Accession NM_032214) is another VGAM2604 host target gene. SLA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:25944, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87860] Another function of VGAM2604 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NM_032214). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2. Solute Carrier Family 22 (organic cation transporter), Member 2 (SLC22A2, Accession

XM_004235) is another VGAM2604 host target gene. SLC22A2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC22A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A2 BINDING SITE, designated SEQ ID:29942, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87861] Another function of VGAM2604 is therefore inhibition of Solute Carrier Family 22 (organic cation transporter), Member 2 (SLC22A2, Accession XM_004235), a gene which is an organic cation transporter that may mediate first step in cation resorption. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC22A2. The function of SLC22A2 has been established by previous studies. Polyspecific organic cation transporters in the liver, kidney, and intestine are critical for elimination of many endogenous amines as well as a wide array of drugs and environmental toxins. Using PCR with primers derived from rat OCT1 (OMIM Ref. No. 602607),

Gorboulev et al. (1997) cloned the human organic cation transporters OCT1 and OCT2 from human kidney cortex cDNA. The predicted 555-amino acid OCT2 protein has 12 putative transmembrane domains and is 70% identical to human OCT1 protein. On Northern blots, OCT2 was expressed as 2.5- and 4.0-kb mRNAs mainly in kidney, although RT-PCR detected OCT2 expression in a few other tissues. Using in situ hybridization and immunohistochemistry, Gorboulev et al. (1997) found that OCT2 is localized at the luminal membrane of the kidney distal tubule. Xenopus oocytes expressing OCT2 showed increased cation uptake. A bidirectional silencer for a 400-kb region that contains 3 imprinted, maternally expressed protein-coding genes (IGF2R, 147280; SLC22A2; SLC22A3) has been shown by targeted deletion to be located in a sequence of 3.7 kb, which also contains the promoter for the imprinted, paternally expressed noncoding Air RNA. Expression of Air is correlated with repression of all 3 genes on the paternal allele; however, Air RNA overlaps just 1 of these genes in an antisense orientation. By inserting a polyadenylation signal that truncates 96% of the RNA transcript, Sleutels et al. (2002) demonstrated that Air RNA is required for silencing. The trun-

cated Air allele maintains imprinted expression and methylation of the Air promoter, but shows complete loss of silencing of the IGF2R/SLC22A2/SLC22A3 gene cluster on the paternal chromosome. Sleutels et al. (2002) concluded that noncoding RNAs have an active role in genomic imprinting

[87862] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[87863] Gorboulev, V.; Ulzheimer, J. C.; Akhoundova, A.; Ulzheimer-Teuber, I.; Karbach, U.; Quester, S.; Baumann, C.; Lang, F.; Busch, A. E.; Koepsell, H. : Cloning and characterization of two human polyspecific organic cation transporters. DNA Cell Biol. 16: 871-881, 1997. ; and

[87864] Sleutels, F.; Zwart, R.; Barlow, D. P. : The non-coding Air RNA is required for silencing autosomal imprinted genes. Nature 415: 810-813, 2002.

[87865] Further studies establishing the function and utilities of SLC22A2 are found in John Hopkins OMIM database record ID 602608, and in sited publications numbered 1114, 1116, 111 and 5233 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Solute Carrier Family 7 (cationic amino acid

transporter, y+ system), Member 8 (SLC7A8, Accession NM_012244) is another VGAM2604 host target gene. SLC7A8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC7A8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC7A8 BINDING SITE, designated SEQ ID:14553, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87866] Another function of VGAM2604 is therefore inhibition of Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 8 (SLC7A8, Accession NM_012244), a gene which helps mediate transport of large and small neutral amino acids. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A8. The function of SLC7A8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1263.SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A, Member 2

(SMARCA2, Accession NM_003070) is another VGAM2604 host target gene. SMARCA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMARCA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMARCA2 BINDING SITE, designated SEQ ID:9035, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87867] Another function of VGAM2604 is therefore inhibition of SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A, Member 2 (SMARCA2, Accession NM_003070), a gene which is involved in chromatin assembly and remodeling. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCA2. The function of SMARCA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.Transient Receptor Potential Cation Channel, Subfamily V, Member 1 (TRPV1, Accession NM_018727) is another VGAM2604 host target

gene. TRPV1 BINDING SITE1 through TRPV1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TRPV1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 through TRPV1 BINDING SITE4, designated SEQ ID:20816, SEQ ID:27996, SEQ ID:28004 and SEQ ID:28013 respectively, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87868] Another function of VGAM2604 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily V, Member 1 (TRPV1, Accession NM_018727), a gene which functions as a receptor for capsaicin. Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1. The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM146.Wingless-type MMTV Integration Site Family, Member 5B (WNT5B, Accession NM_030775) is another VGAM2604 host target gene. WNT5B BINDING

SITE1 and WNT5B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WNT5B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT5B BINDING SITE1 and WNT5B BINDING SITE2, designated SEQ ID:25060 and SEQ ID:26362 respectively, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87869] Another function of VGAM2604 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 5B (WNT5B, Accession NM_030775), a gene which is the ligand for members of the frizzled family of seven transmembrane receptors and may be a signaling molecule . Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT5B. The function of WNT5B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1928.Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769) is another VGAM2604

host target gene. C11orf11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf11 BINDING SITE, designated SEQ ID:44790, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87870] Another function of VGAM2604 is therefore inhibition of Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf11. C2F (Accession NM_006331) is another VGAM2604 host target gene. C2F BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C2F, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C2F BINDING SITE, designated SEQ ID:13030, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87871] Another function of VGAM2604 is therefore inhibition of C2F (Accession NM_006331). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C2F. Cab45 (Accession NM_016176) is another VGAM2604 host target gene. Cab45 BINDING SITE1 and Cab45 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by Cab45, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Cab45 BINDING SITE1 and Cab45 BINDING SITE2, designated SEQ ID:18278 and SEQ ID:18621 respectively, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87872] Another function of VGAM2604 is therefore inhibition of Cab45 (Accession NM_016176). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Cab45. DKFZP434B205 (Accession XM_059966) is another VGAM2604 host target gene. DKFZP434B205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434B205,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434B205 BINDING SITE, designated SEQ ID:37128, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87873] Another function of VGAM2604 is therefore inhibition of DKFZP434B205 (Accession XM_059966). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B205. DKFZP434C128 (Accession XM_036086) is another VGAM2604 host target gene. DKFZP434C128 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C128, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434C128 BINDING SITE, designated SEQ ID:32375, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87874] Another function of VGAM2604 is therefore inhibition of

DKFZP434C128 (Accession XM_036086). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C128. Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259) is another VGAM2604 host target gene. DOCK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DOCK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DOCK3 BINDING SITE, designated SEQ ID:33036, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87875] Another function of VGAM2604 is therefore inhibition of Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DOCK3. EDR2 (Accession XM_018136) is another VGAM2604 host target gene. EDR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EDR2, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EDR2 BINDING SITE, designated SEQ ID:30338, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87876] Another function of VGAM2604 is therefore inhibition of EDR2 (Accession XM_018136). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDR2. FLJ10743 (Accession NM_018201) is another VGAM2604 host target gene. FLJ10743 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10743, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10743 BINDING SITE, designated SEQ ID:20082, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87877] Another function of VGAM2604 is therefore inhibition of FLJ10743 (Accession NM_018201). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ10743. FLJ13197 (Accession NM_024614) is another VGAM2604 host target gene. FLJ13197 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13197, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13197 BINDING SITE, designated SEQ ID:23873, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87878] Another function of VGAM2604 is therefore inhibition of FLJ13197 (Accession NM_024614). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13197. FLJ22659 (Accession NM_024934) is another VGAM2604 host target gene. FLJ22659 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22659, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22659 BINDING SITE, designated SEQ ID:24471, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM

RNA, also designated SEQ ID:5315.

[87879] Another function of VGAM2604 is therefore inhibition of FLJ22659 (Accession NM_024934). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22659. FLJ22814 (Accession NM_024916) is another VGAM2604 host target gene. FLJ22814 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22814, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22814 BINDING SITE, designated SEQ ID:24444, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87880] Another function of VGAM2604 is therefore inhibition of FLJ22814 (Accession NM_024916). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22814. HERV-H LTR-associating 2 (HHLA2, Accession NM_007072) is another VGAM2604 host target gene. HHLA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

HHLA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HHLA2 BINDING SITE, designated SEQ ID:13939, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87881] Another function of VGAM2604 is therefore inhibition of HERV-H LTR-associating 2 (HHLA2, Accession NM_007072). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HHLA2. HSNOV1 (Accession NM_017515) is another VGAM2604 host target gene. HSNOV1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSNOV1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSNOV1 BINDING SITE, designated SEQ ID:18968, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87882] Another function of VGAM2604 is therefore inhibition of

HSNOV1 (Accession NM_017515). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSNOV1. KIAA0252 (Accession XM_031646) is another VGAM2604 host target gene. KIAA0252 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0252, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0252 BINDING SITE, designated SEQ ID:31452, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87883] Another function of VGAM2604 is therefore inhibition of KIAA0252 (Accession XM_031646). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0252. KIAA0416 (Accession NM_015564) is another VGAM2604 host target gene. KIAA0416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0416 BINDING SITE, designated SEQ ID:17835, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87884] Another function of VGAM2604 is therefore inhibition of KIAA0416 (Accession NM_015564). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0416. KIAA0420 (Accession XM_032693) is another VGAM2604 host target gene. KIAA0420 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0420, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0420 BINDING SITE, designated SEQ ID:31731, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87885] Another function of VGAM2604 is therefore inhibition of KIAA0420 (Accession XM_032693). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0420. KIAA0435 (Accession NM_014801) is another

VGAM2604 host target gene. KIAA0435 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0435 BINDING SITE, designated SEQ ID:16725, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87886] Another function of VGAM2604 is therefore inhibition of KIAA0435 (Accession NM_014801). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0435. KIAA0841 (Accession XM_049237) is another VGAM2604 host target gene. KIAA0841 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE, designated SEQ ID:35364, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87887] Another function of VGAM2604 is therefore inhibition of KIAA0841 (Accession XM_049237). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841. KIAA0847 (Accession XM_085298) is another VGAM2604 host target gene. KIAA0847 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0847, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0847 BINDING SITE, designated SEQ ID:38048, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87888] Another function of VGAM2604 is therefore inhibition of KIAA0847 (Accession XM_085298). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0847. KIAA1069 (Accession XM_042635) is another VGAM2604 host target gene. KIAA1069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1069, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1069 BINDING SITE, designated SEQ ID:33725, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87889] Another function of VGAM2604 is therefore inhibition of KIAA1069 (Accession XM_042635). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1069. KIAA1157 (Accession XM_051093) is another VGAM2604 host target gene. KIAA1157 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1157, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1157 BINDING SITE, designated SEQ ID:35755, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87890] Another function of VGAM2604 is therefore inhibition of KIAA1157 (Accession XM_051093). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1157. KIAA1755 (Accession XM_028810) is another VGAM2604 host target gene. KIAA1755 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1755, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1755 BINDING SITE, designated SEQ ID:30754, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87891] Another function of VGAM2604 is therefore inhibition of KIAA1755 (Accession XM_028810). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1755. MEF-2 (Accession XM_034883) is another VGAM2604 host target gene. MEF-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEF-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEF-2 BINDING SITE, designated SEQ ID:32181, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5315.

[87892] Another function of VGAM2604 is therefore inhibition of MEF-2 (Accession XM_034883). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEF-2. MGC13053 (Accession NM_032710) is another VGAM2604 host target gene. MGC13053 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC13053, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13053 BINDING SITE, designated SEQ ID:26425, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87893] Another function of VGAM2604 is therefore inhibition of MGC13053 (Accession NM_032710). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13053. MGC9912 (Accession NM_080664) is another VGAM2604 host target gene. MGC9912 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC9912, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC9912 BINDING SITE, designated SEQ ID:27953, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87894] Another function of VGAM2604 is therefore inhibition of MGC9912 (Accession NM_080664). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9912. Nuclear Factor of Activated T-cells 5, Tonicity-responsive (NFAT5, Accession NM_138714) is another VGAM2604 host target gene. NFAT5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NFAT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFAT5 BINDING SITE, designated SEQ ID:28956, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87895] Another function of VGAM2604 is therefore inhibition of Nuclear Factor of Activated T-cells 5, Tonicity-responsive

(NFAT5, Accession NM_138714). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFAT5. Phosphodiesterase 2A, CGMP-stimulated (PDE2A, Accession NM_002599) is another VGAM2604 host target gene. PDE2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE2A BINDING SITE, designated SEQ ID:8461, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87896] Another function of VGAM2604 is therefore inhibition of Phosphodiesterase 2A, CGMP-stimulated (PDE2A, Accession NM_002599). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE2A. Retinoic Acid Induced 17 (RAI17, Accession XM_166091) is another VGAM2604 host target gene. RAI17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAI17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:43865, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87897] Another function of VGAM2604 is therefore inhibition of Retinoic Acid Induced 17 (RAI17, Accession XM_166091). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17. RBT1 (Accession NM_013368) is another VGAM2604 host target gene. RBT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBT1 BINDING SITE, designated SEQ ID:15014, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87898] Another function of VGAM2604 is therefore inhibition of RBT1 (Accession NM_013368). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBT1.

Small EDRK-rich Factor 2 (SERF2, Accession NM_005770) is another VGAM2604 host target gene. SERF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SERF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERF2 BINDING SITE, designated SEQ ID:12341, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87899] Another function of VGAM2604 is therefore inhibition of Small EDRK-rich Factor 2 (SERF2, Accession NM_005770). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF2. SS-56 (Accession XM_006063) is another VGAM2604 host target gene. SS-56 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS-56, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS-56 BINDING SITE, designated SEQ ID:29986, to the nucleotide sequence of VGAM2604 RNA,

herein designated VGAM RNA, also designated SEQ ID:5315.

[87900] Another function of VGAM2604 is therefore inhibition of SS-56 (Accession XM_006063). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SS-56. Tetratricopeptide Repeat Domain 4 (TTC4, Accession XM_038926) is another VGAM2604 host target gene. TTC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TTC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTC4 BINDING SITE, designated SEQ ID:32959, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87901] Another function of VGAM2604 is therefore inhibition of Tetratricopeptide Repeat Domain 4 (TTC4, Accession XM_038926). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTC4. LOC113763 (Accession NM_138434) is another VGAM2604 host target gene. LOC113763 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by LOC113763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113763 BINDING SITE, designated SEQ ID:28805, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87902] Another function of VGAM2604 is therefore inhibition of LOC113763 (Accession NM_138434). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113763. LOC124221 (Accession XM_058785) is another VGAM2604 host target gene. LOC124221 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC124221, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124221 BINDING SITE, designated SEQ ID:36743, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87903] Another function of VGAM2604 is therefore inhibition of

LOC124221 (Accession XM_058785). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124221. LOC138199 (Accession XM_059950) is another VGAM2604 host target gene. LOC138199 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC138199, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138199 BINDING SITE, designated SEQ ID:37118, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87904] Another function of VGAM2604 is therefore inhibition of LOC138199 (Accession XM_059950). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138199. LOC150113 (Accession XM_104532) is another VGAM2604 host target gene. LOC150113 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150113, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC150113 BINDING SITE, designated SEQ ID:42169, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87905] Another function of VGAM2604 is therefore inhibition of LOC150113 (Accession XM_104532). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150113. LOC152315 (Accession XM_087440) is another VGAM2604 host target gene. LOC152315 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152315, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152315 BINDING SITE, designated SEQ ID:39257, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87906] Another function of VGAM2604 is therefore inhibition of LOC152315 (Accession XM_087440). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152315. LOC152328 (Accession XM_087420) is an-

other VGAM2604 host target gene. LOC152328 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152328, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152328 BINDING SITE, designated SEQ ID:39243, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87907] Another function of VGAM2604 is therefore inhibition of LOC152328 (Accession XM_087420). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152328. LOC158527 (Accession XM_088594) is another VGAM2604 host target gene. LOC158527 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158527 BINDING SITE, designated SEQ ID:39860, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87908] Another function of VGAM2604 is therefore inhibition of LOC158527 (Accession XM_088594). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158527. LOC196500 (Accession XM_113734) is another VGAM2604 host target gene. LOC196500 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196500, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196500 BINDING SITE, designated SEQ ID:42387, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87909] Another function of VGAM2604 is therefore inhibition of LOC196500 (Accession XM_113734). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196500. LOC196759 (Accession XM_113601) is another VGAM2604 host target gene. LOC196759 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196759, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196759 BINDING SITE, designated SEQ ID:42295, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87910] Another function of VGAM2604 is therefore inhibition of LOC196759 (Accession XM_113601). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196759. LOC200205 (Accession XM_114152) is another VGAM2604 host target gene. LOC200205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200205 BINDING SITE, designated SEQ ID:42738, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87911] Another function of VGAM2604 is therefore inhibition of LOC200205 (Accession XM_114152). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC200205. LOC221463 (Accession XM_166374) is another VGAM2604 host target gene. LOC221463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221463 BINDING SITE, designated SEQ ID:44205, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87912] Another function of VGAM2604 is therefore inhibition of LOC221463 (Accession XM_166374). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221463. LOC221922 (Accession XM_166555) is another VGAM2604 host target gene. LOC221922 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221922, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221922 BINDING SITE, designated SEQ ID:44536, to the nucleotide sequence of VGAM2604 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5315.

[87913] Another function of VGAM2604 is therefore inhibition of LOC221922 (Accession XM_166555). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221922. LOC254082 (Accession XM_173165) is another VGAM2604 host target gene. LOC254082 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254082 BINDING SITE, designated SEQ ID:46423, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87914] Another function of VGAM2604 is therefore inhibition of LOC254082 (Accession XM_173165). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254082. LOC257354 (Accession XM_170810) is another VGAM2604 host target gene. LOC257354 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257354, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257354 BINDING SITE, designated SEQ ID:45584, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87915] Another function of VGAM2604 is therefore inhibition of LOC257354 (Accession XM_170810). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257354. LOC257612 (Accession XM_175270) is another VGAM2604 host target gene. LOC257612 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257612, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257612 BINDING SITE, designated SEQ ID:46741, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87916] Another function of VGAM2604 is therefore inhibition of LOC257612 (Accession XM_175270). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC257612. LOC51696 (Accession NM_016217) is another VGAM2604 host target gene. LOC51696 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51696, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51696 BINDING SITE, designated SEQ ID:18314, to the nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87917] Another function of VGAM2604 is therefore inhibition of LOC51696 (Accession NM_016217). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51696. LOC91694 (Accession XM_040082) is another VGAM2604 host target gene. LOC91694 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91694, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91694 BINDING SITE, designated SEQ ID:33250, to the

nucleotide sequence of VGAM2604 RNA, herein designated VGAM RNA, also designated SEQ ID:5315.

[87918] Another function of VGAM2604 is therefore inhibition of LOC91694 (Accession XM_040082). Accordingly, utilities of VGAM2604 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91694. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2605 (VGAM2605) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87919] VGAM2605 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2605 was detected is described hereinabove with reference to Figs. 1-8.

[87920] VGAM2605 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Salmon Pancreas Disease Virus. VGAM2605 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87921] VGAM2605 gene encodes a VGAM2605 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2605 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2605 precursor RNA is designated SEQ ID:2591, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2591 is located at position 9457 relative to the genome of Salmon Pancreas Disease Virus.

[87922] VGAM2605 precursor RNA folds onto itself, forming VGAM2605 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87923] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2605 folded precursor RNA into VGAM2605 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2605 RNA is designated SEQ ID:5316, and is provided hereinbelow with reference to the sequence listing part.

[87924] VGAM2605 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2605 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87925] VGAM2605 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2605 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2605 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87926] The complementary binding of VGAM2605 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2605 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2605 host target RNA into VGAM2605 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87927] It is appreciated that VGAM2605 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2605 host target genes. The mRNA of each one of this plurality of VGAM2605 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2605 RNA, herein designated VGAM RNA, and which when bound by VGAM2605 RNA causes inhibition of translation of respective one or more VGAM2605 host target proteins.

[87928] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2605 gene, herein designated VGAM GENE, on one or more VGAM2605 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87929] It is yet further appreciated that a function of VGAM2605 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2605 include diagnosis, prevention and treatment of viral infection by Salmon Pancreas Disease Virus. Specific functions, and accordingly utilities, of VGAM2605 correlate with, and may be deduced from, the identity of the host target genes which VGAM2605 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87930] Nucleotide sequences of the VGAM2605 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2605 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2605 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2605 are further described hereinbelow with reference to Table 1.

[87931] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2605 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2605 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87932] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2605 gene, herein designated VGAM is inhibition of expression of VGAM2605 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2605 correlate with, and may be deduced from, the identity of the target genes which VGAM2605 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87933] FLJ11850 (Accession NM_022741) is a VGAM2605 host target gene. FLJ11850 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11850, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11850 BINDING SITE, designated SEQ ID:22951, to the nucleotide sequence of VGAM2605 RNA, herein designated VGAM RNA, also designated SEQ ID:5316.

[87934] A function of VGAM2605 is therefore inhibition of FLJ11850 (Accession NM_022741). Accordingly, utilities of

VGAM2605 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11850. RAP2B, Member of RAS Oncogene Family (RAP2B, Accession XM_171061) is another VGAM2605 host target gene. RAP2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAP2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP2B BINDING SITE, designated SEQ ID:45860, to the nucleotide sequence of VGAM2605 RNA, herein designated VGAM RNA, also designated SEQ ID:5316.

[87935] Another function of VGAM2605 is therefore inhibition of RAP2B, Member of RAS Oncogene Family (RAP2B, Accession XM_171061). Accordingly, utilities of VGAM2605 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP2B. LOC121274 (Accession XM_058547) is another VGAM2605 host target gene. LOC121274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC121274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121274 BINDING SITE, designated SEQ ID:36657, to the nucleotide sequence of VGAM2605 RNA, herein designated VGAM RNA, also designated SEQ ID:5316.

[87936] Another function of VGAM2605 is therefore inhibition of LOC121274 (Accession XM_058547). Accordingly, utilities of VGAM2605 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121274. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2606 (VGAM2606) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87937] VGAM2606 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2606 was detected is described hereinabove with reference to Figs. 1-8.

[87938] VGAM2606 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Salmon Pancreas Disease Virus. VGAM2606 host target gene, herein desig-

nated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87939] VGAM2606 gene encodes a VGAM2606 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2606 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2606 precursor RNA is designated SEQ ID:2592, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2592 is located at position 11312 relative to the genome of Salmon Pancreas Disease Virus.

[87940] VGAM2606 precursor RNA folds onto itself, forming VGAM2606 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87941] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2606 folded precursor RNA into VGAM2606

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2606 RNA is designated SEQ ID:5317, and is provided hereinbelow with reference to the sequence listing part.

[87942] VGAM2606 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2606 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87943] VGAM2606 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2606 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2606 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87944] The complementary binding of VGAM2606 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2606 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2606 host target RNA into VGAM2606 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[87945] It is appreciated that VGAM2606 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2606 host target genes. The mRNA of each one of this plurality of VGAM2606 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2606 RNA, herein designated VGAM RNA, and which when bound by VGAM2606 RNA causes inhibition of translation of respective one or more VGAM2606 host target proteins.

[87946] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2606 gene, herein designated VGAM GENE, on one or more VGAM2606 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87947] It is yet further appreciated that a function of VGAM2606 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2606 include diagnosis, prevention and treatment of viral infection by Salmon Pancreas Disease Virus. Specific functions, and accordingly utilities, of VGAM2606 correlate with, and may be deduced from, the identity of the host target genes which VGAM2606 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87948] Nucleotide sequences of the VGAM2606 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2606 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2606 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2606 are further described hereinbelow with reference to Table 1.

[87949] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2606 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2606 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87950] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2606 gene, herein designated VGAM is inhibition of expression of VGAM2606 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2606 correlate with, and may be deduced from, the identity of the target genes which VGAM2606 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87951] Grancalcin, EF-hand Calcium Binding Protein (GCA, Accession NM_012198) is a VGAM2606 host target gene. GCA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GCA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GCA BINDING SITE, designated SEQ ID:14497, to the nucleotide sequence of VGAM2606 RNA, herein designated

VGAM RNA, also designated SEQ ID:5317.

[87952] A function of VGAM2606 is therefore inhibition of Grancalcin, EF-hand Calcium Binding Protein (GCA, Accession NM_012198), a gene which may play a role in granule-membrane fusion and degranulation. Accordingly, utilities of VGAM2606 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GCA. The function of GCA has been established by previous studies. By probing with antibody to the purified protein, Boyhan et al. (1992) cloned GCA, which they called grancalcin, from a promyocytic cell line expression library. The deduced 217-amino acid protein has a calculated molecular mass of 24 kD. The sequence contains an EF-hand calcium-binding region, a potential phosphorylation site, and 2 potential N-glycosylation sites. GCA shares 58% identity over 192 amino acids with sorcin (OMIM Ref. No. 182520), and about 30% identity over the calcium-binding domains of calpains (see OMIM Ref. No. 114220). Northern blot analysis revealed abundant expression of a 1.65-kb transcript in bone marrow and weaker expression in neutrophils, myeloid leukemic cells, and 2 Epstein-Barr virus-transformed B-cell lines. By Western blot analysis, a 28-kD protein was observed in B

and T cells at low concentrations, and at higher levels in neutrophils and macrophages. Subcellular fractionation showed localization to be dependent upon Ca(2+) and Mg(2+). In the absence of divalent cation, grancalcin localized to the cytosolic fraction; with Mg(2+) alone, it partitioned with the granule fraction; and in the presence of Mg(2+) and Ca(2+), it associated with both the granule and membrane fractions. Teahan et al. (1992) purified grancalcin from leukopheresis samples of patients with chronic granulocytic leukemia. The purified protein migrated as a 28-kD protein by SDS-PAGE and formed homodimers of 55 kD upon gel filtration that was independent of reducing agents. No biochemical evidence was found for phosphorylation or glycosylation. Calcium binding was suggested by the difference in migration on SDS/PAGE between calcium-loaded and calcium-depleted preparations, and was confirmed by the binding of Ca(2+) to slot blots of the native protein.

[87953] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[87954] Boyhan, A.; Casimir, C. M.; French, J. K.; Teahan, C. G.; Segal, A. W. : Molecular cloning and characterization of

grancalcin, a novel EF-hand calcium-binding protein abundant in neutrophils and monocytes. J. Biol. Chem. 267: 2928-2933, 1992. ; and

[87955] Teahan, C. G.; Totty, N. F.; Segal, A. W. : Isolation and characterization of grancalcin, a novel 28 kDa EF-hand calcium-binding protein from human neutrophils. Biochem. J. 286: 549-554.

[87956] Further studies establishing the function and utilities of GCA are found in John Hopkins OMIM database record ID 607030, and in sited publications numbered 5384-5385 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.MADS Box Transcription Enhancer Factor 2, Polypeptide C (myocyte enhancer factor 2C) (MEF2C, Accession NM_002397) is another VGAM2606 host target gene. MEF2C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEF2C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEF2C BINDING SITE, designated SEQ ID:8215, to the nucleotide sequence of VGAM2606 RNA, herein designated VGAM RNA, also designated SEQ ID:5317.

[87957] Another function of VGAM2606 is therefore inhibition of MADS Box Transcription Enhancer Factor 2, Polypeptide C (myocyte enhancer factor 2C) (MEF2C, Accession NM_002397), a gene which regulates muscle-specific and mitogen-inducible genes. Accordingly, utilities of VGAM2606 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEF2C. The function of MEF2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM386.Cab45 (Accession NM_016176) is another VGAM2606 host target gene. Cab45 BINDING SITE1 and Cab45 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by Cab45, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Cab45 BINDING SITE1 and Cab45 BINDING SITE2, designated SEQ ID:18279 and SEQ ID:18622 respectively, to the nucleotide sequence of VGAM2606 RNA, herein designated VGAM RNA, also designated SEQ ID:5317.

[87958] Another function of VGAM2606 is therefore inhibition of

Cab45 (Accession NM_016176). Accordingly, utilities of VGAM2606 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Cab45. Mitochondrial Ribosomal Protein L35 (MRPL35, Accession NM_016622) is another VGAM2606 host target gene. MRPL35 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL35, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL35 BINDING SITE, designated SEQ ID:18739, to the nucleotide sequence of VGAM2606 RNA, herein designated VGAM RNA, also designated SEQ ID:5317.

[87959] Another function of VGAM2606 is therefore inhibition of Mitochondrial Ribosomal Protein L35 (MRPL35, Accession NM_016622). Accordingly, utilities of VGAM2606 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL35. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2607 (VGAM2607) viral gene, which modulates expression of

respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87960] VGAM2607 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2607 was detected is described hereinabove with reference to Figs. 1-8.

[87961] VGAM2607 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ljungan Virus. VGAM2607 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87962] VGAM2607 gene encodes a VGAM2607 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2607 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2607 precursor RNA is designated SEQ ID:2593, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2593 is located at position 7425 relative to the genome of Ljungan Virus.

[87963] VGAM2607 precursor RNA folds onto itself, forming VGAM2607 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87964] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2607 folded precursor RNA into VGAM2607 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2607 RNA is designated SEQ ID:5318, and is provided hereinbelow with reference to the sequence listing part.

[87965] VGAM2607 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2607 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87966] VGAM2607 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2607 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2607 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87967] The complementary binding of VGAM2607 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2607 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2607 host target RNA into VGAM2607 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87968] It is appreciated that VGAM2607 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2607 host target genes. The mRNA of each one of this plurality of VGAM2607 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2607 RNA, herein designated VGAM RNA, and which when bound by VGAM2607 RNA causes inhibition of translation of respective one or more VGAM2607 host target proteins.

[87969] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2607 gene, herein designated VGAM GENE, on one or more VGAM2607 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87970] It is yet further appreciated that a function of VGAM2607 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of viral infection by Ljungan Virus. Specific functions, and accordingly utilities, of VGAM2607 correlate with, and may be deduced from, the identity of the host target genes which VGAM2607 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[87971] Nucleotide sequences of the VGAM2607 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2607 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2607 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2607 are further described hereinbelow with reference to Table 1.

[87972] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2607 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2607 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87973] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2607 gene, herein designated VGAM is inhibition of expression of VGAM2607 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2607 correlate with, and may be deduced from, the identity of the target genes which VGAM2607 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87974] BTB (POZ) Domain Containing 1 (BTBD1, Accession NM_025238) is a VGAM2607 host target gene. BTBD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTBD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTBD1 BINDING SITE, designated SEQ ID:24921, to the nucleotide sequence of VGAM2607 RNA, herein designated VGAM RNA, also designated SEQ ID:5318.

[87975] A function of VGAM2607 is therefore inhibition of BTB (POZ) Domain Containing 1 (BTBD1, Accession NM_025238). Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTBD1. DKFZP586N0721 (Accession NM_015400) is another VGAM2607 host target gene. DKFZP586N0721 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586N0721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586N0721 BINDING SITE, designated SEQ ID:17711, to the nucleotide

sequence of VGAM2607 RNA, herein designated VGAM RNA, also designated SEQ ID:5318.

[87976] Another function of VGAM2607 is therefore inhibition of DKFZP586N0721 (Accession NM_015400). Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586N0721. MGC2752 (Accession XM_085842) is another VGAM2607 host target gene. MGC2752 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC2752, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2752 BINDING SITE, designated SEQ ID:38367, to the nucleotide sequence of VGAM2607 RNA, herein designated VGAM RNA, also designated SEQ ID:5318.

[87977] Another function of VGAM2607 is therefore inhibition of MGC2752 (Accession XM_085842). Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2752. LOC146953 (Accession XM_085659) is another VGAM2607 host target gene. LOC146953 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC146953, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146953 BINDING SITE, designated SEQ ID:38285, to the nucleotide sequence of VGAM2607 RNA, herein designated VGAM RNA, also designated SEQ ID:5318.

[87978] Another function of VGAM2607 is therefore inhibition of LOC146953 (Accession XM_085659). Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146953. LOC151647 (Accession XM_087261) is another VGAM2607 host target gene. LOC151647 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151647, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151647 BINDING SITE, designated SEQ ID:39154, to the nucleotide sequence of VGAM2607 RNA, herein designated VGAM RNA, also designated SEQ ID:5318.

[87979] Another function of VGAM2607 is therefore inhibition of LOC151647 (Accession XM_087261). Accordingly, utilities

of VGAM2607 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151647. LOC152453 (Accession XM_087475) is another VGAM2607 host target gene. LOC152453 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152453, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152453 BINDING SITE, designated SEQ ID:39275, to the nucleotide sequence of VGAM2607 RNA, herein designated VGAM RNA, also designated SEQ ID:5318.

[87980] Another function of VGAM2607 is therefore inhibition of LOC152453 (Accession XM_087475). Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152453. LOC254431 (Accession XM_173024) is another VGAM2607 host target gene. LOC254431 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254431, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC254431 BINDING SITE, designated SEQ ID:46291, to the nucleotide sequence of VGAM2607 RNA, herein designated VGAM RNA, also designated SEQ ID:5318.

[87981] Another function of VGAM2607 is therefore inhibition of LOC254431 (Accession XM_173024). Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254431. LOC254778 (Accession XM_171193) is another VGAM2607 host target gene. LOC254778 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254778, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254778 BINDING SITE, designated SEQ ID:45978, to the nucleotide sequence of VGAM2607 RNA, herein designated VGAM RNA, also designated SEQ ID:5318.

[87982] Another function of VGAM2607 is therefore inhibition of LOC254778 (Accession XM_171193). Accordingly, utilities of VGAM2607 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254778. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2608 (VGAM2608) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[87983] VGAM2608 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2608 was detected is described hereinabove with reference to Figs. 1-8.

[87984] VGAM2608 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ljungan Virus. VGAM2608 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[87985] VGAM2608 gene encodes a VGAM2608 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2608 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2608 precursor RNA is designated SEQ ID:2594, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2594 is located at position 6824 relative to the

genome of Ljungan Virus.

[87986] VGAM2608 precursor RNA folds onto itself, forming VGAM2608 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[87987] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2608 folded precursor RNA into VGAM2608 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of VGAM2608 RNA is designated SEQ ID:5319, and is provided hereinbelow with reference to the sequence listing part.

[87988] VGAM2608 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2608 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[87989] VGAM2608 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2608 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2608 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[87990] The complementary binding of VGAM2608 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2608 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2608 host target RNA into VGAM2608 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[87991] It is appreciated that VGAM2608 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2608 host target genes. The mRNA of each one of this plurality of VGAM2608 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2608 RNA, herein designated VGAM RNA, and which when bound by VGAM2608 RNA causes inhibition of translation of respective one or more VGAM2608 host target proteins.

[87992] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2608 gene, herein designated VGAM GENE, on one or more VGAM2608 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[87993] It is yet further appreciated that a function of VGAM2608 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2608 include diagnosis, prevention and treatment of viral infection by Ljungan Virus. Specific functions, and accordingly utilities, of VGAM2608 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2608 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[87994] Nucleotide sequences of the VGAM2608 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2608 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2608 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2608 are further described hereinbelow with reference to Table 1.

[87995] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2608 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2608 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[87996] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2608 gene, herein designated VGAM is inhibition of expression of VGAM2608 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2608 correlate with, and may be deduced

from, the identity of the target genes which VGAM2608 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[87997] DNA (cytosine-5-)-methyltransferase 3 Beta (DNMT3B, Accession NM_006892) is a VGAM2608 host target gene. DNMT3B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNMT3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNMT3B BINDING SITE, designated SEQ ID:13760, to the nucleotide sequence of VGAM2608 RNA, herein designated VGAM RNA, also designated SEQ ID:5319.

[87998] A function of VGAM2608 is therefore inhibition of DNA (cytosine-5-)-methyltransferase 3 Beta (DNMT3B, Accession NM_006892), a gene which is required for genome wide de novo methylation. Accordingly, utilities of VGAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNMT3B. The function of DNMT3B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to VGAM280.Kelch-like 4 (Drosophila) (KLHL4, Accession NM_019117) is another VGAM2608 host target gene. KLHL4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLHL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLHL4 BINDING SITE, designated SEQ ID:21193, to the nucleotide sequence of VGAM2608 RNA, herein designated VGAM RNA, also designated SEQ ID:5319.

[87999] Another function of VGAM2608 is therefore inhibition of Kelch-like 4 (Drosophila) (KLHL4, Accession NM_019117). Accordingly, utilities of VGAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL4. LOC153196 (Accession XM_098323) is another VGAM2608 host target gene. LOC153196 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153196 BINDING SITE, desig-

nated SEQ ID:41588, to the nucleotide sequence of VGAM2608 RNA, herein designated VGAM RNA, also designated SEQ ID:5319.

[88000] Another function of VGAM2608 is therefore inhibition of LOC153196 (Accession XM_098323). Accordingly, utilities of VGAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153196. LOC255096 (Accession XM_174913) is another VGAM2608 host target gene. LOC255096 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255096, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255096 BINDING SITE, designated SEQ ID:46607, to the nucleotide sequence of VGAM2608 RNA, herein designated VGAM RNA, also designated SEQ ID:5319.

[88001] Another function of VGAM2608 is therefore inhibition of LOC255096 (Accession XM_174913). Accordingly, utilities of VGAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255096. LOC256995 (Accession XM_174550) is another VGAM2608 host target gene. LOC256995 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256995, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256995 BINDING SITE, designated SEQ ID:46599, to the nucleotide sequence of VGAM2608 RNA, herein designated VGAM RNA, also designated SEQ ID:5319.

[88002] Another function of VGAM2608 is therefore inhibition of LOC256995 (Accession XM_174550). Accordingly, utilities of VGAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256995. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2609 (VGAM2609) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88003] VGAM2609 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2609 was detected is described hereinabove with reference to Figs. 1-8.

[88004] VGAM2609 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ljungan Virus. VGAM2609 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88005] VGAM2609 gene encodes a VGAM2609 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2609 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2609 precursor RNA is designated SEQ ID:2595, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2595 is located at position 2766 relative to the genome of Ljungan Virus.

[88006] VGAM2609 precursor RNA folds onto itself, forming VGAM2609 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[88007] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2609 folded precursor RNA into VGAM2609 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2609 RNA is designated SEQ ID:5320, and is provided hereinbelow with reference to the sequence listing part.

[88008] VGAM2609 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2609 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88009] VGAM2609 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2609 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2609 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2609 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88010] The complementary binding of VGAM2609 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2609 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2609 host target RNA into VGAM2609 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88011] It is appreciated that VGAM2609 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2609 host target genes. The mRNA of each one of this plurality of VGAM2609 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2609 RNA, herein designated VGAM RNA, and which when bound by VGAM2609 RNA causes inhibition of translation of respective one or more VGAM2609 host target proteins.

[88012] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2609 gene, herein designated VGAM GENE, on one or more VGAM2609 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88013] It is yet further appreciated that a function of VGAM2609 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2609 include diagnosis, prevention and treatment of viral infection by Ljungan Virus. Specific functions, and accordingly utilities, of VGAM2609 correlate with, and may be deduced from, the identity of the host target genes which VGAM2609 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88014] Nucleotide sequences of the VGAM2609 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2609 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2609 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2609 are further described hereinbelow with reference to Table 1.

[88015] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2609 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2609 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88016] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2609 gene, herein designated VGAM is inhibition of expression of VGAM2609 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2609 correlate with, and may be deduced from, the identity of the target genes which VGAM2609 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88017] Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858) is a VGAM2609 host target gene. COL19A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL19A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of COL19A1 BINDING SITE, designated SEQ ID:7591, to the nucleotide sequence of VGAM2609 RNA, herein designated VGAM RNA, also designated SEQ ID:5320.

[88018] A function of VGAM2609 is therefore inhibition of Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858), a gene which may act as a cross-bridge between fibrils and other extracellular matrix molecules. Accordingly, utilities of VGAM2609 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL19A1. The function of COL19A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM19.MADS Box Transcription Enhancer Factor 2, Polypeptide A (myocyte enhancer factor 2A) (MEF2A, Accession NM_005587) is another VGAM2609 host target gene. MEF2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEF2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEF2A BINDING SITE,

designated SEQ ID:12115, to the nucleotide sequence of VGAM2609 RNA, herein designated VGAM RNA, also designated SEQ ID:5320.

[88019] Another function of VGAM2609 is therefore inhibition of MADS Box Transcription Enhancer Factor 2, Polypeptide A (myocyte enhancer factor 2A) (MEF2A, Accession NM_005587), a gene which binds a consensus sequence that regulates transcription. Accordingly, utilities of VGAM2609 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEF2A. The function of MEF2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM46.Cbp/p300-interacting Transactivator, with Glu/Asp-rich Carboxy-terminal Domain, 2 (CITED2, Accession NM_006079) is another VGAM2609 host target gene. CITED2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CITED2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CITED2 BINDING SITE, designated SEQ ID:12727, to the nucleotide sequence of VGAM2609 RNA,

herein designated VGAM RNA, also designated SEQ ID:5320.

[88020] Another function of VGAM2609 is therefore inhibition of Cbp/p300-interacting Transactivator, with Glu/Asp-rich Carboxy-terminal Domain, 2 (CITED2, Accession NM_006079). Accordingly, utilities of VGAM2609 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CITED2. FLJ20666 (Accession NM_018333) is another VGAM2609 host target gene. FLJ20666 BINDING SITE1 and FLJ20666 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ20666, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20666 BINDING SITE1 and FLJ20666 BINDING SITE2, designated SEQ ID:20336 and SEQ ID:19583 respectively, to the nucleotide sequence of VGAM2609 RNA, herein designated VGAM RNA, also designated SEQ ID:5320.

[88021] Another function of VGAM2609 is therefore inhibition of FLJ20666 (Accession NM_018333). Accordingly, utilities of VGAM2609 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20666. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2610 (VGAM2610) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88022] VGAM2610 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2610 was detected is described hereinabove with reference to Figs. 1-8.

[88023] VGAM2610 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ljungan Virus. VGAM2610 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88024] VGAM2610 gene encodes a VGAM2610 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2610 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2610 precursor RNA is designated SEQ ID:2596, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2596 is located at position 7099 relative to the genome of Ljungan Virus.

[88025] VGAM2610 precursor RNA folds onto itself, forming VGAM2610 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88026] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2610 folded precursor RNA into VGAM2610 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2610 RNA is designated SEQ ID:5321, and is provided hereinbelow with reference to the sequence listing part.

[88027] VGAM2610 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2610 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88028] VGAM2610 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2610 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2610 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88029] The complementary binding of VGAM2610 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2610 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2610 host target RNA into VGAM2610 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88030] It is appreciated that VGAM2610 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2610 host target genes. The mRNA of each one of this plurality of VGAM2610 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2610 RNA, herein designated VGAM RNA, and which when bound by VGAM2610 RNA causes

inhibition of translation of respective one or more VGAM2610 host target proteins.

[88031] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2610 gene, herein designated VGAM GENE, on one or more VGAM2610 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88032] It is yet further appreciated that a function of VGAM2610 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2610 include diagnosis, prevention and

treatment of viral infection by Ljungan Virus. Specific functions, and accordingly utilities, of VGAM2610 correlate with, and may be deduced from, the identity of the host target genes which VGAM2610 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88033] Nucleotide sequences of the VGAM2610 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2610 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2610 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2610 are further described hereinbelow with reference to Table 1.

[88034] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2610 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2610 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88035] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2610 gene, herein designated VGAM is inhibition of expression of VGAM2610 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2610 correlate with, and may be deduced from, the identity of the target genes which VGAM2610 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88036] FUS1 (Accession NM_007275) is a VGAM2610 host target gene. FUS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FUS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FUS1 BINDING SITE, designated SEQ ID:14137, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88037] A function of VGAM2610 is therefore inhibition of FUS1 (Accession NM_007275), a gene which may function as a tumor suppressor. Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUS1. The function of FUS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1246.High-mobility Group Nucleosome Binding Do-

main 1 (HMGN1, Accession NM_004965) is another VGAM2610 host target gene. HMGN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMGN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGN1 BINDING SITE, designated SEQ ID:11413, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88038] Another function of VGAM2610 is therefore inhibition of High-mobility Group Nucleosome Binding Domain 1 (HMGN1, Accession NM_004965), a gene which binds to the inner side of the nucleosomal DNA and involves in transcriptional regulation. Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGN1. The function of HMGN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Occludin (OCLN, Accession NM_002538) is another VGAM2610 host target gene. OCLN BINDING SITE is HOST TARGET binding site found in

the 5` untranslated region of mRNA encoded by OCLN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OCLN BINDING SITE, designated SEQ ID:8379, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88039] Another function of VGAM2610 is therefore inhibition of Occludin (OCLN, Accession NM_002538). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OCLN. Phosphatidylinositol-4-phosphate 5-kinase, Type I, Alpha (PIP5K1A, Accession NM_003557) is another VGAM2610 host target gene. PIP5K1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIP5K1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIP5K1A BINDING SITE, designated SEQ ID:9603, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88040] Another function of VGAM2610 is therefore inhibition of

Phosphatidylinositol-4-phosphate 5-kinase, Type I, Alpha (PIP5K1A, Accession NM_003557), a gene which is responsible for the synthesis of PtdIns(4,5)P2. Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP5K1A. The function of PIP5K1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM427.Retinoid X Receptor, Alpha (RXRA, Accession NM_002957) is another VGAM2610 host target gene. RXRA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RXRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RXRA BINDING SITE, designated SEQ ID:8874, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88041] Another function of VGAM2610 is therefore inhibition of Retinoid X Receptor, Alpha (RXRA, Accession NM_002957), a gene which activates genes required for vitamin A metabolism, binds 9-cis retinoic acid. Accordingly, utili-

ties of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RXRA. The function of RXRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM349.Solute Carrier Family 1 (glutamate/neutral amino acid transporter), Member 4 (SLC1A4, Accession NM_003038) is another VGAM2610 host target gene. SLC1A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC1A4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC1A4 BINDING SITE, designated SEQ ID:8996, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88042] Another function of VGAM2610 is therefore inhibition of Solute Carrier Family 1 (glutamate/neutral amino acid transporter), Member 4 (SLC1A4, Accession NM_003038), a gene which transports alanine, serine, cysteine, and threonine. exhibits sodium dependence. Accordingly, utilities of VGAM2610 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with SLC1A4. The function of SLC1A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM859.Staufen, RNA Binding Protein (Drosophila) (STAU, Accession NM_017452) is another VGAM2610 host target gene. STAU BINDING SITE1 through STAU BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by STAU, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE1 through STAU BINDING SITE4, designated SEQ ID:18914, SEQ ID:10942, SEQ ID:18926 and SEQ ID:18920 respectively, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88043] Another function of VGAM2610 is therefore inhibition of Staufen, RNA Binding Protein (Drosophila) (STAU, Accession NM_017452), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stimulating their translation at the site. Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with STAU. The function of STAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM916.Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_133336) is another VGAM2610 host target gene. WHSC1 BINDING SITE1 through WHSC1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WHSC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE1 through WHSC1 BINDING SITE4, designated SEQ ID:28473, SEQ ID:28460, SEQ ID:28443 and SEQ ID:36468 respectively, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88044] Another function of VGAM2610 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_133336), a gene which binds covalently to and repairs g/t mismatches. Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1.

The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.DKFZP434O047 (Accession NM_015594) is another VGAM2610 host target gene. DKFZP434O047 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DK-FZP434O047, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434O047 BINDING SITE, designated SEQ ID:17869, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88045] Another function of VGAM2610 is therefore inhibition of DKFZP434O047 (Accession NM_015594). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434O047. GBTS1 (Accession NM_145173) is another VGAM2610 host target gene. GBTS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GBTS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GBTS1 BINDING SITE, designated SEQ ID:29728, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88046] Another function of VGAM2610 is therefore inhibition of GBTS1 (Accession NM_145173). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBTS1. Heart and Neural Crest Derivatives Expressed 1 (HAND1, Accession NM_004821) is another VGAM2610 host target gene. HAND1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HAND1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HAND1 BINDING SITE, designated SEQ ID:11237, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88047] Another function of VGAM2610 is therefore inhibition of Heart and Neural Crest Derivatives Expressed 1 (HAND1, Accession NM_004821). Accordingly, utilities of

VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAND1. KIAA0481 (Accession XM_050144) is another VGAM2610 host target gene. KIAA0481 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0481, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0481 BINDING SITE, designated SEQ ID:35570, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88048] Another function of VGAM2610 is therefore inhibition of KIAA0481 (Accession XM_050144). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0481. KIAA1554 (Accession XM_170834) is another VGAM2610 host target gene. KIAA1554 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1554, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1554 BINDING SITE, designated SEQ ID:45610, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88049] Another function of VGAM2610 is therefore inhibition of KIAA1554 (Accession XM_170834). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1554. Mitochondrial Ribosomal Protein L30 (MRPL30, Accession NM_016503) is another VGAM2610 host target gene. MRPL30 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MRPL30, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL30 BINDING SITE, designated SEQ ID:18583, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88050] Another function of VGAM2610 is therefore inhibition of Mitochondrial Ribosomal Protein L30 (MRPL30, Accession NM_016503). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL30. P15-2 (Accession

NM_018698) is another VGAM2610 host target gene. P15-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P15-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P15-2 BINDING SITE, designated SEQ ID:20783, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88051] Another function of VGAM2610 is therefore inhibition of P15-2 (Accession NM_018698). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P15-2. Proteasome (prosome, macropain) Inhibitor Subunit 1 (PI31) (PSMF1, Accession NM_006814) is another VGAM2610 host target gene. PSMF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSMF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSMF1 BINDING SITE, designated SEQ ID:13689, to the nucleotide sequence of

VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88052] Another function of VGAM2610 is therefore inhibition of Proteasome (prosome, macropain) Inhibitor Subunit 1 (PI31) (PSMF1, Accession NM_006814). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSMF1. LOC115708 (Accession XM_056552) is another VGAM2610 host target gene. LOC115708 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115708, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115708 BINDING SITE, designated SEQ ID:36407, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88053] Another function of VGAM2610 is therefore inhibition of LOC115708 (Accession XM_056552). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115708. LOC145854 (Accession XM_085259) is another VGAM2610 host target gene. LOC145854 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145854, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145854 BINDING SITE, designated SEQ ID:38009, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88054] Another function of VGAM2610 is therefore inhibition of LOC145854 (Accession XM_085259). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145854. LOC150967 (Accession XM_087060) is another VGAM2610 host target gene. LOC150967 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150967, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150967 BINDING SITE, designated SEQ ID:39035, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88055] Another function of VGAM2610 is therefore inhibition of

LOC150967 (Accession XM_087060). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150967. LOC157624 (Accession XM_098801) is another VGAM2610 host target gene. LOC157624 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157624, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157624 BINDING SITE, designated SEQ ID:41826, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88056] Another function of VGAM2610 is therefore inhibition of LOC157624 (Accession XM_098801). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157624. LOC157918 (Accession XM_098842) is another VGAM2610 host target gene. LOC157918 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC157918 BINDING SITE, designated SEQ ID:41899, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88057] Another function of VGAM2610 is therefore inhibition of LOC157918 (Accession XM_098842). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157918. LOC158956 (Accession XM_039450) is another VGAM2610 host target gene. LOC158956 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158956, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158956 BINDING SITE, designated SEQ ID:33097, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88058] Another function of VGAM2610 is therefore inhibition of LOC158956 (Accession XM_039450). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158956. LOC197320 (Accession XM_113861) is an-

other VGAM2610 host target gene. LOC197320 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC197320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197320 BINDING SITE, designated SEQ ID:42472, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88059] Another function of VGAM2610 is therefore inhibition of LOC197320 (Accession XM_113861). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197320. LOC202025 (Accession XM_117353) is another VGAM2610 host target gene. LOC202025 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202025, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202025 BINDING SITE, designated SEQ ID:43399, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88060] Another function of VGAM2610 is therefore inhibition of LOC202025 (Accession XM_117353). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202025. LOC206426 (Accession XM_116505) is another VGAM2610 host target gene. LOC206426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC206426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC206426 BINDING SITE, designated SEQ ID:43120, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88061] Another function of VGAM2610 is therefore inhibition of LOC206426 (Accession XM_116505). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC206426. LOC222134 (Accession XM_168432) is another VGAM2610 host target gene. LOC222134 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222134, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222134 BINDING SITE, designated SEQ ID:45170, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88062] Another function of VGAM2610 is therefore inhibition of LOC222134 (Accession XM_168432). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222134. LOC255654 (Accession XM_173036) is another VGAM2610 host target gene. LOC255654 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255654 BINDING SITE, designated SEQ ID:46303, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88063] Another function of VGAM2610 is therefore inhibition of LOC255654 (Accession XM_173036). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC255654. LOC257457 (Accession XM_031425) is another VGAM2610 host target gene. LOC257457 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257457, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257457 BINDING SITE, designated SEQ ID:31376, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88064] Another function of VGAM2610 is therefore inhibition of LOC257457 (Accession XM_031425). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257457. LOC51619 (Accession NM_015983) is another VGAM2610 host target gene. LOC51619 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51619, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51619 BINDING SITE, designated SEQ ID:18077, to the nucleotide sequence of VGAM2610 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5321.

[88065] Another function of VGAM2610 is therefore inhibition of LOC51619 (Accession NM_015983). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51619. LOC91759 (Accession XM_040467) is another VGAM2610 host target gene. LOC91759 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91759, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91759 BINDING SITE, designated SEQ ID:33305, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88066] Another function of VGAM2610 is therefore inhibition of LOC91759 (Accession XM_040467). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91759. LOC92539 (Accession XM_045632) is another VGAM2610 host target gene. LOC92539 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92539, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92539 BINDING SITE, designated SEQ ID:34503, to the nucleotide sequence of VGAM2610 RNA, herein designated VGAM RNA, also designated SEQ ID:5321.

[88067] Another function of VGAM2610 is therefore inhibition of LOC92539 (Accession XM_045632). Accordingly, utilities of VGAM2610 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92539. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2611 (VGAM2611) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88068] VGAM2611 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2611 was detected is described hereinabove with reference to Figs. 1-8.

[88069] VGAM2611 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis A Virus.

VGAM2611 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88070] VGAM2611 gene encodes a VGAM2611 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2611 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2611 precursor RNA is designated SEQ ID:2597, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2597 is located at position 3057 relative to the genome of Equine Rhinitis A Virus.

[88071] VGAM2611 precursor RNA folds onto itself, forming VGAM2611 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88072] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2611 folded precursor RNA into VGAM2611 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2611 RNA is designated SEQ ID:5322, and is provided hereinbelow with reference to the sequence listing part.

[88073] VGAM2611 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2611 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88074] VGAM2611 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2611 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2611 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88075] The complementary binding of VGAM2611 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2611 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2611 host target RNA into VGAM2611 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88076] It is appreciated that VGAM2611 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2611 host target genes. The mRNA of each one of this plurality of VGAM2611 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2611 RNA, herein designated VGAM RNA, and which when bound by VGAM2611 RNA causes inhibition of translation of respective one or more VGAM2611 host target proteins.

[88077] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2611 gene, herein designated VGAM GENE, on one or more VGAM2611 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88078] It is yet further appreciated that a function of VGAM2611 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis A Virus. Specific functions, and accordingly utilities, of VGAM2611 correlate with, and may be deduced from, the identity of the host target genes which VGAM2611 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88079] Nucleotide sequences of the VGAM2611 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2611 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2611 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2611 are further described hereinbelow with reference to Table 1.

[88080] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2611 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2611 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88081] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2611 gene, herein designated VGAM is inhibition of expression of VGAM2611 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2611 correlate with, and may be deduced from, the identity of the target genes which VGAM2611 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88082] Arachidonate 15-lipoxygenase (ALOX15, Accession NM_001140) is a VGAM2611 host target gene. ALOX15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALOX15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALOX15 BINDING SITE, designated SEQ

ID:6809, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88083] A function of VGAM2611 is therefore inhibition of Arachidonate 15-lipoxygenase (ALOX15, Accession NM_001140), a gene which converts arachidonic acid to 15s- hydroperoxyeicosatetraenoic acid. Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOX15. The function of ALOX15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM282.Adaptor-related Protein Complex 1, Gamma 1 Subunit (AP1G1, Accession NM_001128) is another VGAM2611 host target gene. AP1G1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP1G1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP1G1 BINDING SITE, designated SEQ ID:6799, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88084] Another function of VGAM2611 is therefore inhibition of Adaptor-related Protein Complex 1, Gamma 1 Subunit (AP1G1, Accession NM_001128), a gene which promotes the formation of clathrin-coated pits and vesicles. Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1G1. The function of AP1G1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM316.Diaphorase (NADH) (cytochrome b-5 reductase) (DIA1, Accession NM_007326) is another VGAM2611 host target gene. DIA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DIA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIA1 BINDING SITE, designated SEQ ID:14246, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88085] Another function of VGAM2611 is therefore inhibition of Diaphorase (NADH) (cytochrome b-5 reductase) (DIA1, Accession NM_007326). Accordingly, utilities of

VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIA1. Discs, Large (Drosophila) Homolog 4 (DLG4, Accession NM_001365) is another VGAM2611 host target gene. DLG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DLG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLG4 BINDING SITE, designated SEQ ID:7045, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88086] Another function of VGAM2611 is therefore inhibition of Discs, Large (Drosophila) Homolog 4 (DLG4, Accession NM_001365), a gene which is a membrane-associated guanylate kinase and may intervene in synaptogenesis. Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLG4. The function of DLG4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Leucine Zipper, Putative Tumor Suppressor 1 (LZTS1, Accession

NM_021020) is another VGAM2611 host target gene. LZTS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LZTS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LZTS1 BINDING SITE, designated SEQ ID:22006, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88087] Another function of VGAM2611 is therefore inhibition of Leucine Zipper, Putative Tumor Suppressor 1 (LZTS1, Accession NM_021020), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans UNC-76. Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTS1. The function of LZTS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM890.RAB, Member of RAS Oncogene Family-like 2A (RABL2A, Accession NM_013412) is another VGAM2611 host target gene. RABL2A BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by RABL2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RABL2A BINDING SITE, designated SEQ ID:15078, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88088] Another function of VGAM2611 is therefore inhibition of RAB, Member of RAS Oncogene Family-like 2A (RABL2A, Accession NM_013412). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2A. RAB, Member of RAS Oncogene Family-like 2B (RABL2B, Accession NM_007081) is another VGAM2611 host target gene. RABL2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RABL2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RABL2B BINDING SITE, designated SEQ ID:13945, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5322.

[88089] Another function of VGAM2611 is therefore inhibition of RAB, Member of RAS Oncogene Family-like 2B (RABL2B, Accession NM_007081). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2B. Solute Carrier Family 19 (folate transporter), Member 1 (SLC19A1, Accession NM_003056) is another VGAM2611 host target gene. SLC19A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC19A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC19A1 BINDING SITE, designated SEQ ID:9021, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88090] Another function of VGAM2611 is therefore inhibition of Solute Carrier Family 19 (folate transporter), Member 1 (SLC19A1, Accession NM_003056). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC19A1. Serine Racemase (SRR, Accession NM_021947)

is another VGAM2611 host target gene. SRR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SRR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRR BINDING SITE, designated SEQ ID:22475, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88091] Another function of VGAM2611 is therefore inhibition of Serine Racemase (SRR, Accession NM_021947). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRR. Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769) is another VGAM2611 host target gene. C11orf11 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C11orf11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf11 BINDING SITE, designated SEQ ID:44784, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5322.

[88092] Another function of VGAM2611 is therefore inhibition of Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf11. Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575) is another VGAM2611 host target gene. C17orf31 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C17orf31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C17orf31 BINDING SITE, designated SEQ ID:18999, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88093] Another function of VGAM2611 is therefore inhibition of Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf31. Chromosome 20 Open Reading Frame 102 (C20orf102, Acces-

sion NM_080607) is another VGAM2611 host target gene. C20orf102 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf102, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf102 BINDING SITE, designated SEQ ID:27925, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88094] Another function of VGAM2611 is therefore inhibition of Chromosome 20 Open Reading Frame 102 (C20orf102, Accession NM_080607). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf102. Chromosome 9 Open Reading Frame 7 (C9orf7, Accession NM_017586) is another VGAM2611 host target gene. C9orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf7 BINDING SITE, des-

ignated SEQ ID:19032, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88095] Another function of VGAM2611 is therefore inhibition of Chromosome 9 Open Reading Frame 7 (C9orf7, Accession NM_017586). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf7. FLJ12788 (Accession NM_022492) is another VGAM2611 host target gene. FLJ12788 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12788, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12788 BINDING SITE, designated SEQ ID:22872, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88096] Another function of VGAM2611 is therefore inhibition of FLJ12788 (Accession NM_022492). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12788. FLJ20211 (Accession NM_017713) is another

VGAM2611 host target gene. FLJ20211 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20211, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20211 BINDING SITE, designated SEQ ID:19297, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88097] Another function of VGAM2611 is therefore inhibition of FLJ20211 (Accession NM_017713). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20211. FLJ20718 (Accession NM_017939) is another VGAM2611 host target gene. FLJ20718 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20718, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20718 BINDING SITE, designated SEQ ID:19634, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88098] Another function of VGAM2611 is therefore inhibition of FLJ20718 (Accession NM_017939). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20718. FLJ22215 (Accession XM_173021) is another VGAM2611 host target gene. FLJ22215 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22215, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22215 BINDING SITE, designated SEQ ID:46281, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88099] Another function of VGAM2611 is therefore inhibition of FLJ22215 (Accession XM_173021). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22215. FLJ32752 (Accession NM_144666) is another VGAM2611 host target gene. FLJ32752 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ32752, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32752 BINDING SITE, designated SEQ ID:29481, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88100] Another function of VGAM2611 is therefore inhibition of FLJ32752 (Accession NM_144666). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32752. KIAA0367 (Accession XM_041018) is another VGAM2611 host target gene. KIAA0367 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0367, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0367 BINDING SITE, designated SEQ ID:33418, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88101] Another function of VGAM2611 is therefore inhibition of KIAA0367 (Accession XM_041018). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0367. KIAA0682 (Accession NM_016196) is another VGAM2611 host target gene. KIAA0682 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0682, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0682 BINDING SITE, designated SEQ ID:18288, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88102] Another function of VGAM2611 is therefore inhibition of KIAA0682 (Accession NM_016196). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0682. KIAA0789 (Accession XM_033113) is another VGAM2611 host target gene. KIAA0789 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0789 BINDING SITE, designated SEQ ID:31846, to the nucleotide sequence of VGAM2611 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5322.

[88103] Another function of VGAM2611 is therefore inhibition of KIAA0789 (Accession XM_033113). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0789. KIAA1862 (Accession XM_044212) is another VGAM2611 host target gene. KIAA1862 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1862, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1862 BINDING SITE, designated SEQ ID:34173, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88104] Another function of VGAM2611 is therefore inhibition of KIAA1862 (Accession XM_044212). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1862. Williams Beuren Syndrome Chromosome Region 21 (WBSCR21, Accession NM_031295) is another VGAM2611 host target gene. WBSCR21 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by WBSCR21, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WBSCR21 BINDING SITE, designated SEQ ID:25327, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88105] Another function of VGAM2611 is therefore inhibition of Williams Beuren Syndrome Chromosome Region 21 (WBSCR21, Accession NM_031295). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR21. LOC143425 (Accession XM_113695) is another VGAM2611 host target gene. LOC143425 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143425, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143425 BINDING SITE, designated SEQ ID:42351, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88106] Another function of VGAM2611 is therefore inhibition of

LOC143425 (Accession XM_113695). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143425. LOC146745 (Accession XM_085577) is another VGAM2611 host target gene. LOC146745 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146745, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146745 BINDING SITE, designated SEQ ID:38230, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88107] Another function of VGAM2611 is therefore inhibition of LOC146745 (Accession XM_085577). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146745. LOC152426 (Accession XM_098225) is another VGAM2611 host target gene. LOC152426 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC152426 BINDING SITE, designated SEQ ID:41496, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88108] Another function of VGAM2611 is therefore inhibition of LOC152426 (Accession XM_098225). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152426. LOC157247 (Accession XM_088275) is another VGAM2611 host target gene. LOC157247 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157247 BINDING SITE, designated SEQ ID:39573, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88109] Another function of VGAM2611 is therefore inhibition of LOC157247 (Accession XM_088275). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157247. LOC201182 (Accession XM_117055) is an-

other VGAM2611 host target gene. LOC201182 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201182, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201182 BINDING SITE, designated SEQ ID:43211, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88110] Another function of VGAM2611 is therefore inhibition of LOC201182 (Accession XM_117055). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201182. LOC201243 (Accession XM_113935) is another VGAM2611 host target gene. LOC201243 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201243, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201243 BINDING SITE, designated SEQ ID:42552, to the nucleotide sequence of VGAM2611 RNA, herein designated VGAM RNA, also designated SEQ ID:5322.

[88111] Another function of VGAM2611 is therefore inhibition of LOC201243 (Accession XM_113935). Accordingly, utilities of VGAM2611 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201243. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2612 (VGAM2612) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88112] VGAM2612 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2612 was detected is described hereinabove with reference to Figs. 1-8.

[88113] VGAM2612 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis A Virus. VGAM2612 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88114] VGAM2612 gene encodes a VGAM2612 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2612 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2612 precursor RNA is designated SEQ ID:2598, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2598 is located at position 2734 relative to the genome of Equine Rhinitis A Virus.

[88115] VGAM2612 precursor RNA folds onto itself, forming VGAM2612 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88116] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2612 folded precursor RNA into VGAM2612 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2612 RNA is designated SEQ ID:5323, and is provided hereinbelow with reference to the sequence listing part.

[88117] VGAM2612 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2612 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88118] VGAM2612 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2612 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2612 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88119] The complementary binding of VGAM2612 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2612 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2612 host target RNA into VGAM2612 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88120] It is appreciated that VGAM2612 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2612 host target genes. The mRNA of each one of this plurality of VGAM2612 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2612 RNA, herein designated VGAM RNA, and which when bound by VGAM2612 RNA causes inhibition of translation of respective one or more VGAM2612 host target proteins.

[88121] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2612 gene, herein designated VGAM GENE, on one or more VGAM2612 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88122] It is yet further appreciated that a function of VGAM2612 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis A Virus. Specific functions, and accordingly utilities, of VGAM2612 correlate with, and may be deduced from, the identity of the host target genes which VGAM2612 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88123] Nucleotide sequences of the VGAM2612 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2612 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2612 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2612 are further described hereinbelow with reference to Table 1.

[88124] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2612 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2612 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[88125] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2612 gene, herein designated VGAM is inhibition of expression of VGAM2612 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2612 correlate with, and may be deduced from, the identity of the target genes which VGAM2612 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88126] Sialidase 3 (membrane sialidase) (NEU3, Accession NM_006656) is a VGAM2612 host target gene. NEU3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NEU3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NEU3 BINDING SITE, designated SEQ ID:13456, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88127] A function of VGAM2612 is therefore inhibition of Sialidase 3 (membrane sialidase) (NEU3, Accession NM_006656). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with NEU3. SMP1 (Accession NM_014313) is another VGAM2612 host target gene. SMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMP1 BINDING SITE, designated SEQ ID:15609, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88128] Another function of VGAM2612 is therefore inhibition of SMP1 (Accession NM_014313), a gene which is a potential integral membrane protein. Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMP1. The function of SMP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM127.Zinc Finger Protein 289, ID1 Regulated (ZNF289, Accession XM_037147) is another VGAM2612 host target gene. ZNF289 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF289, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF289 BINDING SITE, designated SEQ ID:32550, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88129] Another function of VGAM2612 is therefore inhibition of Zinc Finger Protein 289, ID1 Regulated (ZNF289, Accession XM_037147). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF289. Apolipoprotein L, 2 (APOL2, Accession NM_030882) is another VGAM2612 host target gene. APOL2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by APOL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APOL2 BINDING SITE, designated SEQ ID:25161, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88130] Another function of VGAM2612 is therefore inhibition of Apolipoprotein L, 2 (APOL2, Accession NM_030882). Ac-

cordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL2. Apolipoprotein L, 3 (APOL3, Accession NM_014349) is another VGAM2612 host target gene. APOL3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by APOL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APOL3 BINDING SITE, designated SEQ ID:15673, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88131] Another function of VGAM2612 is therefore inhibition of Apolipoprotein L, 3 (APOL3, Accession NM_014349). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL3. DKFZp434E2220 (Accession NM_017612) is another VGAM2612 host target gene. DKFZp434E2220 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp434E2220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434E2220 BINDING SITE, designated SEQ ID:19109, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88132] Another function of VGAM2612 is therefore inhibition of DKFZp434E2220 (Accession NM_017612). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2220. FLJ10388 (Accession NM_018082) is another VGAM2612 host target gene. FLJ10388 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10388, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10388 BINDING SITE, designated SEQ ID:19843, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88133] Another function of VGAM2612 is therefore inhibition of FLJ10388 (Accession NM_018082). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ10388. KIAA0367 (Accession XM_041018) is another VGAM2612 host target gene. KIAA0367 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0367, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0367 BINDING SITE, designated SEQ ID:33415, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88134] Another function of VGAM2612 is therefore inhibition of KIAA0367 (Accession XM_041018). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0367. KIAA0871 (Accession NM_014961) is another VGAM2612 host target gene. KIAA0871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0871 BINDING SITE, designated SEQ ID:17330, to the nucleotide sequence of VGAM2612 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5323.

[88135] Another function of VGAM2612 is therefore inhibition of KIAA0871 (Accession NM_014961). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0871. KIAA0992 (Accession NM_016081) is another VGAM2612 host target gene. KIAA0992 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0992, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0992 BINDING SITE, designated SEQ ID:18159, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88136] Another function of VGAM2612 is therefore inhibition of KIAA0992 (Accession NM_016081). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0992. KIAA1028 (Accession XM_166324) is another VGAM2612 host target gene. KIAA1028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1028, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1028 BINDING SITE, designated SEQ ID:44157, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88137] Another function of VGAM2612 is therefore inhibition of KIAA1028 (Accession XM_166324). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1028. KIAA1203 (Accession XM_049683) is another VGAM2612 host target gene. KIAA1203 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1203, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1203 BINDING SITE, designated SEQ ID:35470, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88138] Another function of VGAM2612 is therefore inhibition of KIAA1203 (Accession XM_049683). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1203. KIAA1954 (Accession XM_085375) is another VGAM2612 host target gene. KIAA1954 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1954, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1954 BINDING SITE, designated SEQ ID:38098, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88139] Another function of VGAM2612 is therefore inhibition of KIAA1954 (Accession XM_085375). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1954. Leiomodin 1 (smooth muscle) (LMOD1, Accession NM_012134) is another VGAM2612 host target gene. LMOD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LMOD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LMOD1 BINDING SITE, designated SEQ

ID:14447, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88140] Another function of VGAM2612 is therefore inhibition of Leiomodin 1 (smooth muscle) (LMOD1, Accession NM_012134). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LMOD1. MGC26914 (Accession NM_144976) is another VGAM2612 host target gene. MGC26914 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC26914, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC26914 BINDING SITE, designated SEQ ID:29586, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88141] Another function of VGAM2612 is therefore inhibition of MGC26914 (Accession NM_144976). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26914. PRO1617 (Accession NM_018587) is another

VGAM2612 host target gene. PRO1617 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1617, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1617 BINDING SITE, designated SEQ ID:20665, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88142] Another function of VGAM2612 is therefore inhibition of PRO1617 (Accession NM_018587). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1617. SKRP1 (Accession NM_080876) is another VGAM2612 host target gene. SKRP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SKRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SKRP1 BINDING SITE, designated SEQ ID:28119, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88143] Another function of VGAM2612 is therefore inhibition of SKRP1 (Accession NM_080876). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SKRP1. SPEC1 (Accession NM_020239) is another VGAM2612 host target gene. SPEC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPEC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPEC1 BINDING SITE, designated SEQ ID:21510, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88144] Another function of VGAM2612 is therefore inhibition of SPEC1 (Accession NM_020239). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPEC1. LOC144747 (Accession XM_084954) is another VGAM2612 host target gene. LOC144747 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144747, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144747 BINDING SITE, designated SEQ ID:37782, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88145] Another function of VGAM2612 is therefore inhibition of LOC144747 (Accession XM_084954). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144747. LOC158293 (Accession XM_088541) is another VGAM2612 host target gene. LOC158293 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158293, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158293 BINDING SITE, designated SEQ ID:39806, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88146] Another function of VGAM2612 is therefore inhibition of LOC158293 (Accession XM_088541). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC158293. LOC162239 (Accession XM_091439) is another VGAM2612 host target gene. LOC162239 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC162239, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162239 BINDING SITE, designated SEQ ID:40051, to the nucleotide sequence of VGAM2612 RNA, herein designated VGAM RNA, also designated SEQ ID:5323.

[88147] Another function of VGAM2612 is therefore inhibition of LOC162239 (Accession XM_091439). Accordingly, utilities of VGAM2612 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162239. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2613 (VGAM2613) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88148] VGAM2613 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2613 was detected is described hereinabove with reference to Figs. 1-8.

[88149] VGAM2613 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis A Virus. VGAM2613 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88150] VGAM2613 gene encodes a VGAM2613 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2613 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2613 precursor RNA is designated SEQ ID:2599, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2599 is located at position 5479 relative to the genome of Equine Rhinitis A Virus.

[88151] VGAM2613 precursor RNA folds onto itself, forming VGAM2613 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88152] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2613 folded precursor RNA into VGAM2613 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2613 RNA is designated SEQ ID:5324, and is provided hereinbelow with reference to the sequence listing part.

[88153] VGAM2613 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2613 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88154] VGAM2613 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2613 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2613 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88155] The complementary binding of VGAM2613 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2613 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2613 host target RNA into VGAM2613 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88156] It is appreciated that VGAM2613 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2613 host target genes. The mRNA of each one of this plurality of VGAM2613 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2613 RNA, herein designated VGAM RNA, and which when bound by VGAM2613 RNA causes inhibition of translation of respective one or more VGAM2613 host target proteins.

[88157] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2613 gene, herein designated VGAM GENE, on one or more VGAM2613 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88158] It is yet further appreciated that a function of VGAM2613 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis A Virus. Specific functions, and accordingly utilities, of VGAM2613 correlate with, and may be deduced from, the identity of the host target genes which VGAM2613 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88159] Nucleotide sequences of the VGAM2613 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2613 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2613 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2613 are further described hereinbelow with reference to Table 1.

[88160] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2613 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2613 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88161] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2613 gene, herein designated VGAM is inhibition of expression of VGAM2613 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2613 correlate with, and may be deduced from, the identity of the target genes which VGAM2613 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88162] Contactin Associated Protein-like 2 (CNTNAP2, Accession NM_014141) is a VGAM2613 host target gene. CNTNAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNTNAP2,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNTNAP2 BINDING SITE, designated SEQ ID:15414, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88163] A function of VGAM2613 is therefore inhibition of Contactin Associated Protein-like 2 (CNTNAP2, Accession NM_014141). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTNAP2. Down Syndrome Critical Region Gene 5 (DSCR5, Accession NM_016430) is another VGAM2613 host target gene. DSCR5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DSCR5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DSCR5 BINDING SITE, designated SEQ ID:18549, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88164] Another function of VGAM2613 is therefore inhibition of

Down Syndrome Critical Region Gene 5 (DSCR5, Accession NM_016430), a gene which is expressed in liver, skeletal muscle, heart, pancreas and testis. Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR5. The function of DSCR5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1720.Forkhead Box M1 (FOXM1, Accession NM_021953) is another VGAM2613 host target gene. FOXM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FOXM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXM1 BINDING SITE, designated SEQ ID:22483, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88165] Another function of VGAM2613 is therefore inhibition of Forkhead Box M1 (FOXM1, Accession NM_021953), a gene which may play a role in the control of cell proliferation. Accordingly, utilities of VGAM2613 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with FOXM1. The function of FOXM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM632.Optic Atrophy 1 (autosomal dominant) (OPA1, Accession NM_130837) is another VGAM2613 host target gene. OPA1 BINDING SITE1 through OPA1 BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OPA1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OPA1 BINDING SITE1 through OPA1 BINDING SITE5, designated SEQ ID:28352, SEQ ID:28320, SEQ ID:28336, SEQ ID:28344 and SEQ ID:28328 respectively, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88166] Another function of VGAM2613 is therefore inhibition of Optic Atrophy 1 (autosomal dominant) (OPA1, Accession NM_130837). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OPA1. Protocadherin Alpha

11 (PCDHA11, Accession NM_031861) is another VGAM2613 host target gene. PCDHA11 BINDING SITE1 and PCDHA11 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDHA11, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA11 BINDING SITE1 and PCDHA11 BINDING SITE2, designated SEQ ID:25621 and SEQ ID:11311 respectively, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88167] Another function of VGAM2613 is therefore inhibition of Protocadherin Alpha 11 (PCDHA11, Accession NM_031861). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA11. FLJ13657 (Accession NM_024828) is another VGAM2613 host target gene. FLJ13657 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13657, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of FLJ13657 BINDING SITE, designated SEQ ID:24220, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88168] Another function of VGAM2613 is therefore inhibition of FLJ13657 (Accession NM_024828). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13657. KIAA0753 (Accession NM_014804) is another VGAM2613 host target gene. KIAA0753 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0753, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0753 BINDING SITE, designated SEQ ID:16736, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88169] Another function of VGAM2613 is therefore inhibition of KIAA0753 (Accession NM_014804). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0753. MAIL (Accession NM_031419) is another

VGAM2613 host target gene. MAIL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAIL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAIL BINDING SITE, designated SEQ ID:25405, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88170] Another function of VGAM2613 is therefore inhibition of MAIL (Accession NM_031419). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAIL. Pellino Homolog 2 (Drosophila) (PELI2, Accession NM_021255) is another VGAM2613 host target gene. PELI2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PELI2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PELI2 BINDING SITE, designated SEQ ID:22232, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88171] Another function of VGAM2613 is therefore inhibition of Pellino Homolog 2 (Drosophila) (PELI2, Accession NM_021255). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PELI2. LOC130026 (Accession NM_138468) is another VGAM2613 host target gene. LOC130026 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130026 BINDING SITE, designated SEQ ID:28818, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88172] Another function of VGAM2613 is therefore inhibition of LOC130026 (Accession NM_138468). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130026. LOC200314 (Accession XM_117225) is another VGAM2613 host target gene. LOC200314 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200314, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200314 BINDING SITE, designated SEQ ID:43294, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88173] Another function of VGAM2613 is therefore inhibition of LOC200314 (Accession XM_117225). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200314. LOC55885 (Accession NM_018640) is another VGAM2613 host target gene. LOC55885 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC55885, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC55885 BINDING SITE, designated SEQ ID:20711, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88174] Another function of VGAM2613 is therefore inhibition of LOC55885 (Accession NM_018640). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC55885. LOC92465 (Accession XM_045250) is another VGAM2613 host target gene. LOC92465 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92465 BINDING SITE, designated SEQ ID:34394, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88175] Another function of VGAM2613 is therefore inhibition of LOC92465 (Accession XM_045250). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92465. LOC93259 (Accession XM_050105) is another VGAM2613 host target gene. LOC93259 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93259 BINDING SITE, designated SEQ ID:35559, to the

nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88176] Another function of VGAM2613 is therefore inhibition of LOC93259 (Accession XM_050105). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93259. LOC96597 (Accession XM_039922) is another VGAM2613 host target gene. LOC96597 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC96597, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC96597 BINDING SITE, designated SEQ ID:33228, to the nucleotide sequence of VGAM2613 RNA, herein designated VGAM RNA, also designated SEQ ID:5324.

[88177] Another function of VGAM2613 is therefore inhibition of LOC96597 (Accession XM_039922). Accordingly, utilities of VGAM2613 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC96597. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2614 (VGAM2614) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88178] VGAM2614 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2614 was detected is described hereinabove with reference to Figs. 1-8.

[88179] VGAM2614 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis B Virus. VGAM2614 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88180] VGAM2614 gene encodes a VGAM2614 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2614 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2614 precursor RNA is designated SEQ ID:2600, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2600 is located at position 6330 relative to the genome of Equine Rhinitis B Virus.

[88181] VGAM2614 precursor RNA folds onto itself, forming VGAM2614 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88182] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2614 folded precursor RNA into VGAM2614 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2614 RNA is designated SEQ ID:5325, and is provided hereinbelow with reference to the sequence listing part.

[88183] VGAM2614 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2614 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2614 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88184] VGAM2614 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2614 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2614 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88185] The complementary binding of VGAM2614 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2614 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2614 host target RNA into VGAM2614 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88186] It is appreciated that VGAM2614 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2614 host target genes. The mRNA of each one of this plurality of VGAM2614 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2614 RNA, herein designated VGAM RNA, and which when bound by VGAM2614 RNA causes inhibition of translation of respective one or more VGAM2614 host target proteins.

[88187] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2614 gene, herein designated VGAM GENE, on one or more VGAM2614 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88188] It is yet further appreciated that a function of VGAM2614 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2614 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis B Virus. Specific functions, and accordingly utilities, of VGAM2614 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2614 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88189] Nucleotide sequences of the VGAM2614 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2614 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2614 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2614 are further described hereinbelow with reference to Table 1.

[88190] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2614 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2614 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88191] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2614 gene, herein designated VGAM is inhibition of expression of VGAM2614 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2614 correlate with, and may be deduced from, the identity of the target genes which VGAM2614

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88192] EDR3 (Accession XM_172303) is a VGAM2614 host target gene. EDR3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EDR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EDR3 BINDING SITE, designated SEQ ID:46067, to the nucleotide sequence of VGAM2614 RNA, herein designated VGAM RNA, also designated SEQ ID:5325.

[88193] A function of VGAM2614 is therefore inhibition of EDR3 (Accession XM_172303). Accordingly, utilities of VGAM2614 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDR3. KIAA1393 (Accession XM_050793) is another VGAM2614 host target gene. KIAA1393 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:35685, to the nucleotide sequence of

VGAM2614 RNA, herein designated VGAM RNA, also designated SEQ ID:5325.

[88194] Another function of VGAM2614 is therefore inhibition of KIAA1393 (Accession XM_050793). Accordingly, utilities of VGAM2614 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2615 (VGAM2615) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88195] VGAM2615 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2615 was detected is described hereinabove with reference to Figs. 1-8.

[88196] VGAM2615 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis B Virus. VGAM2615 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88197] VGAM2615 gene encodes a VGAM2615 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2615 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2615 precursor RNA is designated SEQ ID:2601, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2601 is located at position 2100 relative to the genome of Equine Rhinitis B Virus.

[88198] VGAM2615 precursor RNA folds onto itself, forming VGAM2615 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88199] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2615 folded precursor RNA into VGAM2615 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2615 RNA is designated SEQ ID:5326, and is provided hereinbelow with reference to the sequence listing part.

[88200] VGAM2615 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2615 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88201] VGAM2615 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2615 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2615 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88202] The complementary binding of VGAM2615 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2615 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2615 host target RNA into VGAM2615 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88203] It is appreciated that VGAM2615 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2615 host target genes. The mRNA of each one of this plurality of VGAM2615 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2615 RNA, herein designated VGAM RNA, and which when bound by VGAM2615 RNA causes inhibition of translation of respective one or more VGAM2615 host target proteins.

[88204] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2615 gene, herein designated VGAM GENE, on one or more VGAM2615 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88205] It is yet further appreciated that a function of VGAM2615 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis B Virus. Specific functions, and accordingly utilities, of VGAM2615 correlate with, and may be deduced from, the identity of the host target genes which VGAM2615 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88206] Nucleotide sequences of the VGAM2615 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2615 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2615 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2615 are further described hereinbelow with reference to Table 1.

[88207] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2615 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2615 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88208] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2615 gene, herein designated VGAM is inhibition of expression of VGAM2615 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2615 correlate with, and may be deduced from, the identity of the target genes which VGAM2615 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88209] CD244 (Accession NM_016382) is a VGAM2615 host target gene. CD244 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD244, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD244 BINDING SITE, designated SEQ ID:18526, to the nucleotide sequence of VGAM2615 RNA, herein designated VGAM RNA, also designated SEQ ID:5326.

[88210] A function of VGAM2615 is therefore inhibition of CD244 (Accession NM_016382), a gene which can interfere with a

step as proximal as phosphorylation of an activation receptor. Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD244. The function of CD244 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1224.EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838) is another VGAM2615 host target gene. EGFL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGFL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGFL5 BINDING SITE, designated SEQ ID:41873, to the nucleotide sequence of VGAM2615 RNA, herein designated VGAM RNA, also designated SEQ ID:5326.

[88211] Another function of VGAM2615 is therefore inhibition of EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838). Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGFL5. FLJ11730 (Accession

NM_022756) is another VGAM2615 host target gene. FLJ11730 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11730, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11730 BINDING SITE, designated SEQ ID:22993, to the nucleotide sequence of VGAM2615 RNA, herein designated VGAM RNA, also designated SEQ ID:5326.

[88212] Another function of VGAM2615 is therefore inhibition of FLJ11730 (Accession NM_022756). Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11730. Golgi Autoantigen, Golgin Subfamily A, 1 (GOLGA1, Accession NM_002077) is another VGAM2615 host target gene. GOLGA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GOLGA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GOLGA1 BINDING SITE, designated SEQ ID:7856, to the nucleotide sequence of

VGAM2615 RNA, herein designated VGAM RNA, also designated SEQ ID:5326.

[88213] Another function of VGAM2615 is therefore inhibition of Golgi Autoantigen, Golgin Subfamily A, 1 (GOLGA1, Accession NM_002077). Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA1. KIAA0447 (Accession XM_049733) is another VGAM2615 host target gene. KIAA0447 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0447, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0447 BINDING SITE, designated SEQ ID:35494, to the nucleotide sequence of VGAM2615 RNA, herein designated VGAM RNA, also designated SEQ ID:5326.

[88214] Another function of VGAM2615 is therefore inhibition of KIAA0447 (Accession XM_049733). Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0447. ZAK (Accession NM_133646) is another VGAM2615 host target gene. ZAK BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by ZAK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZAK BINDING SITE, designated SEQ ID:28604, to the nucleotide sequence of VGAM2615 RNA, herein designated VGAM RNA, also designated SEQ ID:5326.

[88215] Another function of VGAM2615 is therefore inhibition of ZAK (Accession NM_133646). Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAK. LOC115110 (Accession XM_049825) is another VGAM2615 host target gene. LOC115110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115110 BINDING SITE, designated SEQ ID:35510, to the nucleotide sequence of VGAM2615 RNA, herein designated VGAM RNA, also designated SEQ ID:5326.

[88216] Another function of VGAM2615 is therefore inhibition of

LOC115110 (Accession XM_049825). Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115110. LOC197342 (Accession XM_113869) is another VGAM2615 host target gene. LOC197342 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197342, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197342 BINDING SITE, designated SEQ ID:42487, to the nucleotide sequence of VGAM2615 RNA, herein designated VGAM RNA, also designated SEQ ID:5326.

[88217] Another function of VGAM2615 is therefore inhibition of LOC197342 (Accession XM_113869). Accordingly, utilities of VGAM2615 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197342. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2616 (VGAM2616) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[88218] VGAM2616 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2616 was detected is described hereinabove with reference to Figs. 1-8.

[88219] VGAM2616 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis B Virus. VGAM2616 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88220] VGAM2616 gene encodes a VGAM2616 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2616 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2616 precursor RNA is designated SEQ ID:2602, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2602 is located at position 4799 relative to the genome of Equine Rhinitis B Virus.

[88221] VGAM2616 precursor RNA folds onto itself, forming VGAM2616 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88222] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2616 folded precursor RNA into VGAM2616 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2616 RNA is designated SEQ ID:5327, and is provided hereinbelow with reference to the sequence listing part.

[88223] VGAM2616 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2616 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88224] VGAM2616 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2616 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2616 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[88225] The complementary binding of VGAM2616 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2616 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2616 host target RNA into VGAM2616 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88226] It is appreciated that VGAM2616 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2616 host target genes. The mRNA of each one of this plurality of VGAM2616 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2616 RNA, herein designated VGAM RNA, and which when bound by VGAM2616 RNA causes inhibition of translation of respective one or more VGAM2616 host target proteins.

[88227] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2616 gene, herein designated VGAM GENE, on one

or more VGAM2616 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88228] It is yet further appreciated that a function of VGAM2616 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2616 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis B Virus. Specific functions, and accordingly utilities, of VGAM2616 correlate with, and may be deduced from, the identity of the host target genes which VGAM2616 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88229] Nucleotide sequences of the VGAM2616 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2616 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2616 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2616 are further described hereinbelow with reference to Table 1.

[88230] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2616 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2616 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88231] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2616 gene, herein designated VGAM is inhibition of expression of VGAM2616 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2616 correlate with, and may be deduced from, the identity of the target genes which VGAM2616 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88232] inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1, Acces-

sion NM_005536) is a VGAM2616 host target gene. IMPA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IMPA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IMPA1 BINDING SITE, designated SEQ ID:12059, to the nucleotide sequence of VGAM2616 RNA, herein designated VGAM RNA, also designated SEQ ID:5327.

[88233] A function of VGAM2616 is therefore inhibition of inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1, Accession NM_005536), a gene which is responsible for the provision of inositol required for synthesis of phosphatidylinositol and polyphosphoinositides. Accordingly, utilities of VGAM2616 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPA1. The function of IMPA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM134.PHD Finger Protein 3 (PHF3, Accession NM_015153) is another VGAM2616 host target gene. PHF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PHF3,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PHF3 BINDING SITE, designated SEQ ID:17511, to the nucleotide sequence of VGAM2616 RNA, herein designated VGAM RNA, also designated SEQ ID:5327.

[88234] Another function of VGAM2616 is therefore inhibition of PHD Finger Protein 3 (PHF3, Accession NM_015153). Accordingly, utilities of VGAM2616 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHF3. Testis-specific Transcript, Y-linked 9 (TTTY9, Accession NM_031927) is another VGAM2616 host target gene. TTTY9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TTTY9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTTY9 BINDING SITE, designated SEQ ID:25680, to the nucleotide sequence of VGAM2616 RNA, herein designated VGAM RNA, also designated SEQ ID:5327.

[88235] Another function of VGAM2616 is therefore inhibition of Testis-specific Transcript, Y-linked 9 (TTTY9, Accession

NM_031927). Accordingly, utilities of VGAM2616 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTTY9. LOC124801 (Accession XM_058850) is another VGAM2616 host target gene. LOC124801 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124801, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124801 BINDING SITE, designated SEQ ID:36764, to the nucleotide sequence of VGAM2616 RNA, herein designated VGAM RNA, also designated SEQ ID:5327.

[88236] Another function of VGAM2616 is therefore inhibition of LOC124801 (Accession XM_058850). Accordingly, utilities of VGAM2616 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124801. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2617 (VGAM2617) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[88237] VGAM2617 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2617 was detected is described hereinabove with reference to Figs. 1-8.

[88238] VGAM2617 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis B Virus. VGAM2617 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88239] VGAM2617 gene encodes a VGAM2617 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2617 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2617 precursor RNA is designated SEQ ID:2603, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2603 is located at position 8196 relative to the genome of Equine Rhinitis B Virus.

[88240] VGAM2617 precursor RNA folds onto itself, forming VGAM2617 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88241] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2617 folded precursor RNA into VGAM2617 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2617 RNA is designated SEQ ID:5328, and is provided hereinbelow with reference to the sequence listing part.

[88242] VGAM2617 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2617 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88243] VGAM2617 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2617 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2617 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[88244] The complementary binding of VGAM2617 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2617 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2617 host target RNA into VGAM2617 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88245] It is appreciated that VGAM2617 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2617 host target genes. The mRNA of each one of this plurality of VGAM2617 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2617 RNA, herein designated VGAM RNA, and which when bound by VGAM2617 RNA causes inhibition of translation of respective one or more VGAM2617 host target proteins.

[88246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2617 gene, herein designated VGAM GENE, on one

or more VGAM2617 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88247] It is yet further appreciated that a function of VGAM2617 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis B Virus. Specific functions, and accordingly utilities, of VGAM2617 correlate with, and may be deduced from, the identity of the host target genes which VGAM2617 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88248] Nucleotide sequences of the VGAM2617 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2617 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2617 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2617 are further described hereinbelow with reference to Table 1.

[88249] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2617 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2617 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88250] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2617 gene, herein designated VGAM is inhibition of expression of VGAM2617 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2617 correlate with, and may be deduced from, the identity of the target genes which VGAM2617 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88251] Clathrin, Heavy Polypeptide-like 1 (CLTCL1, Accession

XM_033096) is a VGAM2617 host target gene. CLTCL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLTCL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLTCL1 BINDING SITE, designated SEQ ID:31837, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88252] A function of VGAM2617 is therefore inhibition of Clathrin, Heavy Polypeptide-like 1 (CLTCL1, Accession XM_033096), a gene which is involved in vesicle budding. Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLTCL1. The function of CLTCL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM42.V-crk Sarcoma Virus CT10 Oncogene Homolog (avian)-like (CRKL, Accession NM_005207) is another VGAM2617 host target gene. CRKL BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CRKL, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRKL BINDING SITE, designated SEQ ID:11708, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88253] Another function of VGAM2617 is therefore inhibition of V-crk Sarcoma Virus CT10 Oncogene Homolog (avian)-like (CRKL, Accession NM_005207). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRKL. 24-dehydrocholesterol Reductase (DHCR24, Accession NM_014762) is another VGAM2617 host target gene. DHCR24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DHCR24 BINDING SITE, designated SEQ ID:16527, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88254] Another function of VGAM2617 is therefore inhibition of 24-dehydrocholesterol Reductase (DHCR24, Accession

NM_014762), a gene which catalyzes the reduction of sterol intermediates. Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHCR24. The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM235.Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193) is another VGAM2617 host target gene. FZD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:14490, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88255] Another function of VGAM2617 is therefore inhibition of Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled receptor family, has seven transmembrane domains. Accordingly, utilities of VGAM2617 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with FZD4. The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.SRY (sex determining region Y)-box 4 (SOX4, Accession NM_003107) is another VGAM2617 host target gene. SOX4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX4 BINDING SITE, designated SEQ ID:9077, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88256] Another function of VGAM2617 is therefore inhibition of SRY (sex determining region Y)-box 4 (SOX4, Accession NM_003107), a gene which binds with high affinity to the t-cell enhancer motif 5'-aacaaag-3' motif. Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX4. The function of SOX4 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM409.BDG-29 (Accession XM_051343) is another VGAM2617 host target gene. BDG-29 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BDG-29, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BDG-29 BINDING SITE, designated SEQ ID:35820, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88257] Another function of VGAM2617 is therefore inhibition of BDG-29 (Accession XM_051343). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDG-29. FLJ21687 (Accession NM_024859) is another VGAM2617 host target gene. FLJ21687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21687 BINDING SITE, designated SEQ ID:24291, to the nucleotide

sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88258] Another function of VGAM2617 is therefore inhibition of FLJ21687 (Accession NM_024859). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21687. poly(rC) Binding Protein 4 (PCBP4, Accession NM_020418) is another VGAM2617 host target gene. PCBP4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCBP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCBP4 BINDING SITE, designated SEQ ID:21678, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88259] Another function of VGAM2617 is therefore inhibition of poly(rC) Binding Protein 4 (PCBP4, Accession NM_020418). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCBP4. PIF1 (Accession XM_027898) is another VGAM2617 host target gene. PIF1 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIF1 BINDING SITE, designated SEQ ID:30588, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88260] Another function of VGAM2617 is therefore inhibition of PIF1 (Accession XM_027898). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIF1. SHARP (Accession NM_015001) is another VGAM2617 host target gene. SHARP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SHARP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHARP BINDING SITE, designated SEQ ID:17369, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88261] Another function of VGAM2617 is therefore inhibition of

SHARP (Accession NM_015001). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHARP. LOC123096 (Accession XM_058679) is another VGAM2617 host target gene. LOC123096 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC123096, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC123096 BINDING SITE, designated SEQ ID:36722, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88262] Another function of VGAM2617 is therefore inhibition of LOC123096 (Accession XM_058679). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC123096. LOC155438 (Accession XM_098722) is another VGAM2617 host target gene. LOC155438 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC155438 BINDING SITE, designated SEQ ID:41768, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88263] Another function of VGAM2617 is therefore inhibition of LOC155438 (Accession XM_098722). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155438. LOC220110 (Accession XM_167882) is another VGAM2617 host target gene. LOC220110 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220110 BINDING SITE, designated SEQ ID:44895, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88264] Another function of VGAM2617 is therefore inhibition of LOC220110 (Accession XM_167882). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220110. LOC254219 (Accession XM_172913) is an-

other VGAM2617 host target gene. LOC254219 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254219 BINDING SITE, designated SEQ ID:46174, to the nucleotide sequence of VGAM2617 RNA, herein designated VGAM RNA, also designated SEQ ID:5328.

[88265] Another function of VGAM2617 is therefore inhibition of LOC254219 (Accession XM_172913). Accordingly, utilities of VGAM2617 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254219. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2618 (VGAM2618) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88266] VGAM2618 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2618 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[88267] VGAM2618 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis B Virus. VGAM2618 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88268] VGAM2618 gene encodes a VGAM2618 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2618 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2618 precursor RNA is designated SEQ ID:2604, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2604 is located at position 6170 relative to the genome of Equine Rhinitis B Virus.

[88269] VGAM2618 precursor RNA folds onto itself, forming VGAM2618 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88270] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2618 folded precursor RNA into VGAM2618 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2618 RNA is designated SEQ ID:5329, and is provided hereinbelow with reference to the sequence listing part.

[88271] VGAM2618 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2618 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88272] VGAM2618 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2618 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2618 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2618 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88273] The complementary binding of VGAM2618 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2618 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2618 host target RNA into VGAM2618 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88274] It is appreciated that VGAM2618 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2618 host target genes. The mRNA of each one of this plurality of VGAM2618 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2618 RNA, herein designated VGAM RNA, and which when bound by VGAM2618 RNA causes inhibition of translation of respective one or more VGAM2618 host target proteins.

[88275] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2618 gene, herein designated VGAM GENE, on one or more VGAM2618 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88276] It is yet further appreciated that a function of VGAM2618 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis B Virus. Specific functions, and accordingly utilities, of VGAM2618 correlate with, and may be deduced from, the identity of the host target genes which VGAM2618 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88277] Nucleotide sequences of the VGAM2618 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2618 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2618 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2618 are further described hereinbelow with reference to Table 1.

[88278] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2618 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2618 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88279] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2618 gene, herein designated VGAM is inhibition of expression of VGAM2618 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2618 correlate with, and may be deduced from, the identity of the target genes which VGAM2618 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88280] Dehydrogenase/reductase (SDR family) Member 2 (DHRS2, Accession NM_005794) is a VGAM2618 host target gene. DHRS2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DHRS2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DHRS2 BINDING SITE, designated SEQ ID:12374, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88281] A function of VGAM2618 is therefore inhibition of Dehydrogenase/reductase (SDR family) Member 2 (DHRS2, Accession NM_005794). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHRS2. GREB1 (Accession XM_051545) is another VGAM2618 host target gene. GREB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GREB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE, designated SEQ ID:35852, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88282] Another function of VGAM2618 is therefore inhibition of GREB1 (Accession XM_051545). Accordingly, utilities of

VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GREB1. KIAA0286 (Accession XM_043118) is another VGAM2618 host target gene. KIAA0286 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0286 BINDING SITE, designated SEQ ID:33905, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88283] Another function of VGAM2618 is therefore inhibition of KIAA0286 (Accession XM_043118). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0286. KIAA0565 (Accession XM_039912) is another VGAM2618 host target gene. KIAA0565 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0565 BINDING SITE, designated SEQ ID:33217, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88284] Another function of VGAM2618 is therefore inhibition of KIAA0565 (Accession XM_039912). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0565. PRO1600 (Accession NM_014095) is another VGAM2618 host target gene. PRO1600 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO1600, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1600 BINDING SITE, designated SEQ ID:15314, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88285] Another function of VGAM2618 is therefore inhibition of PRO1600 (Accession NM_014095). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1600. LOC148824 (Accession XM_097527) is another VGAM2618 host target gene. LOC148824 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148824, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148824 BINDING SITE, designated SEQ ID:40908, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88286] Another function of VGAM2618 is therefore inhibition of LOC148824 (Accession XM_097527). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148824. LOC157292 (Accession XM_098740) is another VGAM2618 host target gene. LOC157292 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157292, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157292 BINDING SITE, designated SEQ ID:41775, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88287] Another function of VGAM2618 is therefore inhibition of

LOC157292 (Accession XM_098740). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157292. LOC157507 (Accession XM_088312) is another VGAM2618 host target gene. LOC157507 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157507, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157507 BINDING SITE, designated SEQ ID:39604, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88288] Another function of VGAM2618 is therefore inhibition of LOC157507 (Accession XM_088312). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157507. LOC201287 (Accession XM_113947) is another VGAM2618 host target gene. LOC201287 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201287, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC201287 BINDING SITE, designated SEQ ID:42560, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88289] Another function of VGAM2618 is therefore inhibition of LOC201287 (Accession XM_113947). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201287. LOC254082 (Accession XM_173165) is another VGAM2618 host target gene. LOC254082 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254082 BINDING SITE, designated SEQ ID:46421, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88290] Another function of VGAM2618 is therefore inhibition of LOC254082 (Accession XM_173165). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254082. LOC256207 (Accession XM_170837) is an-

other VGAM2618 host target gene. LOC256207 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256207, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256207 BINDING SITE, designated SEQ ID:45618, to the nucleotide sequence of VGAM2618 RNA, herein designated VGAM RNA, also designated SEQ ID:5329.

[88291] Another function of VGAM2618 is therefore inhibition of LOC256207 (Accession XM_170837). Accordingly, utilities of VGAM2618 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256207. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2619 (VGAM2619) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88292] VGAM2619 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2619 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[88293] VGAM2619 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Rhinitis B Virus. VGAM2619 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88294] VGAM2619 gene encodes a VGAM2619 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2619 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2619 precursor RNA is designated SEQ ID:2605, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2605 is located at position 4452 relative to the genome of Equine Rhinitis B Virus.

[88295] VGAM2619 precursor RNA folds onto itself, forming VGAM2619 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88296] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2619 folded precursor RNA into VGAM2619 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2619 RNA is designated SEQ ID:5330, and is provided hereinbelow with reference to the sequence listing part.

[88297] VGAM2619 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2619 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88298] VGAM2619 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2619 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2619 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2619 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88299] The complementary binding of VGAM2619 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2619 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2619 host target RNA into VGAM2619 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88300] It is appreciated that VGAM2619 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2619 host target genes. The mRNA of each one of this plurality of VGAM2619 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2619 RNA, herein designated VGAM RNA, and which when bound by VGAM2619 RNA causes inhibition of translation of respective one or more VGAM2619 host target proteins.

[88301] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2619 gene, herein designated VGAM GENE, on one or more VGAM2619 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88302] It is yet further appreciated that a function of VGAM2619 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2619 include diagnosis, prevention and treatment of viral infection by Equine Rhinitis B Virus. Specific functions, and accordingly utilities, of VGAM2619 correlate with, and may be deduced from, the identity of the host target genes which VGAM2619 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88303] Nucleotide sequences of the VGAM2619 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2619 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2619 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2619 are further described hereinbelow with reference to Table 1.

[88304] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2619 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2619 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88305] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2619 gene, herein designated VGAM is inhibition of expression of VGAM2619 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2619 correlate with, and may be deduced from, the identity of the target genes which VGAM2619 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88306] NKX3A (Accession NM_006167) is a VGAM2619 host target gene. NKX3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NKX3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of NKX3A BINDING SITE, designated SEQ ID:12825, to the nucleotide sequence of VGAM2619 RNA, herein designated VGAM RNA, also designated SEQ ID:5330.

[88307] A function of VGAM2619 is therefore inhibition of NKX3A (Accession NM_006167), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities of VGAM2619 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NKX3A. The function of NKX3A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM481.Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_133336) is another VGAM2619 host target gene. WHSC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by WHSC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:28478, to the nucleotide sequence of VGAM2619 RNA, herein designated VGAM RNA,

also designated SEQ ID:5330.

[88308] Another function of VGAM2619 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_133336), a gene which binds covalently to and repairs g/t mismatches. Accordingly, utilities of VGAM2619 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1. The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.DKFZP564K1964 (Accession NM_015544) is another VGAM2619 host target gene. DKFZP564K1964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564K1964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564K1964 BINDING SITE, designated SEQ ID:17805, to the nucleotide sequence of VGAM2619 RNA, herein designated VGAM RNA, also designated SEQ ID:5330.

[88309] Another function of VGAM2619 is therefore inhibition of DKFZP564K1964 (Accession NM_015544). Accordingly,

utilities of VGAM2619 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564K1964. P114-RHO-GEF (Accession NM_015318) is another VGAM2619 host target gene. P114-RHO-GEF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P114-RHO-GEF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P114-RHO-GEF BINDING SITE, designated SEQ ID:17636, to the nucleotide sequence of VGAM2619 RNA, herein designated VGAM RNA, also designated SEQ ID:5330.

[88310] Another function of VGAM2619 is therefore inhibition of P114-RHO-GEF (Accession NM_015318). Accordingly, utilities of VGAM2619 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P114-RHO-GEF. LOC221042 (Accession XM_167669) is another VGAM2619 host target gene. LOC221042 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of LOC221042 BINDING SITE, designated SEQ ID:44750, to the nucleotide sequence of VGAM2619 RNA, herein designated VGAM RNA, also designated SEQ ID:5330.

[88311] Another function of VGAM2619 is therefore inhibition of LOC221042 (Accession XM_167669). Accordingly, utilities of VGAM2619 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221042. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2620 (VGAM2620) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88312] VGAM2620 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2620 was detected is described hereinabove with reference to Figs. 1-8.

[88313] VGAM2620 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Enterovirus A (PEV8). VGAM2620 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88314] VGAM2620 gene encodes a VGAM2620 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2620 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2620 precursor RNA is designated SEQ ID:2606, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2606 is located at position 2601 relative to the genome of Porcine Enterovirus A (PEV8).

[88315] VGAM2620 precursor RNA folds onto itself, forming VGAM2620 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88316] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2620 folded precursor RNA into VGAM2620

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2620 RNA is designated SEQ ID:5331, and is provided hereinbelow with reference to the sequence listing part.

[88317] VGAM2620 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2620 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88318] VGAM2620 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2620 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2620 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88319] The complementary binding of VGAM2620 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2620 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2620 host target RNA into VGAM2620 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[88320] It is appreciated that VGAM2620 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2620 host target genes. The mRNA of each one of this plurality of VGAM2620 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2620 RNA, herein designated VGAM RNA, and which when bound by VGAM2620 RNA causes inhibition of translation of respective one or more VGAM2620 host target proteins.

[88321] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2620 gene, herein designated VGAM GENE, on one or more VGAM2620 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88322] It is yet further appreciated that a function of VGAM2620 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of viral infection by Porcine Enterovirus A (PEV8). Specific functions, and accordingly utilities, of VGAM2620 correlate with, and may be deduced from, the identity of the host target genes which VGAM2620 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88323] Nucleotide sequences of the VGAM2620 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2620 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2620 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2620 are further described hereinbelow with reference to Table 1.

[88324] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2620 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2620 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88325] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2620 gene, herein designated VGAM is inhibition of expression of VGAM2620 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2620 correlate with, and may be deduced from, the identity of the target genes which VGAM2620 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88326] CDC7 Cell Division Cycle 7-like 1 (S. cerevisiae) (CDC7L1, Accession NM_003503) is a VGAM2620 host target gene. CDC7L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDC7L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDC7L1 BINDING SITE, designated SEQ ID:9591, to the nucleotide sequence of VGAM2620 RNA,

herein designated VGAM RNA, also designated SEQ ID:5331.

[88327] A function of VGAM2620 is therefore inhibition of CDC7 Cell Division Cycle 7-like 1 (S. cerevisiae) (CDC7L1, Accession NM_003503), a gene which may phosphorylate critical substrates that regulate the G1/S phase transition and/or DNA replication in mammalian cells. Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC7L1. The function of CDC7L1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1431.Olfactomedin 1 (OLFM1, Accession NM_014279) is another VGAM2620 host target gene. OLFM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OLFM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OLFM1 BINDING SITE, designated SEQ ID:15557, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88328] Another function of VGAM2620 is therefore inhibition of Olfactomedin 1 (OLFM1, Accession NM_014279). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OLFM1. Phosphatidylinositol Glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA, Accession NM_002641) is another VGAM2620 host target gene. PIGA BINDING SITE1 through PIGA BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PIGA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIGA BINDING SITE1 through PIGA BINDING SITE3, designated SEQ ID:8498, SEQ ID:21711 and SEQ ID:21718 respectively, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88329] Another function of VGAM2620 is therefore inhibition of Phosphatidylinositol Glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA, Accession NM_002641). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGA. FLJ14621 (Accession NM_032811) is

another VGAM2620 host target gene. FLJ14621 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14621, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14621 BINDING SITE, designated SEQ ID:26582, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88330] Another function of VGAM2620 is therefore inhibition of FLJ14621 (Accession NM_032811). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14621. KIAA1033 (Accession XM_035313) is another VGAM2620 host target gene. KIAA1033 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1033, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1033 BINDING SITE, designated SEQ ID:32229, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88331] Another function of VGAM2620 is therefore inhibition of KIAA1033 (Accession XM_035313). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1033. KIAA1128 (Accession XM_043596) is another VGAM2620 host target gene. KIAA1128 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1128, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1128 BINDING SITE, designated SEQ ID:33967, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88332] Another function of VGAM2620 is therefore inhibition of KIAA1128 (Accession XM_043596). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1128. MGC5590 (Accession NM_024058) is another VGAM2620 host target gene. MGC5590 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC5590, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5590 BINDING SITE, designated SEQ ID:23495, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88333] Another function of VGAM2620 is therefore inhibition of MGC5590 (Accession NM_024058). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5590. Phosphodiesterase 10A (PDE10A, Accession NM_006661) is another VGAM2620 host target gene. PDE10A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE10A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE10A BINDING SITE, designated SEQ ID:13463, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88334] Another function of VGAM2620 is therefore inhibition of Phosphodiesterase 10A (PDE10A, Accession NM_006661). Accordingly, utilities of VGAM2620 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with PDE10A. Tripartite Motif-containing 2 (TRIM2, Accession NM_015271) is another VGAM2620 host target gene. TRIM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM2 BINDING SITE, designated SEQ ID:17597, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88335] Another function of VGAM2620 is therefore inhibition of Tripartite Motif-containing 2 (TRIM2, Accession NM_015271). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM2. LOC146159 (Accession XM_085344) is another VGAM2620 host target gene. LOC146159 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146159, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC146159 BINDING SITE, designated SEQ ID:38075, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88336] Another function of VGAM2620 is therefore inhibition of LOC146159 (Accession XM_085344). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146159. LOC152559 (Accession XM_087487) is another VGAM2620 host target gene. LOC152559 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152559, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152559 BINDING SITE, designated SEQ ID:39282, to the nucleotide sequence of VGAM2620 RNA, herein designated VGAM RNA, also designated SEQ ID:5331.

[88337] Another function of VGAM2620 is therefore inhibition of LOC152559 (Accession XM_087487). Accordingly, utilities of VGAM2620 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152559. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2621 (VGAM2621) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88338] VGAM2621 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2621 was detected is described hereinabove with reference to Figs. 1-8.

[88339] VGAM2621 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Enterovirus A (PEV8). VGAM2621 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88340] VGAM2621 gene encodes a VGAM2621 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2621 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2621 precursor RNA is designated SEQ ID:2607, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2607 is located at position 6168 relative to the genome of Porcine Enterovirus A (PEV8).

[88341] VGAM2621 precursor RNA folds onto itself, forming VGAM2621 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88342] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2621 folded precursor RNA into VGAM2621 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2621 RNA is designated SEQ ID:5332, and is provided hereinbelow with reference to the sequence listing part.

[88343] VGAM2621 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2621 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88344] VGAM2621 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2621 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2621 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2621 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88345] The complementary binding of VGAM2621 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2621 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2621 host target RNA into VGAM2621 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88346] It is appreciated that VGAM2621 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2621 host target genes. The mRNA of each one of this plurality of VGAM2621 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2621 RNA, herein designated VGAM RNA, and which when bound by VGAM2621 RNA causes inhibition of translation of respective one or more

VGAM2621 host target proteins.

[88347] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2621 gene, herein designated VGAM GENE, on one or more VGAM2621 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88348] It is yet further appreciated that a function of VGAM2621 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2621 include diagnosis, prevention and treatment of viral infection by Porcine Enterovirus A

(PEV8). Specific functions, and accordingly utilities, of VGAM2621 correlate with, and may be deduced from, the identity of the host target genes which VGAM2621 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88349] Nucleotide sequences of the VGAM2621 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2621 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2621 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2621 are further described hereinbelow with reference to Table 1.

[88350] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2621 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2621 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88351] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2621 gene, herein designated VGAM is inhibition of expression of VGAM2621 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2621 correlate with, and may be deduced from, the identity of the target genes which VGAM2621 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88352] KIAA0884 (Accession XM_046660) is a VGAM2621 host target gene. KIAA0884 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0884, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0884 BINDING SITE, designated SEQ ID:34770, to the nucleotide sequence of VGAM2621 RNA, herein designated VGAM RNA, also designated SEQ ID:5332.

[88353] A function of VGAM2621 is therefore inhibition of KIAA0884 (Accession XM_046660). Accordingly, utilities of VGAM2621 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0884. LOC130507 (Accession XM_059440) is another VGAM2621 host target gene. LOC130507 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130507, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130507 BINDING SITE, designated SEQ ID:36995, to the nucleotide sequence of VGAM2621 RNA, herein designated VGAM RNA, also designated SEQ ID:5332.

[88354] Another function of VGAM2621 is therefore inhibition of LOC130507 (Accession XM_059440). Accordingly, utilities of VGAM2621 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130507. LOC221710 (Accession XM_166471) is another VGAM2621 host target gene. LOC221710 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221710, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221710 BINDING SITE, designated SEQ ID:44395, to the nucleotide sequence of VGAM2621 RNA, herein designated VGAM RNA, also designated SEQ ID:5332.

[88355] Another function of VGAM2621 is therefore inhibition of LOC221710 (Accession XM_166471). Accordingly, utilities of VGAM2621 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221710. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2622 (VGAM2622) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88356] VGAM2622 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2622 was detected is described hereinabove with reference to Figs. 1-8.

[88357] VGAM2622 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Enterovirus A (PEV8). VGAM2622 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88358] VGAM2622 gene encodes a VGAM2622 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2622 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2622 precursor RNA is designated SEQ ID:2608, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2608 is located at position 3608 relative to the genome of Porcine Enterovirus A (PEV8).

[88359] VGAM2622 precursor RNA folds onto itself, forming VGAM2622 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88360] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2622 folded precursor RNA into VGAM2622 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2622 RNA is designated SEQ ID:5333, and is provided hereinbelow with reference to the sequence listing part.

[88361] VGAM2622 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2622 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88362] VGAM2622 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2622 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2622 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88363] The complementary binding of VGAM2622 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2622 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2622 host target RNA into VGAM2622 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88364] It is appreciated that VGAM2622 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2622 host target genes. The mRNA of each one of this plurality of VGAM2622 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2622 RNA, herein designated VGAM RNA, and which when bound by VGAM2622 RNA causes

inhibition of translation of respective one or more VGAM2622 host target proteins.

[88365] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2622 gene, herein designated VGAM GENE, on one or more VGAM2622 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88366] It is yet further appreciated that a function of VGAM2622 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2622 include diagnosis, prevention and

treatment of viral infection by Porcine Enterovirus A (PEV8). Specific functions, and accordingly utilities, of VGAM2622 correlate with, and may be deduced from, the identity of the host target genes which VGAM2622 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88367] Nucleotide sequences of the VGAM2622 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2622 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2622 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2622 are further described hereinbelow with reference to Table 1.

[88368] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2622 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2622 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88369] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2622 gene, herein designated VGAM is inhibition of expression of VGAM2622 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2622 correlate with, and may be deduced from, the identity of the target genes which VGAM2622 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88370] Secreted Protein, Acidic, Cysteine-rich (osteonectin) (SPARC, Accession NM_003118) is a VGAM2622 host target gene. SPARC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPARC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPARC BINDING SITE, designated SEQ ID:9088, to the nucleotide sequence of VGAM2622 RNA, herein designated VGAM RNA, also designated SEQ ID:5333.

[88371] A function of VGAM2622 is therefore inhibition of Secreted Protein, Acidic, Cysteine-rich (osteonectin) (SPARC, Accession NM_003118), a gene which .appears to regulate cell growth through interactions with the extracellular matrix and cytokines. binds calcium and copper, several types of collagen, albumin, thrombospondin, pdgf and cell membranes. Accordingly, utilities of VGAM2622 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SPARC. The function of SPARC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1652.FLJ12592 (Accession NM_032169) is another VGAM2622 host target gene. FLJ12592 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12592, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12592 BINDING SITE, designated SEQ ID:25873, to the nucleotide sequence of VGAM2622 RNA, herein designated VGAM RNA, also designated SEQ ID:5333.

[88372] Another function of VGAM2622 is therefore inhibition of FLJ12592 (Accession NM_032169). Accordingly, utilities of VGAM2622 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12592. FLJ25359 (Accession NM_144587) is another VGAM2622 host target gene. FLJ25359 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ25359, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ25359 BINDING SITE, designated SEQ ID:29407, to the nucleotide sequence of VGAM2622 RNA, herein designated VGAM RNA, also designated SEQ ID:5333.

[88373] Another function of VGAM2622 is therefore inhibition of FLJ25359 (Accession NM_144587). Accordingly, utilities of VGAM2622 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25359. KIAA1155 (Accession XM_030864) is another VGAM2622 host target gene. KIAA1155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE, designated SEQ ID:31199, to the nucleotide sequence of VGAM2622 RNA, herein designated VGAM RNA, also designated SEQ ID:5333.

[88374] Another function of VGAM2622 is therefore inhibition of KIAA1155 (Accession XM_030864). Accordingly, utilities of VGAM2622 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1155. MGC2474 (Accession NM_023931) is another VGAM2622 host target gene. MGC2474 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE, designated SEQ ID:23420, to the nucleotide sequence of VGAM2622 RNA, herein designated VGAM RNA, also designated SEQ ID:5333.

[88375] Another function of VGAM2622 is therefore inhibition of MGC2474 (Accession NM_023931). Accordingly, utilities of VGAM2622 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2474. Suppression of Tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13, Accession NM_003932) is another VGAM2622 host target gene. ST13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ST13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of ST13 BINDING SITE, designated SEQ ID:10034, to the nucleotide sequence of VGAM2622 RNA, herein designated VGAM RNA, also designated SEQ ID:5333.

[88376] Another function of VGAM2622 is therefore inhibition of Suppression of Tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13, Accession NM_003932). Accordingly, utilities of VGAM2622 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ST13. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2623 (VGAM2623) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88377] VGAM2623 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2623 was detected is described hereinabove with reference to Figs. 1-8.

[88378] VGAM2623 gene, herein designated VGAM GENE, is a viral gene contained in the genome of A-2 Plaque Virus. VGAM2623 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[88379] VGAM2623 gene encodes a VGAM2623 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2623 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2623 precursor RNA is designated SEQ ID:2609, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2609 is located at position 4786 relative to the genome of A-2 Plaque Virus.

[88380] VGAM2623 precursor RNA folds onto itself, forming VGAM2623 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88381] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2623 folded precursor RNA into VGAM2623 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2623 RNA is designated SEQ ID:5334, and is provided hereinbelow with reference to the sequence listing part.

[88382] VGAM2623 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2623 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88383] VGAM2623 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2623 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2623 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88384] The complementary binding of VGAM2623 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2623 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2623 host target RNA into VGAM2623 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88385] It is appreciated that VGAM2623 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2623 host target genes. The mRNA of each one of this plurality of VGAM2623 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2623 RNA, herein designated VGAM RNA, and which when bound by VGAM2623 RNA causes inhibition of translation of respective one or more VGAM2623 host target proteins.

[88386] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2623 gene, herein designated VGAM GENE, on one or more VGAM2623 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88387] It is yet further appreciated that a function of VGAM2623 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of viral infection by A-2 Plaque Virus. Specific functions, and accordingly utilities, of VGAM2623 correlate with, and may be deduced from, the identity of the host target genes which VGAM2623 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88388] Nucleotide sequences of the VGAM2623 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2623 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2623 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2623 are further described hereinbelow with reference to Table 1.

[88389] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2623 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2623 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88390] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2623 gene, herein designated VGAM is inhibition of expression of VGAM2623 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2623 correlate with, and may be deduced from, the identity of the target genes which VGAM2623 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88391] Chorionic Gonadotropin, Beta Polypeptide (CGB, Accession NM_000737) is a VGAM2623 host target gene. CGB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CGB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGB BINDING SITE, designated SEQ ID:6393, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88392] A function of VGAM2623 is therefore inhibition of Chorionic Gonadotropin, Beta Polypeptide (CGB, Accession NM_000737), a gene which stimulates the ovaries to synthesize the steroids. Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGB. The function of CGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.Guanine Nucleotide Binding Protein (G protein), Alpha Activating Activity Polypeptide O (GNAO1, Accession XM_165653) is another VGAM2623 host target gene. GNAO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNAO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNAO1 BINDING SITE, designated SEQ ID:43720, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88393] Another function of VGAM2623 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Alpha Ac-

tivating Activity Polypeptide O (GNAO1, Accession XM_165653), a gene which functions as modulators or transducers in various transmembrane signaling systems. Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNAO1. The function of GNAO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM665.Microfibrillar-associated Protein 3 (MFAP3, Accession NM_005927) is another VGAM2623 host target gene. MFAP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MFAP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MFAP3 BINDING SITE, designated SEQ ID:12554, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88394] Another function of VGAM2623 is therefore inhibition of Microfibrillar-associated Protein 3 (MFAP3, Accession NM_005927). Accordingly, utilities of VGAM2623 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with MFAP3. MAX Binding Protein (MNT, Accession NM_020310) is another VGAM2623 host target gene. MNT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MNT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MNT BINDING SITE, designated SEQ ID:21561, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88395] Another function of VGAM2623 is therefore inhibition of MAX Binding Protein (MNT, Accession NM_020310). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MNT. Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 5 (SLC9A5, Accession XM_007868) is another VGAM2623 host target gene. SLC9A5 BINDING SITE1 and SLC9A5 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC9A5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING

SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC9A5 BINDING SITE1 and SLC9A5 BINDING SITE2, designated SEQ ID:30063 and SEQ ID:10934 respectively, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88396] Another function of VGAM2623 is therefore inhibition of Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 5 (SLC9A5, Accession XM_007868). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC9A5. Thy-1 Cell Surface Antigen (THY1, Accession NM_006288) is another VGAM2623 host target gene. THY1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by THY1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of THY1 BINDING SITE, designated SEQ ID:12976, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88397] Another function of VGAM2623 is therefore inhibition of Thy-1 Cell Surface Antigen (THY1, Accession

NM_006288), a gene which plays a role in cell-cell or cell-ligand interactions during synaptogenesis. Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THY1. The function of THY1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM396.Calneuron 1 (CALN1, Accession NM_031468) is another VGAM2623 host target gene. CALN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CALN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CALN1 BINDING SITE, designated SEQ ID:25522, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88398] Another function of VGAM2623 is therefore inhibition of Calneuron 1 (CALN1, Accession NM_031468). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALN1. Cell Division Cycle Associated 4 (CDCA4, Ac-

cession NM_017955) is another VGAM2623 host target gene. CDCA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDCA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDCA4 BINDING SITE, designated SEQ ID:19660, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88399] Another function of VGAM2623 is therefore inhibition of Cell Division Cycle Associated 4 (CDCA4, Accession NM_017955). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDCA4. Chorionic Gonadotropin, Beta Polypeptide 5 (CGB5, Accession NM_033043) is another VGAM2623 host target gene. CGB5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CGB5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGB5 BINDING SITE, designated SEQ ID:26930,

to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88400] Another function of VGAM2623 is therefore inhibition of Chorionic Gonadotropin, Beta Polypeptide 5 (CGB5, Accession NM_033043). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGB5. Chorionic Gonadotropin, Beta Polypeptide 7 (CGB7, Accession NM_033142) is another VGAM2623 host target gene. CGB7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CGB7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGB7 BINDING SITE, designated SEQ ID:26994, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88401] Another function of VGAM2623 is therefore inhibition of Chorionic Gonadotropin, Beta Polypeptide 7 (CGB7, Accession NM_033142). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGB7. Chorionic Gonadotropin, Beta Polypeptide 8 (CGB8, Accession

NM_033183) is another VGAM2623 host target gene. CGB8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CGB8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGB8 BINDING SITE, designated SEQ ID:27045, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88402] Another function of VGAM2623 is therefore inhibition of Chorionic Gonadotropin, Beta Polypeptide 8 (CGB8, Accession NM_033183). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGB8. DKFZp762E1312 (Accession NM_018410) is another VGAM2623 host target gene. DKFZp762E1312 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp762E1312, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp762E1312 BINDING SITE, designated SEQ ID:20450, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM

RNA, also designated SEQ ID:5334.

[88403] Another function of VGAM2623 is therefore inhibition of DKFZp762E1312 (Accession NM_018410). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762E1312. FLJ12783 (Accession NM_031426) is another VGAM2623 host target gene. FLJ12783 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12783, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12783 BINDING SITE, designated SEQ ID:25417, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88404] Another function of VGAM2623 is therefore inhibition of FLJ12783 (Accession NM_031426). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12783. FLJ14437 (Accession NM_032578) is another VGAM2623 host target gene. FLJ14437 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14437, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14437 BINDING SITE, designated SEQ ID:26308, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88405] Another function of VGAM2623 is therefore inhibition of FLJ14437 (Accession NM_032578). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14437. FLJ14810 (Accession NM_032843) is another VGAM2623 host target gene. FLJ14810 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14810, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14810 BINDING SITE, designated SEQ ID:26634, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88406] Another function of VGAM2623 is therefore inhibition of FLJ14810 (Accession NM_032843). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ14810. FLJ20174 (Accession NM_017699) is another VGAM2623 host target gene. FLJ20174 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20174, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20174 BINDING SITE, designated SEQ ID:19268, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88407] Another function of VGAM2623 is therefore inhibition of FLJ20174 (Accession NM_017699). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20174. KIAA0449 (Accession NM_017596) is another VGAM2623 host target gene. KIAA0449 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0449, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0449 BINDING SITE, designated SEQ ID:19051, to the

nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88408] Another function of VGAM2623 is therefore inhibition of KIAA0449 (Accession NM_017596). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0449. KIAA0545 (Accession XM_032278) is another VGAM2623 host target gene. KIAA0545 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0545, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0545 BINDING SITE, designated SEQ ID:31635, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88409] Another function of VGAM2623 is therefore inhibition of KIAA0545 (Accession XM_032278). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0545. KIAA1010 (Accession XM_050742) is another VGAM2623 host target gene. KIAA1010 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1010 BINDING SITE, designated SEQ ID:35670, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88410] Another function of VGAM2623 is therefore inhibition of KIAA1010 (Accession XM_050742). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1010. KIAA1089 (Accession XM_044148) is another VGAM2623 host target gene. KIAA1089 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1089, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1089 BINDING SITE, designated SEQ ID:34140, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88411] Another function of VGAM2623 is therefore inhibition of KIAA1089 (Accession XM_044148). Accordingly, utilities

of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1089. KIAA1110 (Accession XM_029973) is another VGAM2623 host target gene. KIAA1110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1110 BINDING SITE, designated SEQ ID:30984, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88412] Another function of VGAM2623 is therefore inhibition of KIAA1110 (Accession XM_029973). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1110. KIAA1272 (Accession XM_046600) is another VGAM2623 host target gene. KIAA1272 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1272, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1272 BINDING SITE, designated SEQ ID:34761, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88413] Another function of VGAM2623 is therefore inhibition of KIAA1272 (Accession XM_046600). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1272. KIAA1855 (Accession XM_166453) is another VGAM2623 host target gene. KIAA1855 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1855, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1855 BINDING SITE, designated SEQ ID:44356, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88414] Another function of VGAM2623 is therefore inhibition of KIAA1855 (Accession XM_166453). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1855. MGC16279 (Accession XM_031808) is another VGAM2623 host target gene. MGC16279 BINDING SITE1

and MGC16279 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MGC16279, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16279 BINDING SITE1 and MGC16279 BINDING SITE2, designated SEQ ID:31488 and SEQ ID:26734 respectively, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88415] Another function of VGAM2623 is therefore inhibition of MGC16279 (Accession XM_031808). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16279. Myosin XVIIIB (MYO18B, Accession NM_032608) is another VGAM2623 host target gene. MYO18B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYO18B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYO18B BINDING SITE, designated SEQ ID:26331, to the nucleotide sequence of VGAM2623 RNA,

herein designated VGAM RNA, also designated SEQ ID:5334.

[88416] Another function of VGAM2623 is therefore inhibition of Myosin XVIIIB (MYO18B, Accession NM_032608). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO18B. PGS1 (Accession NM_024419) is another VGAM2623 host target gene. PGS1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PGS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PGS1 BINDING SITE, designated SEQ ID:23657, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88417] Another function of VGAM2623 is therefore inhibition of PGS1 (Accession NM_024419). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGS1. Ring Finger Protein 36 (RNF36, Accession NM_080745) is another VGAM2623 host target gene. RNF36 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by RNF36, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF36 BINDING SITE, designated SEQ ID:28032, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88418] Another function of VGAM2623 is therefore inhibition of Ring Finger Protein 36 (RNF36, Accession NM_080745). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF36. Transmembrane 4 Superfamily Member 11 (plasmolipin) (TM4SF11, Accession NM_015993) is another VGAM2623 host target gene. TM4SF11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TM4SF11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TM4SF11 BINDING SITE, designated SEQ ID:18084, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88419] Another function of VGAM2623 is therefore inhibition of Transmembrane 4 Superfamily Member 11 (plasmolipin) (TM4SF11, Accession NM_015993). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TM4SF11. LOC115129 (Accession XM_055292) is another VGAM2623 host target gene. LOC115129 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115129, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115129 BINDING SITE, designated SEQ ID:36252, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88420] Another function of VGAM2623 is therefore inhibition of LOC115129 (Accession XM_055292). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115129. LOC144114 (Accession XM_090198) is another VGAM2623 host target gene. LOC144114 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144114, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144114 BINDING SITE, designated SEQ ID:39993, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88421] Another function of VGAM2623 is therefore inhibition of LOC144114 (Accession XM_090198). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144114. LOC146184 (Accession XM_096942) is another VGAM2623 host target gene. LOC146184 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146184, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146184 BINDING SITE, designated SEQ ID:40661, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88422] Another function of VGAM2623 is therefore inhibition of LOC146184 (Accession XM_096942). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC146184. LOC158156 (Accession XM_088496) is another VGAM2623 host target gene. LOC158156 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158156, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158156 BINDING SITE, designated SEQ ID:39740, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88423] Another function of VGAM2623 is therefore inhibition of LOC158156 (Accession XM_088496). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158156. LOC196483 (Accession XM_016909) is another VGAM2623 host target gene. LOC196483 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196483, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196483 BINDING SITE, designated SEQ ID:30291, to

the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88424] Another function of VGAM2623 is therefore inhibition of LOC196483 (Accession XM_016909). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196483. LOC196955 (Accession XM_085210) is another VGAM2623 host target gene. LOC196955 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196955 BINDING SITE, designated SEQ ID:37933, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88425] Another function of VGAM2623 is therefore inhibition of LOC196955 (Accession XM_085210). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196955. LOC204970 (Accession XM_114795) is another VGAM2623 host target gene. LOC204970 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC204970, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC204970 BINDING SITE, designated SEQ ID:43068, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88426] Another function of VGAM2623 is therefore inhibition of LOC204970 (Accession XM_114795). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC204970. LOC220739 (Accession XM_167548) is another VGAM2623 host target gene. LOC220739 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220739 BINDING SITE, designated SEQ ID:44656, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88427] Another function of VGAM2623 is therefore inhibition of LOC220739 (Accession XM_167548). Accordingly, utilities

of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220739. LOC221466 (Accession XM_168087) is another VGAM2623 host target gene. LOC221466 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221466, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221466 BINDING SITE, designated SEQ ID:44992, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88428] Another function of VGAM2623 is therefore inhibition of LOC221466 (Accession XM_168087). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221466. LOC255974 (Accession XM_173706) is another VGAM2623 host target gene. LOC255974 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255974, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC255974 BINDING SITE, designated SEQ ID:46556, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88429] Another function of VGAM2623 is therefore inhibition of LOC255974 (Accession XM_173706). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255974. LOC51337 (Accession NM_016647) is another VGAM2623 host target gene. LOC51337 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51337 BINDING SITE, designated SEQ ID:18762, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88430] Another function of VGAM2623 is therefore inhibition of LOC51337 (Accession NM_016647). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51337. LOC90092 (Accession XM_028862) is another VGAM2623 host target gene. LOC90092 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90092 BINDING SITE, designated SEQ ID:30786, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88431] Another function of VGAM2623 is therefore inhibition of LOC90092 (Accession XM_028862). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90092. LOC96652 (Accession XM_037474) is another VGAM2623 host target gene. LOC96652 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC96652, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC96652 BINDING SITE, designated SEQ ID:32628, to the nucleotide sequence of VGAM2623 RNA, herein designated VGAM RNA, also designated SEQ ID:5334.

[88432] Another function of VGAM2623 is therefore inhibition of

LOC96652 (Accession XM_037474). Accordingly, utilities of VGAM2623 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC96652. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2624 (VGAM2624) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88433] VGAM2624 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2624 was detected is described hereinabove with reference to Figs. 1-8.

[88434] VGAM2624 gene, herein designated VGAM GENE, is a viral gene contained in the genome of A-2 Plaque Virus. VGAM2624 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88435] VGAM2624 gene encodes a VGAM2624 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2624 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2624 precursor RNA is designated SEQ ID:2610, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2610 is located at position 5482 relative to the genome of A-2 Plaque Virus.

[88436] VGAM2624 precursor RNA folds onto itself, forming VGAM2624 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88437] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2624 folded precursor RNA into VGAM2624 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide se-

quence of VGAM2624 RNA is designated SEQ ID:5335, and is provided hereinbelow with reference to the sequence listing part.

[88438] VGAM2624 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2624 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88439] VGAM2624 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2624 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2624 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88440] The complementary binding of VGAM2624 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2624 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2624 host target RNA into VGAM2624 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88441] It is appreciated that VGAM2624 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2624 host target genes. The mRNA of each one of this plurality of VGAM2624 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2624 RNA, herein designated VGAM RNA, and which when bound by VGAM2624 RNA causes inhibition of translation of respective one or more VGAM2624 host target proteins.

[88442] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2624 gene, herein designated VGAM GENE, on one or more VGAM2624 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88443] It is yet further appreciated that a function of VGAM2624

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2624 include diagnosis, prevention and treatment of viral infection by A-2 Plaque Virus. Specific functions, and accordingly utilities, of VGAM2624 correlate with, and may be deduced from, the identity of the host target genes which VGAM2624 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88444] Nucleotide sequences of the VGAM2624 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2624 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2624 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2624 are further described hereinbelow with reference to Table 1.

[88445] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2624 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2624 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88446] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2624 gene, herein designated VGAM is inhibition of expression of VGAM2624 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2624 correlate with, and may be deduced from, the identity of the target genes which VGAM2624 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88447] Platelet-derived Growth Factor Receptor, Beta Polypeptide (PDGFRB, Accession XM_038350) is a VGAM2624 host target gene. PDGFRB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDGFRB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFRB BINDING SITE, designated SEQ ID:32818, to the nucleotide sequence of VGAM2624 RNA, herein designated VGAM RNA, also designated SEQ ID:5335.

[88448] A function of VGAM2624 is therefore inhibition of Platelet-derived Growth Factor Receptor, Beta Polypeptide (PDGFRB, Accession XM_038350), a gene which Platelet-derived growth factor receptor beta chain; tyrosine kinase

receptor. Accordingly, utilities of VGAM2624 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFRB. The function of PDGFRB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.Ras Association (RalGDS/AF-6) Domain Family 1 (RASSF1, Accession NM_007182) is another VGAM2624 host target gene. RASSF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASSF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASSF1 BINDING SITE, designated SEQ ID:14039, to the nucleotide sequence of VGAM2624 RNA, herein designated VGAM RNA, also designated SEQ ID:5335.

[88449] Another function of VGAM2624 is therefore inhibition of Ras Association (RalGDS/AF-6) Domain Family 1 (RASSF1, Accession NM_007182), a gene which is a candidate renal tumor suppressor. Accordingly, utilities of VGAM2624 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF1. The function of

RASSF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.LOC157681 (Accession XM_088363) is another VGAM2624 host target gene. LOC157681 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157681, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157681 BINDING SITE, designated SEQ ID:39642, to the nucleotide sequence of VGAM2624 RNA, herein designated VGAM RNA, also designated SEQ ID:5335.

[88450] Another function of VGAM2624 is therefore inhibition of LOC157681 (Accession XM_088363). Accordingly, utilities of VGAM2624 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157681. LOC221431 (Accession XM_166380) is another VGAM2624 host target gene. LOC221431 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221431, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC221431 BINDING SITE, designated SEQ ID:44225, to the nucleotide sequence of VGAM2624 RNA, herein designated VGAM RNA, also designated SEQ ID:5335.

[88451] Another function of VGAM2624 is therefore inhibition of LOC221431 (Accession XM_166380). Accordingly, utilities of VGAM2624 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221431. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2625 (VGAM2625) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88452] VGAM2625 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2625 was detected is described hereinabove with reference to Figs. 1-8.

[88453] VGAM2625 gene, herein designated VGAM GENE, is a viral gene contained in the genome of A-2 Plaque Virus. VGAM2625 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[88454] VGAM2625 gene encodes a VGAM2625 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2625 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2625 precursor RNA is designated SEQ ID:2611, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2611 is located at position 6077 relative to the genome of A-2 Plaque Virus.

[88455] VGAM2625 precursor RNA folds onto itself, forming VGAM2625 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88456] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2625 folded precursor RNA into VGAM2625 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2625 RNA is designated SEQ ID:5336, and is provided hereinbelow with reference to the sequence listing part.

[88457] VGAM2625 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2625 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88458] VGAM2625 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2625 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2625 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88459] The complementary binding of VGAM2625 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2625 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2625 host target RNA into VGAM2625 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88460] It is appreciated that VGAM2625 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2625 host target genes. The mRNA of each one of this plurality of VGAM2625 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2625 RNA, herein designated VGAM RNA, and which when bound by VGAM2625 RNA causes inhibition of translation of respective one or more VGAM2625 host target proteins.

[88461] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2625 gene, herein designated VGAM GENE, on one or more VGAM2625 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88462] It is yet further appreciated that a function of VGAM2625 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2625 include diagnosis, prevention and treatment of viral infection by A-2 Plaque Virus. Specific functions, and accordingly utilities, of VGAM2625 correlate with, and may be deduced from, the identity of the host target genes which VGAM2625 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88463] Nucleotide sequences of the VGAM2625 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2625 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2625 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2625 are further described hereinbelow with reference to Table 1.

[88464] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2625 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2625 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88465] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2625 gene, herein designated VGAM is inhibition of expression of VGAM2625 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2625 correlate with, and may be deduced from, the identity of the target genes which VGAM2625 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88466] Potassium Voltage-gated Channel, Shaker-related Subfamily, Member 6 (KCNA6, Accession NM_002235) is a VGAM2625 host target gene. KCNA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNA6 BINDING SITE, designated SEQ ID:8015, to the nucleotide sequence of VGAM2625 RNA, herein designated VGAM RNA,

also designated SEQ ID:5336.

[88467] A function of VGAM2625 is therefore inhibition of Potassium Voltage-gated Channel, Shaker-related Subfamily, Member 6 (KCNA6, Accession NM_002235), a gene which mediates the voltage-dependent potassium ion permeability of excitable membranes. Accordingly, utilities of VGAM2625 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNA6. The function of KCNA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM893.LOC161823 (Accession XM_091156) is another VGAM2625 host target gene. LOC161823 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC161823, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161823 BINDING SITE, designated SEQ ID:40030, to the nucleotide sequence of VGAM2625 RNA, herein designated VGAM RNA, also designated SEQ ID:5336.

[88468] Another function of VGAM2625 is therefore inhibition of LOC161823 (Accession XM_091156). Accordingly, utilities

of VGAM2625 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161823. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2626 (VGAM2626) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88469] VGAM2626 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2626 was detected is described hereinabove with reference to Figs. 1-8.

[88470] VGAM2626 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian Encephalomyelitis Virus. VGAM2626 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88471] VGAM2626 gene encodes a VGAM2626 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2626 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2626 precursor RNA is designated SEQ ID:2612, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2612 is located at position 6595 relative to the genome of Avian Encephalomyelitis Virus.

[88472] VGAM2626 precursor RNA folds onto itself, forming VGAM2626 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88473] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2626 folded precursor RNA into VGAM2626 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2626 RNA is designated SEQ ID:5337, and

is provided hereinbelow with reference to the sequence listing part.

[88474] VGAM2626 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2626 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88475] VGAM2626 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2626 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2626 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88476] The complementary binding of VGAM2626 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2626 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2626 host target RNA into VGAM2626 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88477] It is appreciated that VGAM2626 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2626 host target genes. The mRNA of each one of this plurality of VGAM2626 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2626 RNA, herein designated VGAM RNA, and which when bound by VGAM2626 RNA causes inhibition of translation of respective one or more VGAM2626 host target proteins.

[88478] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2626 gene, herein designated VGAM GENE, on one or more VGAM2626 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88479] It is yet further appreciated that a function of VGAM2626 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of viral infection by Avian Encephalomyelitis Virus. Specific functions, and accordingly utilities, of VGAM2626 correlate with, and may be deduced from, the identity of the host target genes which VGAM2626 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88480] Nucleotide sequences of the VGAM2626 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2626 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2626 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2626 are further described hereinbelow with reference to Table 1.

[88481] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2626 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2626 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88482] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2626 gene, herein designated VGAM is inhibition of expression of VGAM2626 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2626 correlate with, and may be deduced from, the identity of the target genes which VGAM2626 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88483] Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 2 (KCNS2, Accession XM_043106) is a VGAM2626 host target gene. KCNS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNS2 BINDING SITE, designated SEQ ID:33899, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88484] A function of VGAM2626 is therefore inhibition of Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 2 (KCNS2, Accession XM_043106), a gene which mediates the voltage-dependent potassium ion permeability of excitable membranes. Accordingly, utili-

ties of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNS2. The function of KCNS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.Transient Receptor Potential Cation Channel, Subfamily M, Member 2 (TRPM2, Accession NM_003307) is another VGAM2626 host target gene. TRPM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPM2 BINDING SITE, designated SEQ ID:9311, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88485] Another function of VGAM2626 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily M, Member 2 (TRPM2, Accession NM_003307), a gene which may be a calcium channel. Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPM2.

The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1928.DKFZp434A1010 (Accession XM_049185) is another VGAM2626 host target gene. DKFZp434A1010 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DK-FZp434A1010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434A1010 BINDING SITE, designated SEQ ID:35345, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88486] Another function of VGAM2626 is therefore inhibition of DKFZp434A1010 (Accession XM_049185). Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434A1010. FLJ11383 (Accession NM_024938) is another VGAM2626 host target gene. FLJ11383 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11383, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11383 BINDING SITE, designated SEQ ID:24480, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88487] Another function of VGAM2626 is therefore inhibition of FLJ11383 (Accession NM_024938). Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11383. FLJ13102 (Accession NM_024887) is another VGAM2626 host target gene. FLJ13102 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13102, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13102 BINDING SITE, designated SEQ ID:24341, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88488] Another function of VGAM2626 is therefore inhibition of FLJ13102 (Accession NM_024887). Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13102. KIAA0286 (Accession XM_043118) is another VGAM2626 host target gene. KIAA0286 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0286 BINDING SITE, designated SEQ ID:33906, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88489] Another function of VGAM2626 is therefore inhibition of KIAA0286 (Accession XM_043118). Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0286. KIAA0737 (Accession NM_014828) is another VGAM2626 host target gene. KIAA0737 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0737, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0737 BINDING SITE, designated SEQ ID:16819, to the nucleotide sequence of VGAM2626 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5337.

[88490] Another function of VGAM2626 is therefore inhibition of KIAA0737 (Accession NM_014828). Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0737. MGC3020 (Accession NM_024048) is another VGAM2626 host target gene. MGC3020 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3020, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3020 BINDING SITE, designated SEQ ID:23482, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88491] Another function of VGAM2626 is therefore inhibition of MGC3020 (Accession NM_024048). Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3020. Protein Tyrosine Phosphatase Type IVA, Member 1 (PTP4A1, Accession NM_003463) is another VGAM2626 host target gene. PTP4A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by PTP4A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTP4A1 BINDING SITE, designated SEQ ID:9532, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88492] Another function of VGAM2626 is therefore inhibition of Protein Tyrosine Phosphatase Type IVA, Member 1 (PTP4A1, Accession NM_003463). Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTP4A1. LOC144519 (Accession XM_084890) is another VGAM2626 host target gene. LOC144519 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144519 BINDING SITE, designated SEQ ID:37758, to the nucleotide sequence of VGAM2626 RNA, herein designated VGAM RNA, also designated SEQ ID:5337.

[88493] Another function of VGAM2626 is therefore inhibition of

LOC144519 (Accession XM_084890). Accordingly, utilities of VGAM2626 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144519. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2627 (VGAM2627) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88494] VGAM2627 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2627 was detected is described hereinabove with reference to Figs. 1-8.

[88495] VGAM2627 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian Encephalomyelitis Virus. VGAM2627 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88496] VGAM2627 gene encodes a VGAM2627 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2627 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2627 precursor RNA is designated SEQ ID:2613, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2613 is located at position 5436 relative to the genome of Avian Encephalomyelitis Virus.

[88497] VGAM2627 precursor RNA folds onto itself, forming VGAM2627 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88498] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2627 folded precursor RNA into VGAM2627 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide se-

quence of VGAM2627 RNA is designated SEQ ID:5338, and is provided hereinbelow with reference to the sequence listing part.

[88499] VGAM2627 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2627 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88500] VGAM2627 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2627 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2627 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88501] The complementary binding of VGAM2627 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2627 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2627 host target RNA into VGAM2627 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88502] It is appreciated that VGAM2627 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2627 host target genes. The mRNA of each one of this plurality of VGAM2627 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2627 RNA, herein designated VGAM RNA, and which when bound by VGAM2627 RNA causes inhibition of translation of respective one or more VGAM2627 host target proteins.

[88503] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2627 gene, herein designated VGAM GENE, on one or more VGAM2627 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88504] It is yet further appreciated that a function of VGAM2627

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of viral infection by Avian Encephalomyelitis Virus. Specific functions, and accordingly utilities, of VGAM2627 correlate with, and may be deduced from, the identity of the host target genes which VGAM2627 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88505] Nucleotide sequences of the VGAM2627 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2627 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2627 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2627 are further described hereinbelow with reference to Table 1.

[88506] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2627 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2627 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88507] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2627 gene, herein designated VGAM is inhibition of expression of VGAM2627 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2627 correlate with, and may be deduced from, the identity of the target genes which VGAM2627 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88508] B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898) is a VGAM2627 host target gene. BCL11B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL11B BINDING SITE, designated SEQ ID:23166, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88509] A function of VGAM2627 is therefore inhibition of B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with BCL11B. Corticotropin Releasing Hormone Receptor 1 (CRHR1, Accession NM_004382) is another VGAM2627 host target gene. CRHR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRHR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRHR1 BINDING SITE, designated SEQ ID:10604, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88510] Another function of VGAM2627 is therefore inhibition of Corticotropin Releasing Hormone Receptor 1 (CRHR1, Accession NM_004382), a gene which likely mediates physiological and behavioral response to stress. Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRHR1. The function of CRHR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM435.Enoyl-Coenzyme A, Hydratase/3-hydroxyacyl Coenzyme A Dehydrogenase

(EHHADH, Accession NM_001966) is another VGAM2627 host target gene. EHHADH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EHHADH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EHHADH BINDING SITE, designated SEQ ID:7694, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88511] Another function of VGAM2627 is therefore inhibition of Enoyl-Coenzyme A, Hydratase/3-hydroxyacyl Coenzyme A Dehydrogenase (EHHADH, Accession NM_001966), a gene which functions in the peroxisomal beta-oxidation pathway. Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHHADH. The function of EHHADH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.F-box and WD-40 Domain Protein 1B (FBXW1B, Accession NM_012300) is another VGAM2627 host target gene. FBXW1B BINDING SITE1 through FBXW1B

BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FBXW1B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXW1B BINDING SITE1 through FBXW1B BINDING SITE3, designated SEQ ID:14663, SEQ ID:27365 and SEQ ID:27375 respectively, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88512] Another function of VGAM2627 is therefore inhibition of F-box and WD-40 Domain Protein 1B (FBXW1B, Accession NM_012300), a gene which somehow is involved in the process of neuronal cell differentiation or brain development. Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW1B. The function of FBXW1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.Muscleblind-like (Drosophila) (MBNL, Accession NM_021038) is another VGAM2627 host target gene. MBNL BINDING SITE is HOST TARGET binding site found in

the 5` untranslated region of mRNA encoded by MBNL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MBNL BINDING SITE, designated SEQ ID:22023, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88513] Another function of VGAM2627 is therefore inhibition of Muscleblind-like (Drosophila) (MBNL, Accession NM_021038), a gene which binds to cug triplet repeat expansion dsrna (by similarity). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBNL. The function of MBNL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.Phosphorylase Kinase, Alpha 2 (liver) (PHKA2, Accession NM_000292) is another VGAM2627 host target gene. PHKA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PHKA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of PHKA2 BINDING SITE, designated SEQ ID:5834, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88514] Another function of VGAM2627 is therefore inhibition of Phosphorylase Kinase, Alpha 2 (liver) (PHKA2, Accession NM_000292). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHKA2. Protein Tyrosine Phosphatase, Receptor Type, O (PTPRO, Accession NM_002848) is another VGAM2627 host target gene. PTPRO BINDING SITE1 through PTPRO BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPRO, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRO BINDING SITE1 through PTPRO BINDING SITE5, designated SEQ ID:8741, SEQ ID:25034, SEQ ID:25006, SEQ ID:25014 and SEQ ID:25023 respectively, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88515] Another function of VGAM2627 is therefore inhibition of

Protein Tyrosine Phosphatase, Receptor Type, O (PTPRO, Accession NM_002848), a gene which may function as a cell contact receptor that mediates and controls cell-cell signals. Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRO. The function of PTPRO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM140.Transmembrane 4 Superfamily Member 6 (TM4SF6, Accession NM_003270) is another VGAM2627 host target gene. TM4SF6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TM4SF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TM4SF6 BINDING SITE, designated SEQ ID:9285, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88516] Another function of VGAM2627 is therefore inhibition of Transmembrane 4 Superfamily Member 6 (TM4SF6, Accession NM_003270), a gene which plays a role in the

regulation of cell development, activation, growth and motility. Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TM4SF6. The function of TM4SF6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM84.DKFZP564K0822 (Accession XM_168378) is another VGAM2627 host target gene. DKFZP564K0822 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564K0822, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564K0822 BINDING SITE, designated SEQ ID:45139, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88517] Another function of VGAM2627 is therefore inhibition of DKFZP564K0822 (Accession XM_168378). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564K0822. FLJ10856 (Accession NM_018247)

is another VGAM2627 host target gene. FLJ10856 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10856 BINDING SITE, designated SEQ ID:20217, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88518] Another function of VGAM2627 is therefore inhibition of FLJ10856 (Accession NM_018247). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10856. KIAA0087 (Accession NM_014769) is another VGAM2627 host target gene. KIAA0087 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0087, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0087 BINDING SITE, designated SEQ ID:16559, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88519] Another function of VGAM2627 is therefore inhibition of KIAA0087 (Accession NM_014769). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0087. KIAA0461 (Accession XM_047883) is another VGAM2627 host target gene. KIAA0461 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0461, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0461 BINDING SITE, designated SEQ ID:35070, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88520] Another function of VGAM2627 is therefore inhibition of KIAA0461 (Accession XM_047883). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0461. KIAA1319 (Accession NM_020770) is another VGAM2627 host target gene. KIAA1319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1319, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1319 BINDING SITE, designated SEQ ID:21868, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88521] Another function of VGAM2627 is therefore inhibition of KIAA1319 (Accession NM_020770). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1319. KIAA1954 (Accession XM_085375) is another VGAM2627 host target gene. KIAA1954 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1954, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1954 BINDING SITE, designated SEQ ID:38092, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88522] Another function of VGAM2627 is therefore inhibition of KIAA1954 (Accession XM_085375). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1954. Protein Tyrosine Phosphatase, Receptor Type, N Polypeptide 2 (PTPRN2, Accession NM_130842) is another VGAM2627 host target gene. PTPRN2 BINDING SITE1 and PTPRN2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPRN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRN2 BINDING SITE1 and PTPRN2 BINDING SITE2, designated SEQ ID:28369 and SEQ ID:28374 respectively, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88523] Another function of VGAM2627 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, N Polypeptide 2 (PTPRN2, Accession NM_130842). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRN2. SCAMP5 (Accession NM_138967) is another VGAM2627 host target gene. SCAMP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAMP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAMP5 BINDING SITE, designated SEQ ID:29071, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88524] Another function of VGAM2627 is therefore inhibition of SCAMP5 (Accession NM_138967). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP5. ZNF-U69274 (Accession NM_014415) is another VGAM2627 host target gene. ZNF-U69274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF-U69274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF-U69274 BINDING SITE, designated SEQ ID:15760, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88525] Another function of VGAM2627 is therefore inhibition of ZNF-U69274 (Accession NM_014415). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with ZNF-U69274. Zinc Finger Protein 304 (ZNF304, Accession NM_020657) is another VGAM2627 host target gene. ZNF304 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF304, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF304 BINDING SITE, designated SEQ ID:21830, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88526] Another function of VGAM2627 is therefore inhibition of Zinc Finger Protein 304 (ZNF304, Accession NM_020657). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF304. LOC120856 (Accession XM_058509) is another VGAM2627 host target gene. LOC120856 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120856 BINDING SITE, desig-

nated SEQ ID:36639, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88527] Another function of VGAM2627 is therefore inhibition of LOC120856 (Accession XM_058509). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120856. LOC128844 (Accession XM_066199) is another VGAM2627 host target gene. LOC128844 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC128844, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128844 BINDING SITE, designated SEQ ID:37319, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88528] Another function of VGAM2627 is therefore inhibition of LOC128844 (Accession XM_066199). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128844. LOC161734 (Accession XM_102109) is another VGAM2627 host target gene. LOC161734 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC161734, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161734 BINDING SITE, designated SEQ ID:42109, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88529] Another function of VGAM2627 is therefore inhibition of LOC161734 (Accession XM_102109). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161734. LOC219445 (Accession XM_166212) is another VGAM2627 host target gene. LOC219445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219445 BINDING SITE, designated SEQ ID:44012, to the nucleotide sequence of VGAM2627 RNA, herein designated VGAM RNA, also designated SEQ ID:5338.

[88530] Another function of VGAM2627 is therefore inhibition of

LOC219445 (Accession XM_166212). Accordingly, utilities of VGAM2627 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219445. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2628 (VGAM2628) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88531] VGAM2628 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2628 was detected is described hereinabove with reference to Figs. 1-8.

[88532] VGAM2628 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian Encephalomyelitis Virus. VGAM2628 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88533] VGAM2628 gene encodes a VGAM2628 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2628 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2628 precursor RNA is designated SEQ ID:2614, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2614 is located at position 4961 relative to the genome of Avian Encephalomyelitis Virus.

[88534] VGAM2628 precursor RNA folds onto itself, forming VGAM2628 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88535] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2628 folded precursor RNA into VGAM2628 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM2628 RNA is designated SEQ ID:5339, and is provided hereinbelow with reference to the sequence listing part.

[88536] VGAM2628 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2628 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88537] VGAM2628 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2628 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2628 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88538] The complementary binding of VGAM2628 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2628 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2628 host target RNA into VGAM2628 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88539] It is appreciated that VGAM2628 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2628 host target genes. The mRNA of each one of this plurality of VGAM2628 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2628 RNA, herein designated VGAM RNA, and which when bound by VGAM2628 RNA causes inhibition of translation of respective one or more VGAM2628 host target proteins.

[88540] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2628 gene, herein designated VGAM GENE, on one or more VGAM2628 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88541] It is yet further appreciated that a function of VGAM2628

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of viral infection by Avian Encephalomyelitis Virus. Specific functions, and accordingly utilities, of VGAM2628 correlate with, and may be deduced from, the identity of the host target genes which VGAM2628 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88542] Nucleotide sequences of the VGAM2628 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2628 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2628 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2628 are further described hereinbelow with reference to Table 1.

[88543] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2628 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2628 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88544] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2628 gene, herein designated VGAM is inhibition of expression of VGAM2628 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2628 correlate with, and may be deduced from, the identity of the target genes which VGAM2628 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88545] Amiloride Binding Protein 1 (amine oxidase (copper-containing)) (ABP1, Accession XM_032220) is a VGAM2628 host target gene. ABP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABP1 BINDING SITE, designated SEQ ID:31614, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88546] A function of VGAM2628 is therefore inhibition of Amiloride Binding Protein 1 (amine oxidase (copper-containing)) (ABP1, Accession XM_032220), a gene which catalyzes the degradation of compounds such

as putrescine. Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABP1. The function of ABP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.A Kinase (PRKA) Anchor Protein 2 (AKAP2, Accession NM_007203) is another VGAM2628 host target gene. AKAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP2 BINDING SITE, designated SEQ ID:14059, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88547] Another function of VGAM2628 is therefore inhibition of A Kinase (PRKA) Anchor Protein 2 (AKAP2, Accession NM_007203), a gene which binds to regulatory subunit (rii) of protein kinase a. Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP2.

The function of AKAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM18.Centrin, EF-hand Protein, 1 (CETN1, Accession XM_170866) is another VGAM2628 host target gene. CETN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CETN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CETN1 BINDING SITE, designated SEQ ID:45638, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88548] Another function of VGAM2628 is therefore inhibition of Centrin, EF-hand Protein, 1 (CETN1, Accession XM_170866). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CETN1. Erythrocyte Membrane Protein Band 4.1 (elliptocytosis 1, RH-linked) (EPB41, Accession NM_004437) is another VGAM2628 host target gene. EPB41 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by EPB41, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPB41 BINDING SITE, designated SEQ ID:10721, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88549] Another function of VGAM2628 is therefore inhibition of Erythrocyte Membrane Protein Band 4.1 (elliptocytosis 1, RH-linked) (EPB41, Accession NM_004437), a gene which protein 4.1 is a major structural element of the erythrocyte membrane skeleton. it plays a key role in regulating membrane physical properties of mechanical stability and deformability by stabilizing spectrin-actin interaction. binds with a high affinity to glycophorin and with lower affinity to band iii protein. associates with the nuclear mitotic apparatus. Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB41. The function of EPB41 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1709.Follistatin-like 1 (FSTL1, Accession

NM_007085) is another VGAM2628 host target gene. FSTL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FSTL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FSTL1 BINDING SITE, designated SEQ ID:13948, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88550] Another function of VGAM2628 is therefore inhibition of Follistatin-like 1 (FSTL1, Accession NM_007085), a gene which may modulate the action of some growth factors on cell proliferation and differentiation. Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FSTL1. The function of FSTL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM791.Glutamate Receptor, Metabotropic 4 (GRM4, Accession NM_000841) is another VGAM2628 host target gene. GRM4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRM4, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRM4 BINDING SITE, designated SEQ ID:6502, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88551] Another function of VGAM2628 is therefore inhibition of Glutamate Receptor, Metabotropic 4 (GRM4, Accession NM_000841), a gene which is mediated by a g-protein that inhibits adenylate cyclase activity. Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM4. The function of GRM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1052.Methyltransferase-like 1 (METTL1, Accession NM_023032) is another VGAM2628 host target gene. METTL1 BINDING SITE1 and METTL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by METTL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

METTL1 BINDING SITE1 and METTL1 BINDING SITE2, designated SEQ ID:23305 and SEQ ID:23310 respectively, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88552] Another function of VGAM2628 is therefore inhibition of Methyltransferase-like 1 (METTL1, Accession NM_023032). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with METTL1. Neuroligin 1 (NLGN1, Accession NM_014932) is another VGAM2628 host target gene. NLGN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NLGN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NLGN1 BINDING SITE, designated SEQ ID:17229, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88553] Another function of VGAM2628 is therefore inhibition of Neuroligin 1 (NLGN1, Accession NM_014932), a gene which may trigger the de novo formation of presynaptic structure. Accordingly, utilities of VGAM2628 include di-

agnosis, prevention and treatment of diseases and clinical conditions associated with NLGN1. The function of NLGN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM659.5'-nucleotidase, Cytosolic II (NT5C2, Accession NM_012229) is another VGAM2628 host target gene. NT5C2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NT5C2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NT5C2 BINDING SITE, designated SEQ ID:14526, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88554] Another function of VGAM2628 is therefore inhibition of 5'-nucleotidase, Cytosolic II (NT5C2, Accession NM_012229). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NT5C2. Proprotein Convertase Subtilisin/kexin Type 2 (PCSK2, Accession NM_002594) is another VGAM2628 host target gene.

PCSK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCSK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCSK2 BINDING SITE, designated SEQ ID:8453, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88555] Another function of VGAM2628 is therefore inhibition of Proprotein Convertase Subtilisin/kexin Type 2 (PCSK2, Accession NM_002594), a gene which is involved in the processing of hormone and other protein precursors at sites comprised of pairs of basic amino acid residues. Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK2. The function of PCSK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1120.BHC80 (Accession NM_016621) is another VGAM2628 host target gene. BHC80 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BHC80, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BHC80 BINDING SITE, designated SEQ ID:18728, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88556] Another function of VGAM2628 is therefore inhibition of BHC80 (Accession NM_016621). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHC80. Baculoviral IAP Repeat-containing 3 (BIRC3, Accession XM_040715) is another VGAM2628 host target gene. BIRC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIRC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIRC3 BINDING SITE, designated SEQ ID:33368, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88557] Another function of VGAM2628 is therefore inhibition of Baculoviral IAP Repeat-containing 3 (BIRC3, Accession XM_040715). Accordingly, utilities of VGAM2628 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC3. Chromosome 20 Open Reading Frame 121 (C20orf121, Accession NM_024331) is another VGAM2628 host target gene. C20orf121 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf121 BINDING SITE, designated SEQ ID:23629, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88558] Another function of VGAM2628 is therefore inhibition of Chromosome 20 Open Reading Frame 121 (C20orf121, Accession NM_024331). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf121. CASPR3 (Accession NM_033655) is another VGAM2628 host target gene. CASPR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CASPR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASPR3 BINDING SITE, designated SEQ ID:27385, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88559] Another function of VGAM2628 is therefore inhibition of CASPR3 (Accession NM_033655). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASPR3. Calsyntenin 2 (CLSTN2, Accession NM_022131) is another VGAM2628 host target gene. CLSTN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLSTN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLSTN2 BINDING SITE, designated SEQ ID:22691, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88560] Another function of VGAM2628 is therefore inhibition of Calsyntenin 2 (CLSTN2, Accession NM_022131). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with CLSTN2. CRIPT (Accession XM_057669) is another VGAM2628 host target gene. CRIPT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRIPT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRIPT BINDING SITE, designated SEQ ID:36537, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88561] Another function of VGAM2628 is therefore inhibition of CRIPT (Accession XM_057669). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRIPT. DnaJ (Hsp40) Homolog, Subfamily C, Member 6 (DNAJC6, Accession NM_014787) is another VGAM2628 host target gene. DNAJC6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNAJC6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNAJC6 BINDING SITE, designated SEQ ID:16657, to the nucleotide sequence of VGAM2628 RNA,

herein designated VGAM RNA, also designated SEQ ID:5339.

[88562] Another function of VGAM2628 is therefore inhibition of DnaJ (Hsp40) Homolog, Subfamily C, Member 6 (DNAJC6, Accession NM_014787). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJC6. FLJ10392 (Accession NM_018084) is another VGAM2628 host target gene. FLJ10392 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10392, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10392 BINDING SITE, designated SEQ ID:19845, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88563] Another function of VGAM2628 is therefore inhibition of FLJ10392 (Accession NM_018084). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10392. FLJ20552 (Accession NM_017876) is another VGAM2628 host target gene. FLJ20552 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20552, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20552 BINDING SITE, designated SEQ ID:19547, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88564] Another function of VGAM2628 is therefore inhibition of FLJ20552 (Accession NM_017876). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20552. FLJ21195 (Accession NM_022469) is another VGAM2628 host target gene. FLJ21195 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21195 BINDING SITE, designated SEQ ID:22823, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88565] Another function of VGAM2628 is therefore inhibition of

FLJ21195 (Accession NM_022469). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21195. KIAA1950 (Accession XM_166532) is another VGAM2628 host target gene. KIAA1950 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1950, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1950 BINDING SITE, designated SEQ ID:44485, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88566] Another function of VGAM2628 is therefore inhibition of KIAA1950 (Accession XM_166532). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1950. KR18 (Accession NM_033288) is another VGAM2628 host target gene. KR18 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KR18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of KR18 BINDING SITE, designated SEQ ID:27115, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88567] Another function of VGAM2628 is therefore inhibition of KR18 (Accession NM_033288). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KR18. Lysosomal-associated Membrane Protein 3 (LAMP3, Accession XM_003022) is another VGAM2628 host target gene. LAMP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LAMP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:29915, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88568] Another function of VGAM2628 is therefore inhibition of Lysosomal-associated Membrane Protein 3 (LAMP3, Accession XM_003022). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with LAMP3. RER1 (Accession NM_007033) is another VGAM2628 host target gene. RER1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RER1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RER1 BINDING SITE, designated SEQ ID:13902, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88569] Another function of VGAM2628 is therefore inhibition of RER1 (Accession NM_007033). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RER1. SCYA28 (Accession NM_019846) is another VGAM2628 host target gene. SCYA28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCYA28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCYA28 BINDING SITE, designated SEQ ID:21249, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5339.

[88570] Another function of VGAM2628 is therefore inhibition of SCYA28 (Accession NM_019846). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYA28. Serine Threonine Kinase 39 (STE20/SPS1 homolog, yeast) (STK39, Accession NM_013233) is another VGAM2628 host target gene. STK39 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STK39, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK39 BINDING SITE, designated SEQ ID:14892, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88571] Another function of VGAM2628 is therefore inhibition of Serine Threonine Kinase 39 (STE20/SPS1 homolog, yeast) (STK39, Accession NM_013233). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK39. Tyrosine Kinase, Non-receptor, 1 (TNK1, Accession NM_003985) is another VGAM2628 host target gene.

TNK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNK1 BINDING SITE, designated SEQ ID:10134, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88572] Another function of VGAM2628 is therefore inhibition of Tyrosine Kinase, Non-receptor, 1 (TNK1, Accession NM_003985). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNK1. LOC132880 (Accession XM_059609) is another VGAM2628 host target gene. LOC132880 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132880, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132880 BINDING SITE, designated SEQ ID:37029, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88573] Another function of VGAM2628 is therefore inhibition of LOC132880 (Accession XM_059609). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132880. LOC147138 (Accession XM_085717) is another VGAM2628 host target gene. LOC147138 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147138, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147138 BINDING SITE, designated SEQ ID:38307, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88574] Another function of VGAM2628 is therefore inhibition of LOC147138 (Accession XM_085717). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147138. LOC147727 (Accession XM_085862) is another VGAM2628 host target gene. LOC147727 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147727, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147727 BINDING SITE, designated SEQ ID:38380, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88575] Another function of VGAM2628 is therefore inhibition of LOC147727 (Accession XM_085862). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147727. LOC155081 (Accession XM_088145) is another VGAM2628 host target gene. LOC155081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155081 BINDING SITE, designated SEQ ID:39542, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88576] Another function of VGAM2628 is therefore inhibition of LOC155081 (Accession XM_088145). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC155081. LOC201245 (Accession XM_113326) is another VGAM2628 host target gene. LOC201245 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201245, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201245 BINDING SITE, designated SEQ ID:42228, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88577] Another function of VGAM2628 is therefore inhibition of LOC201245 (Accession XM_113326). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201245. LOC202802 (Accession XM_114560) is another VGAM2628 host target gene. LOC202802 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202802, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202802 BINDING SITE, designated SEQ ID:42987, to the nucleotide sequence of VGAM2628 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5339.

[88578] Another function of VGAM2628 is therefore inhibition of LOC202802 (Accession XM_114560). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202802. LOC222228 (Accession XM_168627) is another VGAM2628 host target gene. LOC222228 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222228 BINDING SITE, designated SEQ ID:45273, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88579] Another function of VGAM2628 is therefore inhibition of LOC222228 (Accession XM_168627). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222228. LOC222233 (Accession XM_168560) is another VGAM2628 host target gene. LOC222233 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222233, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222233 BINDING SITE, designated SEQ ID:45242, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88580] Another function of VGAM2628 is therefore inhibition of LOC222233 (Accession XM_168560). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222233. LOC57406 (Accession NM_020676) is another VGAM2628 host target gene. LOC57406 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57406, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57406 BINDING SITE, designated SEQ ID:21837, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88581] Another function of VGAM2628 is therefore inhibition of LOC57406 (Accession NM_020676). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC57406. LOC92568 (Accession XM_045852) is another VGAM2628 host target gene. LOC92568 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92568, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92568 BINDING SITE, designated SEQ ID:34575, to the nucleotide sequence of VGAM2628 RNA, herein designated VGAM RNA, also designated SEQ ID:5339.

[88582] Another function of VGAM2628 is therefore inhibition of LOC92568 (Accession XM_045852). Accordingly, utilities of VGAM2628 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92568. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2629 (VGAM2629) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88583] VGAM2629 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2629 was detected is described hereinabove with reference to Figs. 1-8.

[88584] VGAM2629 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Avian Encephalomyelitis Virus. VGAM2629 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88585] VGAM2629 gene encodes a VGAM2629 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2629 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2629 precursor RNA is designated SEQ ID:2615, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2615 is located at position 2698 relative to the genome of Avian Encephalomyelitis Virus.

[88586] VGAM2629 precursor RNA folds onto itself, forming VGAM2629 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88587] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2629 folded precursor RNA into VGAM2629 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2629 RNA is designated SEQ ID:5340, and is provided hereinbelow with reference to the sequence listing part.

[88588] VGAM2629 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2629 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88589] VGAM2629 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2629 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2629 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88590] The complementary binding of VGAM2629 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2629 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2629 host target RNA into VGAM2629 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88591] It is appreciated that VGAM2629 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2629 host target genes. The mRNA of each one of this plurality of VGAM2629 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2629 RNA, herein designated VGAM RNA, and which when bound by VGAM2629 RNA causes inhibition of translation of respective one or more VGAM2629 host target proteins.

[88592] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2629 gene, herein designated VGAM GENE, on one or more VGAM2629 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88593] It is yet further appreciated that a function of VGAM2629 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of viral infection by Avian Encephalomyelitis Virus. Specific functions, and accordingly utilities, of VGAM2629 correlate with, and may be deduced from, the identity of the host target genes which VGAM2629 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88594] Nucleotide sequences of the VGAM2629 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2629 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2629 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2629 are further described hereinbelow with reference to Table 1.

[88595] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2629 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2629 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88596] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2629 gene, herein designated VGAM is inhibition of expression of VGAM2629 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2629 correlate with, and may be deduced from, the identity of the target genes which VGAM2629 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88597] Hepatocyte Growth Factor (hepapoietin A; scatter factor) (HGF, Accession XM_168542) is a VGAM2629 host target gene. HGF BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by HGF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HGF BINDING SITE, designated SEQ ID:45217, to the nucleotide sequence of VGAM2629 RNA, herein designated VGAM RNA, also designated SEQ ID:5340.

[88598] A function of VGAM2629 is therefore inhibition of Hepatocyte Growth Factor (hepapoietin A; scatter factor) (HGF, Accession XM_168542), a gene which may be required for normal embryonic development; strongly similar to murine Hgf, has kringle domains. Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HGF. The function of HGF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM174.Regulatory Factor X, 2 (influences HLA class II expression) (RFX2, Accession NM_000635) is another VGAM2629 host target gene. RFX2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RFX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RFX2 BINDING SITE, designated SEQ ID:6269, to the nucleotide sequence of VGAM2629 RNA, herein designated VGAM RNA, also designated SEQ ID:5340.

[88599] Another function of VGAM2629 is therefore inhibition of Regulatory Factor X, 2 (influences HLA class II expression) (RFX2, Accession NM_000635), a gene which acts as a dimer to regulate the expression of many genes. Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFX2. The function of RFX2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM622.FLJ12934 (Accession NM_022899) is another VGAM2629 host target gene. FLJ12934 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12934 BINDING SITE, designated SEQ ID:23178, to the nucleotide sequence of VGAM2629 RNA,

herein designated VGAM RNA, also designated SEQ ID:5340.

[88600] Another function of VGAM2629 is therefore inhibition of FLJ12934 (Accession NM_022899). Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12934. FLJ13868 (Accession NM_022744) is another VGAM2629 host target gene. FLJ13868 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13868, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13868 BINDING SITE, designated SEQ ID:22954, to the nucleotide sequence of VGAM2629 RNA, herein designated VGAM RNA, also designated SEQ ID:5340.

[88601] Another function of VGAM2629 is therefore inhibition of FLJ13868 (Accession NM_022744). Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13868. Paternally Expressed 10 (PEG10, Accession NM_015068) is another VGAM2629 host target gene. PEG10 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by PEG10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEG10 BINDING SITE, designated SEQ ID:17425, to the nucleotide sequence of VGAM2629 RNA, herein designated VGAM RNA, also designated SEQ ID:5340.

[88602] Another function of VGAM2629 is therefore inhibition of Paternally Expressed 10 (PEG10, Accession NM_015068). Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEG10. UPLC1 (Accession NM_017707) is another VGAM2629 host target gene. UPLC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UPLC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UPLC1 BINDING SITE, designated SEQ ID:19283, to the nucleotide sequence of VGAM2629 RNA, herein designated VGAM RNA, also designated SEQ ID:5340.

[88603] Another function of VGAM2629 is therefore inhibition of UPLC1 (Accession NM_017707). Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UPLC1. LOC149271 (Accession XM_086475) is another VGAM2629 host target gene. LOC149271 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149271 BINDING SITE, designated SEQ ID:38674, to the nucleotide sequence of VGAM2629 RNA, herein designated VGAM RNA, also designated SEQ ID:5340.

[88604] Another function of VGAM2629 is therefore inhibition of LOC149271 (Accession XM_086475). Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149271. LOC90333 (Accession XM_030958) is another VGAM2629 host target gene. LOC90333 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90333, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90333 BINDING SITE, designated SEQ ID:31218, to the nucleotide sequence of VGAM2629 RNA, herein designated VGAM RNA, also designated SEQ ID:5340.

[88605] Another function of VGAM2629 is therefore inhibition of LOC90333 (Accession XM_030958). Accordingly, utilities of VGAM2629 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90333. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2630 (VGAM2630) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88606] VGAM2630 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2630 was detected is described hereinabove with reference to Figs. 1-8.

[88607] VGAM2630 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana Bat Virus. VGAM2630 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[88608] VGAM2630 gene encodes a VGAM2630 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2630 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2630 precursor RNA is designated SEQ ID:2616, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2616 is located at position 2276 relative to the genome of Tamana Bat Virus.

[88609] VGAM2630 precursor RNA folds onto itself, forming VGAM2630 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88610] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2630 folded precursor RNA into VGAM2630

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM2630 RNA is designated SEQ ID:5341, and is provided hereinbelow with reference to the sequence listing part.

[88611] VGAM2630 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2630 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88612] VGAM2630 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2630 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2630 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88613] The complementary binding of VGAM2630 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2630 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2630 host target RNA into VGAM2630 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[88614] It is appreciated that VGAM2630 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2630 host target genes. The mRNA of each one of this plurality of VGAM2630 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2630 RNA, herein designated VGAM RNA, and which when bound by VGAM2630 RNA causes inhibition of translation of respective one or more VGAM2630 host target proteins.

[88615] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2630 gene, herein designated VGAM GENE, on one or more VGAM2630 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88616] It is yet further appreciated that a function of VGAM2630 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2630 include diagnosis, prevention and treatment of viral infection by Tamana Bat Virus. Specific functions, and accordingly utilities, of VGAM2630 correlate with, and may be deduced from, the identity of the host target genes which VGAM2630 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88617] Nucleotide sequences of the VGAM2630 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2630 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2630 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2630 are further described hereinbelow with reference to Table 1.

[88618] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2630 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2630 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88619] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2630 gene, herein designated VGAM is inhibition of expression of VGAM2630 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2630 correlate with, and may be deduced from, the identity of the target genes which VGAM2630 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88620] General Transcription Factor IIH, Polypeptide 1, 62kDa (GTF2H1, Accession NM_005316) is a VGAM2630 host target gene. GTF2H1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTF2H1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTF2H1 BINDING SITE, designated SEQ ID:11793, to the nucleotide sequence of

VGAM2630 RNA, herein designated VGAM RNA, also designated SEQ ID:5341.

[88621] A function of VGAM2630 is therefore inhibition of General Transcription Factor IIH, Polypeptide 1, 62kDa (GTF2H1, Accession NM_005316), a gene which is subunit of RNA polymerase II transcription initiation factor IIH; involved in transcription and DNA repair mechanisms. Accordingly, utilities of VGAM2630 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2H1. The function of GTF2H1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1407.VAMP (vesicle-associated membrane protein)-associated Protein B and C (VAPB, Accession NM_004738) is another VGAM2630 host target gene. VAPB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VAPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VAPB BINDING SITE, designated SEQ ID:11133, to the nucleotide sequence of VGAM2630 RNA, herein designated VGAM RNA, also designated SEQ ID:5341.

[88622] Another function of VGAM2630 is therefore inhibition of VAMP (vesicle-associated membrane protein)-associated Protein B and C (VAPB, Accession NM_004738). Accordingly, utilities of VGAM2630 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VAPB. C1orf27 (Accession NM_017847) is another VGAM2630 host target gene. C1orf27 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C1orf27, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf27 BINDING SITE, designated SEQ ID:19509, to the nucleotide sequence of VGAM2630 RNA, herein designated VGAM RNA, also designated SEQ ID:5341.

[88623] Another function of VGAM2630 is therefore inhibition of C1orf27 (Accession NM_017847). Accordingly, utilities of VGAM2630 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf27. SRB7 Suppressor of RNA Polymerase B Homolog (yeast) (SURB7, Accession NM_004264) is another VGAM2630 host target gene. SURB7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by SURB7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SURB7 BINDING SITE, designated SEQ ID:10465, to the nucleotide sequence of VGAM2630 RNA, herein designated VGAM RNA, also designated SEQ ID:5341.

[88624] Another function of VGAM2630 is therefore inhibition of SRB7 Suppressor of RNA Polymerase B Homolog (yeast) (SURB7, Accession NM_004264). Accordingly, utilities of VGAM2630 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURB7. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2631 (VGAM2631) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88625] VGAM2631 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2631 was detected is described hereinabove with reference to Figs. 1-8.

[88626] VGAM2631 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Tamana Bat Virus. VGAM2631 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88627] VGAM2631 gene encodes a VGAM2631 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2631 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2631 precursor RNA is designated SEQ ID:2617, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2617 is located at position 9727 relative to the genome of Tamana Bat Virus.

[88628] VGAM2631 precursor RNA folds onto itself, forming VGAM2631 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88629] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2631 folded precursor RNA into VGAM2631 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2631 RNA is designated SEQ ID:5342, and is provided hereinbelow with reference to the sequence listing part.

[88630] VGAM2631 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2631 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88631] VGAM2631 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2631 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2631 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88632] The complementary binding of VGAM2631 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2631 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2631

host target RNA into VGAM2631 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88633] It is appreciated that VGAM2631 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2631 host target genes. The mRNA of each one of this plurality of VGAM2631 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2631 RNA, herein designated VGAM RNA, and which when bound by VGAM2631 RNA causes inhibition of translation of respective one or more VGAM2631 host target proteins.

[88634] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2631 gene, herein designated VGAM GENE, on one or more VGAM2631 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88635] It is yet further appreciated that a function of VGAM2631 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of viral infection by Tamana Bat Virus. Specific functions, and accordingly utilities, of VGAM2631 correlate with, and may be deduced from, the identity of the host target genes which VGAM2631 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88636] Nucleotide sequences of the VGAM2631 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2631 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2631 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2631 are further

described hereinbelow with reference to Table 1.

[88637] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2631 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2631 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88638] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2631 gene, herein designated VGAM is inhibition of expression of VGAM2631 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2631 correlate with, and may be deduced from, the identity of the target genes which VGAM2631 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88639] Adenylate Kinase 2 (AK2, Accession NM_013411) is a VGAM2631 host target gene. AK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AK2 BINDING SITE, desig-

nated SEQ ID:15076, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88640] A function of VGAM2631 is therefore inhibition of Adenylate Kinase 2 (AK2, Accession NM_013411), a gene which essential for maintenance and cell growth. Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AK2. The function of AK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1113.FKRP (Accession NM_024301) is another VGAM2631 host target gene. FKRP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FKRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKRP BINDING SITE, designated SEQ ID:23591, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88641] Another function of VGAM2631 is therefore inhibition of FKRP (Accession NM_024301). Accordingly, utilities of

VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKRP. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle) (PPP1R3A, Accession NM_002711) is another VGAM2631 host target gene. PPP1R3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R3A BINDING SITE, designated SEQ ID:8564, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88642] Another function of VGAM2631 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle) (PPP1R3A, Accession NM_002711), a gene which regulates phosphatase activity towards glycogen synthase, active in skeletal muscle. Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R3A. The function of PPP1R3A and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1872.Solute Carrier Family 14 (urea transporter), Member 2 (SLC14A2, Accession NM_007163) is another VGAM2631 host target gene. SLC14A2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC14A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC14A2 BINDING SITE, designated SEQ ID:14006, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88643] Another function of VGAM2631 is therefore inhibition of Solute Carrier Family 14 (urea transporter), Member 2 (SLC14A2, Accession NM_007163), a gene which is a renal urea transporter 2. Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC14A2. The function of SLC14A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM74.Sorting Nexin 9 (SNX9, Accession NM_016224) is another VGAM2631 host target gene. SNX9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNX9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNX9 BINDING SITE, designated SEQ ID:18331, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88644] Another function of VGAM2631 is therefore inhibition of Sorting Nexin 9 (SNX9, Accession NM_016224). Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX9. Chromosome 1 Open Reading Frame 34 (C1orf34, Accession XM_027172) is another VGAM2631 host target gene. C1orf34 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf34, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf34 BINDING SITE, designated SEQ ID:30434, to the nucleotide sequence of

VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88645] Another function of VGAM2631 is therefore inhibition of Chromosome 1 Open Reading Frame 34 (C1orf34, Accession XM_027172). Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf34. DKFZP564O1664 (Accession NM_030800) is another VGAM2631 host target gene. DKFZP564O1664 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O1664, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564O1664 BINDING SITE, designated SEQ ID:25101, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88646] Another function of VGAM2631 is therefore inhibition of DKFZP564O1664 (Accession NM_030800). Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O1664. MGC16186 (Accession

NM_032372) is another VGAM2631 host target gene. MGC16186 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC16186, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16186 BINDING SITE, designated SEQ ID:26160, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88647] Another function of VGAM2631 is therefore inhibition of MGC16186 (Accession NM_032372). Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16186. Testis-specific Kinase 2 (TESK2, Accession XM_032399) is another VGAM2631 host target gene. TESK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TESK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TESK2 BINDING SITE, designated SEQ ID:31648, to the nucleotide sequence of VGAM2631 RNA,

herein designated VGAM RNA, also designated SEQ ID:5342.

[88648] Another function of VGAM2631 is therefore inhibition of Testis-specific Kinase 2 (TESK2, Accession XM_032399). Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TESK2. LOC150157 (Accession XM_097823) is another VGAM2631 host target gene. LOC150157 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150157, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150157 BINDING SITE, designated SEQ ID:41144, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88649] Another function of VGAM2631 is therefore inhibition of LOC150157 (Accession XM_097823). Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150157. LOC201685 (Accession XM_117325) is another VGAM2631 host target gene. LOC201685 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201685, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201685 BINDING SITE, designated SEQ ID:43384, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88650] Another function of VGAM2631 is therefore inhibition of LOC201685 (Accession XM_117325). Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201685. LOC253150 (Accession XM_170948) is another VGAM2631 host target gene. LOC253150 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253150, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253150 BINDING SITE, designated SEQ ID:45732, to the nucleotide sequence of VGAM2631 RNA, herein designated VGAM RNA, also designated SEQ ID:5342.

[88651] Another function of VGAM2631 is therefore inhibition of

LOC253150 (Accession XM_170948). Accordingly, utilities of VGAM2631 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253150. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2632 (VGAM2632) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88652] VGAM2632 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2632 was detected is described hereinabove with reference to Figs. 1-8.

[88653] VGAM2632 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana Bat Virus. VGAM2632 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88654] VGAM2632 gene encodes a VGAM2632 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2632 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2632 precursor RNA is designated SEQ ID:2618, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2618 is located at position 1113 relative to the genome of Tamana Bat Virus.

[88655] VGAM2632 precursor RNA folds onto itself, forming VGAM2632 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88656] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2632 folded precursor RNA into VGAM2632 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide se-

quence of VGAM2632 RNA is designated SEQ ID:5343, and is provided hereinbelow with reference to the sequence listing part.

[88657] VGAM2632 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2632 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88658] VGAM2632 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2632 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2632 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88659] The complementary binding of VGAM2632 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2632 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2632 host target RNA into VGAM2632 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88660] It is appreciated that VGAM2632 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2632 host target genes. The mRNA of each one of this plurality of VGAM2632 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2632 RNA, herein designated VGAM RNA, and which when bound by VGAM2632 RNA causes inhibition of translation of respective one or more VGAM2632 host target proteins.

[88661] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2632 gene, herein designated VGAM GENE, on one or more VGAM2632 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88662] It is yet further appreciated that a function of VGAM2632

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2632 include diagnosis, prevention and treatment of viral infection by Tamana Bat Virus. Specific functions, and accordingly utilities, of VGAM2632 correlate with, and may be deduced from, the identity of the host target genes which VGAM2632 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88663] Nucleotide sequences of the VGAM2632 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2632 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2632 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2632 are further described hereinbelow with reference to Table 1.

[88664] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2632 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2632 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88665] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2632 gene, herein designated VGAM is inhibition of expression of VGAM2632 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2632 correlate with, and may be deduced from, the identity of the target genes which VGAM2632 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88666] FLJ10996 (Accession NM_019044) is a VGAM2632 host target gene. FLJ10996 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10996, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10996 BINDING SITE, designated SEQ ID:21126, to the nucleotide sequence of VGAM2632 RNA, herein designated VGAM RNA, also designated SEQ ID:5343.

[88667] A function of VGAM2632 is therefore inhibition of FLJ10996 (Accession NM_019044). Accordingly, utilities of VGAM2632 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10996. Fig. 1 further provides a conceptual description

of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2633 (VGAM2633) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88668] VGAM2633 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2633 was detected is described hereinabove with reference to Figs. 1-8.

[88669] VGAM2633 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana Bat Virus. VGAM2633 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88670] VGAM2633 gene encodes a VGAM2633 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2633 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2633 precursor RNA is designated SEQ ID:2619, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2619 is located at position 3876 relative to the genome of Tamana Bat Virus.

[88671] VGAM2633 precursor RNA folds onto itself, forming VGAM2633 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[88672] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2633 folded precursor RNA into VGAM2633 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2633 RNA is designated SEQ ID:5344, and is provided hereinbelow with reference to the sequence listing part.

[88673] VGAM2633 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2633 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2633 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88674] VGAM2633 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2633 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2633 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2633 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2633 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88675] The complementary binding of VGAM2633 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2633 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2633 host target RNA into VGAM2633 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88676] It is appreciated that VGAM2633 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2633 host target genes. The mRNA of each one of this plurality of VGAM2633 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2633 RNA, herein designated VGAM RNA, and which when bound by VGAM2633 RNA causes inhibition of translation of respective one or more VGAM2633 host target proteins.

[88677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2633 gene, herein designated VGAM GENE, on one or more VGAM2633 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88678] It is yet further appreciated that a function of VGAM2633 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of viral infection by Tamana Bat Virus. Specific functions, and accordingly utilities, of VGAM2633 correlate with, and may be deduced from, the identity of the host target genes which VGAM2633 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88679] Nucleotide sequences of the VGAM2633 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2633 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2633 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2633 are further described hereinbelow with reference to Table 1.

[88680] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2633 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2633 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88681] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2633 gene, herein designated VGAM is inhibition of expression of VGAM2633 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2633 correlate with, and may be deduced from, the identity of the target genes which VGAM2633 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88682] Cyclin D-type Binding-protein 1 (CCNDBP1, Accession NM_037370) is a VGAM2633 host target gene. CCNDBP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CCNDBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of CCNDBP1 BINDING SITE, designated SEQ ID:27398, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88683] A function of VGAM2633 is therefore inhibition of Cyclin D-type Binding-protein 1 (CCNDBP1, Accession NM_037370). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNDBP1. Collagen, Type VI, Alpha 3 (COL6A3, Accession NM_004369) is another VGAM2633 host target gene. COL6A3 BINDING SITE1 and COL6A3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COL6A3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL6A3 BINDING SITE1 and COL6A3 BINDING SITE2, designated SEQ ID:10588 and SEQ ID:27672 respectively, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88684] Another function of VGAM2633 is therefore inhibition of

Collagen, Type VI, Alpha 3 (COL6A3, Accession NM_004369). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A3. BDG-29 (Accession XM_051343) is another VGAM2633 host target gene. BDG-29 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BDG-29, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BDG-29 BINDING SITE, designated SEQ ID:35819, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88685] Another function of VGAM2633 is therefore inhibition of BDG-29 (Accession XM_051343). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDG-29. FLJ20275 (Accession NM_017737) is another VGAM2633 host target gene. FLJ20275 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20275, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20275 BINDING SITE, designated SEQ ID:19323, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88686] Another function of VGAM2633 is therefore inhibition of FLJ20275 (Accession NM_017737). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20275. HBP1 (Accession NM_012257) is another VGAM2633 host target gene. HBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HBP1 BINDING SITE, designated SEQ ID:14560, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88687] Another function of VGAM2633 is therefore inhibition of HBP1 (Accession NM_012257). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HBP1.

Hypermethylated In Cancer 2 (HIC2, Accession XM_036937) is another VGAM2633 host target gene. HIC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIC2 BINDING SITE, designated SEQ ID:32530, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88688] Another function of VGAM2633 is therefore inhibition of Hypermethylated In Cancer 2 (HIC2, Accession XM_036937). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC2. MAN1 (Accession NM_014319) is another VGAM2633 host target gene. MAN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAN1 BINDING SITE, designated SEQ ID:15617, to the nucleotide sequence of VGAM2633 RNA,

herein designated VGAM RNA, also designated SEQ ID:5344.

[88689] Another function of VGAM2633 is therefore inhibition of MAN1 (Accession NM_014319). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAN1. MGC16142 (Accession NM_032763) is another VGAM2633 host target gene. MGC16142 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC16142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16142 BINDING SITE, designated SEQ ID:26509, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88690] Another function of VGAM2633 is therefore inhibition of MGC16142 (Accession NM_032763). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16142. MGC2827 (Accession NM_023940) is another VGAM2633 host target gene. MGC2827 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by MGC2827, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2827 BINDING SITE, designated SEQ ID:23426, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88691] Another function of VGAM2633 is therefore inhibition of MGC2827 (Accession NM_023940). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2827. Tetratricopeptide Repeat Domain 4 (TTC4, Accession XM_038926) is another VGAM2633 host target gene. TTC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TTC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTC4 BINDING SITE, designated SEQ ID:32961, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88692] Another function of VGAM2633 is therefore inhibition of Tetratricopeptide Repeat Domain 4 (TTC4, Accession

XM_038926). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTC4. LOC150606 (Accession XM_097928) is another VGAM2633 host target gene. LOC150606 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150606, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150606 BINDING SITE, designated SEQ ID:41235, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88693] Another function of VGAM2633 is therefore inhibition of LOC150606 (Accession XM_097928). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150606. LOC91813 (Accession XM_040862) is another VGAM2633 host target gene. LOC91813 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC91813 BINDING SITE, designated SEQ ID:33401, to the nucleotide sequence of VGAM2633 RNA, herein designated VGAM RNA, also designated SEQ ID:5344.

[88694] Another function of VGAM2633 is therefore inhibition of LOC91813 (Accession XM_040862). Accordingly, utilities of VGAM2633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91813. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2634 (VGAM2634) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88695] VGAM2634 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2634 was detected is described hereinabove with reference to Figs. 1-8.

[88696] VGAM2634 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana Bat Virus. VGAM2634 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[88697] VGAM2634 gene encodes a VGAM2634 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2634 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2634 precursor RNA is designated SEQ ID:2620, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2620 is located at position 3523 relative to the genome of Tamana Bat Virus.

[88698] VGAM2634 precursor RNA folds onto itself, forming VGAM2634 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88699] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2634 folded precursor RNA into VGAM2634 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2634 RNA is designated SEQ ID:5345, and is provided hereinbelow with reference to the sequence listing part.

[88700] VGAM2634 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2634 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88701] VGAM2634 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2634 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2634 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88702] The complementary binding of VGAM2634 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2634 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2634 host target RNA into VGAM2634 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88703] It is appreciated that VGAM2634 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2634 host target genes. The mRNA of each one of this plurality of VGAM2634 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2634 RNA, herein designated VGAM RNA, and which when bound by VGAM2634 RNA causes inhibition of translation of respective one or more VGAM2634 host target proteins.

[88704] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2634 gene, herein designated VGAM GENE, on one or more VGAM2634 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88705] It is yet further appreciated that a function of VGAM2634 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of viral infection by Tamana Bat Virus. Specific functions, and accordingly utilities, of VGAM2634 correlate with, and may be deduced from, the identity of the host target genes which VGAM2634 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88706] Nucleotide sequences of the VGAM2634 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2634 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2634 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2634 are further described hereinbelow with reference to Table 1.

[88707] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2634 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2634 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88708] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2634 gene, herein designated VGAM is inhibition of expression of VGAM2634 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2634 correlate with, and may be deduced from, the identity of the target genes which VGAM2634 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88709] ATPase, Ca++ Transporting, Cardiac Muscle, Slow Twitch 2 (ATP2A2, Accession NM_001681) is a VGAM2634 host target gene. ATP2A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP2A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP2A2 BINDING SITE, designated SEQ ID:7403, to the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5345.

[88710] A function of VGAM2634 is therefore inhibition of ATPase, Ca++ Transporting, Cardiac Muscle, Slow Twitch 2 (ATP2A2, Accession NM_001681). Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP2A2. Cartilage Associated Protein (CRTAP, Accession NM_006371) is another VGAM2634 host target gene. CRTAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRTAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRTAP BINDING SITE, designated SEQ ID:13064, to the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, also designated SEQ ID:5345.

[88711] Another function of VGAM2634 is therefore inhibition of Cartilage Associated Protein (CRTAP, Accession NM_006371), a gene which is a novel developmentally regulated chick embryo protein. Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAP.

The function of CRTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.RNTRE (Accession NM_014688) is another VGAM2634 host target gene. RNTRE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNTRE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNTRE BINDING SITE, designated SEQ ID:16189, to the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, also designated SEQ ID:5345.

[88712] Another function of VGAM2634 is therefore inhibition of RNTRE (Accession NM_014688), a gene which may be involved in cell proliferation. Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNTRE. The function of RNTRE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM379.T-box 5 (TBX5, Accession NM_080717) is another VGAM2634 host target gene. TBX5 BINDING SITE1

and TBX5 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TBX5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBX5 BINDING SITE1 and TBX5 BINDING SITE2, designated SEQ ID:28015 and SEQ ID:5691 respectively, to the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, also designated SEQ ID:5345.

[88713] Another function of VGAM2634 is therefore inhibition of T-box 5 (TBX5, Accession NM_080717). Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX5. Elongation of Very Long Chain Fatty Acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (ELOVL2, Accession NM_017770) is another VGAM2634 host target gene. ELOVL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELOVL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELOVL2 BINDING SITE, designated SEQ ID:19389, to the nucleotide sequence of VGAM2634 RNA,

herein designated VGAM RNA, also designated SEQ ID:5345.

[88714] Another function of VGAM2634 is therefore inhibition of Elongation of Very Long Chain Fatty Acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (ELOVL2, Accession NM_017770). Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELOVL2. FLJ13110 (Accession NM_022912) is another VGAM2634 host target gene. FLJ13110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13110 BINDING SITE, designated SEQ ID:23224, to the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, also designated SEQ ID:5345.

[88715] Another function of VGAM2634 is therefore inhibition of FLJ13110 (Accession NM_022912). Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13110. LOC200339 (Accession XM_117226) is another

VGAM2634 host target gene. LOC200339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200339, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200339 BINDING SITE, designated SEQ ID:43303, to the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, also designated SEQ ID:5345.

[88716] Another function of VGAM2634 is therefore inhibition of LOC200339 (Accession XM_117226). Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200339. LOC257407 (Accession XM_173078) is another VGAM2634 host target gene. LOC257407 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257407, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257407 BINDING SITE, designated SEQ ID:46338, to the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, also designated SEQ ID:5345.

[88717] Another function of VGAM2634 is therefore inhibition of LOC257407 (Accession XM_173078). Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257407. LOC92997 (Accession XM_048690) is another VGAM2634 host target gene. LOC92997 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92997, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92997 BINDING SITE, designated SEQ ID:35222, to the nucleotide sequence of VGAM2634 RNA, herein designated VGAM RNA, also designated SEQ ID:5345.

[88718] Another function of VGAM2634 is therefore inhibition of LOC92997 (Accession XM_048690). Accordingly, utilities of VGAM2634 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92997. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2635 (VGAM2635) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[88719] VGAM2635 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2635 was detected is described hereinabove with reference to Figs. 1-8.

[88720] VGAM2635 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tamana Bat Virus. VGAM2635 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88721] VGAM2635 gene encodes a VGAM2635 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2635 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2635 precursor RNA is designated SEQ ID:2621, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2621 is located at position 2105 relative to the genome of Tamana Bat Virus.

[88722] VGAM2635 precursor RNA folds onto itself, forming VGAM2635 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88723] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2635 folded precursor RNA into VGAM2635 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2635 RNA is designated SEQ ID:5346, and is provided hereinbelow with reference to the sequence listing part.

[88724] VGAM2635 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2635 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88725] VGAM2635 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2635 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2635 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88726] The complementary binding of VGAM2635 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2635 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2635 host target RNA into VGAM2635 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88727] It is appreciated that VGAM2635 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2635 host target genes. The mRNA of each one of this plurality of VGAM2635 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2635 RNA, herein designated VGAM RNA, and which when bound by VGAM2635 RNA causes inhibition of translation of respective one or more VGAM2635 host target proteins.

[88728] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2635 gene, herein designated VGAM GENE, on one or more VGAM2635 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88729] It is yet further appreciated that a function of VGAM2635 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of viral infection by Tamana Bat Virus. Specific functions, and accordingly utilities, of VGAM2635 correlate with, and may be deduced from, the identity of the host target genes which VGAM2635 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[88730] Nucleotide sequences of the VGAM2635 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2635 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2635 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2635 are further described hereinbelow with reference to Table 1.

[88731] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2635 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2635 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88732] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2635 gene, herein designated VGAM is inhibition of expression of VGAM2635 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2635 correlate with, and may be deduced from, the identity of the target genes which VGAM2635 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88733] UDP-Gal:betaGlcNAc Beta 1,3-galactosyltransferase, Polypeptide 2 (B3GALT2, Accession NM_003783) is a VGAM2635 host target gene. B3GALT2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by B3GALT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B3GALT2 BINDING SITE, designated SEQ ID:9872, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88734] A function of VGAM2635 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,3-galactosyltransferase, Polypeptide 2 (B3GALT2, Accession NM_003783). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GALT2. Like-glycosyltransferase (LARGE, Accession NM_004737) is another VGAM2635 host target gene. LARGE BINDING SITE1 and LARGE BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LARGE, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of LARGE BINDING SITE1 and LARGE BINDING SITE2, designated SEQ ID:11127 and SEQ ID:28599 respectively, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88735] Another function of VGAM2635 is therefore inhibition of Like-glycosyltransferase (LARGE, Accession NM_004737), a gene which is a member of the N-acetylglucosaminyltransferase family. Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LARGE. The function of LARGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM205.Megalencephalic Leukoencephalopathy with Subcortical Cysts 1 (MLC1, Accession NM_139202) is another VGAM2635 host target gene. MLC1 BINDING SITE1 and MLC1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MLC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLC1 BINDING SITE1 and

MLC1 BINDING SITE2, designated SEQ ID:29218 and SEQ ID:14909 respectively, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88736] Another function of VGAM2635 is therefore inhibition of Megalencephalic Leukoencephalopathy with Subcortical Cysts 1 (MLC1, Accession NM_139202). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLC1. RAD52 Homolog (S. cerevisiae) (RAD52, Accession NM_134422) is another VGAM2635 host target gene. RAD52 BINDING SITE1 through RAD52 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RAD52, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE1 through RAD52 BINDING SITE3, designated SEQ ID:28649, SEQ ID:28657 and SEQ ID:28665 respectively, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88737] Another function of VGAM2635 is therefore inhibition of

RAD52 Homolog (S. cerevisiae) (RAD52, Accession NM_134422). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52. Chromosome 21 Open Reading Frame 93 (C21orf93, Accession NM_145179) is another VGAM2635 host target gene. C21orf93 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C21orf93, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf93 BINDING SITE, designated SEQ ID:29741, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88738] Another function of VGAM2635 is therefore inhibition of Chromosome 21 Open Reading Frame 93 (C21orf93, Accession NM_145179). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf93. DKFZP434H132 (Accession XM_057020) is another VGAM2635 host target gene. DKFZP434H132 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by DKFZP434H132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434H132 BINDING SITE, designated SEQ ID:36448, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88739] Another function of VGAM2635 is therefore inhibition of DKFZP434H132 (Accession XM_057020). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H132. Forkhead Box H1 (FOXH1, Accession NM_003923) is another VGAM2635 host target gene. FOXH1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FOXH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXH1 BINDING SITE, designated SEQ ID:10011, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88740] Another function of VGAM2635 is therefore inhibition of Forkhead Box H1 (FOXH1, Accession NM_003923). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXH1. KIAA1468 (Accession XM_166289) is another VGAM2635 host target gene. KIAA1468 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1468 BINDING SITE, designated SEQ ID:44099, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88741] Another function of VGAM2635 is therefore inhibition of KIAA1468 (Accession XM_166289). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1468. Triple Homeobox 1 (TIX1, Accession XM_029734) is another VGAM2635 host target gene. TIX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIX1, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIX1 BINDING SITE, designated SEQ ID:30928, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88742] Another function of VGAM2635 is therefore inhibition of Triple Homeobox 1 (TIX1, Accession XM_029734). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIX1. LOC148759 (Accession XM_097517) is another VGAM2635 host target gene. LOC148759 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148759, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148759 BINDING SITE, designated SEQ ID:40904, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88743] Another function of VGAM2635 is therefore inhibition of LOC148759 (Accession XM_097517). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC148759. LOC153937 (Accession XM_087813) is another VGAM2635 host target gene. LOC153937 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153937, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153937 BINDING SITE, designated SEQ ID:39447, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88744] Another function of VGAM2635 is therefore inhibition of LOC153937 (Accession XM_087813). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153937. LOC200845 (Accession XM_114305) is another VGAM2635 host target gene. LOC200845 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200845, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200845 BINDING SITE, designated SEQ ID:42863, to

the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88745] Another function of VGAM2635 is therefore inhibition of LOC200845 (Accession XM_114305). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200845. LOC220776 (Accession XM_043388) is another VGAM2635 host target gene. LOC220776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220776 BINDING SITE, designated SEQ ID:33932, to the nucleotide sequence of VGAM2635 RNA, herein designated VGAM RNA, also designated SEQ ID:5346.

[88746] Another function of VGAM2635 is therefore inhibition of LOC220776 (Accession XM_043388). Accordingly, utilities of VGAM2635 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220776. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2636 (VGAM2636) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88747] VGAM2636 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2636 was detected is described hereinabove with reference to Figs. 1-8.

[88748] VGAM2636 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sheeppox Virus. VGAM2636 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88749] VGAM2636 gene encodes a VGAM2636 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2636 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2636 precursor RNA is designated SEQ ID:2622, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2622 is located at position 25048 relative to the genome of Sheeppox Virus.

[88750] VGAM2636 precursor RNA folds onto itself, forming VGAM2636 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88751] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2636 folded precursor RNA into VGAM2636 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2636 RNA is designated SEQ ID:5347, and is provided hereinbelow with reference to the sequence listing part.

[88752] VGAM2636 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2636 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2636 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88753] VGAM2636 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2636 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2636 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88754] The complementary binding of VGAM2636 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2636 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2636 host target RNA into VGAM2636 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88755] It is appreciated that VGAM2636 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2636 host target genes. The mRNA of each one of this plurality of VGAM2636 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2636 RNA, herein designated VGAM RNA, and which when bound by VGAM2636 RNA causes inhibition of translation of respective one or more VGAM2636 host target proteins.

[88756] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2636 gene, herein designated VGAM GENE, on one or more VGAM2636 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88757] It is yet further appreciated that a function of VGAM2636 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2636 include diagnosis, prevention and treatment of viral infection by Sheeppox Virus. Specific functions, and accordingly utilities, of VGAM2636 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2636 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88758] Nucleotide sequences of the VGAM2636 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2636 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2636 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2636 are further described hereinbelow with reference to Table 1.

[88759] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2636 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2636 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88760] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2636 gene, herein designated VGAM is inhibition of expression of VGAM2636 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2636 correlate with, and may be deduced from, the identity of the target genes which VGAM2636

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88761] Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071) is a VGAM2636 host target gene. NCOA6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NCOA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE, designated SEQ ID:15286, to the nucleotide sequence of VGAM2636 RNA, herein designated VGAM RNA, also designated SEQ ID:5347.

[88762] A function of VGAM2636 is therefore inhibition of Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071), a gene which activates gene transcription through ligand-dependent association with coactivators. Accordingly, utilities of VGAM2636 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6. The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.Solute Carrier Family 1 (glial high affinity glutamate transporter), Member 3 (SLC1A3,

Accession NM_004172) is another VGAM2636 host target gene. SLC1A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC1A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC1A3 BINDING SITE, designated SEQ ID:10385, to the nucleotide sequence of VGAM2636 RNA, herein designated VGAM RNA, also designated SEQ ID:5347.

[88763] Another function of VGAM2636 is therefore inhibition of Solute Carrier Family 1 (glial high affinity glutamate transporter), Member 3 (SLC1A3, Accession NM_004172), a gene which is a transporter molecule that regulates neurotransmitter concentrations at excitatory synapses of the mammalian cns. Accordingly, utilities of VGAM2636 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A3. The function of SLC1A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM294.Glutamine-fructose-6-phosphate Transaminase 1 (GFPT1, Accession NM_002056) is another

VGAM2636 host target gene. GFPT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GFPT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GFPT1 BINDING SITE, designated SEQ ID:7817, to the nucleotide sequence of VGAM2636 RNA, herein designated VGAM RNA, also designated SEQ ID:5347.

[88764] Another function of VGAM2636 is therefore inhibition of Glutamine-fructose-6-phosphate Transaminase 1 (GFPT1, Accession NM_002056). Accordingly, utilities of VGAM2636 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFPT1. Glutamate Receptor, Ionotropic, N-methyl-D-aspartate 3A (GRIN3A, Accession NM_133445) is another VGAM2636 host target gene. GRIN3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRIN3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRIN3A BINDING SITE, designated SEQ ID:28527, to the nucleotide sequence of

VGAM2636 RNA, herein designated VGAM RNA, also designated SEQ ID:5347.

[88765] Another function of VGAM2636 is therefore inhibition of Glutamate Receptor, Ionotropic, N-methyl-D-aspartate 3A (GRIN3A, Accession NM_133445). Accordingly, utilities of VGAM2636 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN3A. KIAA1674 (Accession XM_044065) is another VGAM2636 host target gene. KIAA1674 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1674, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1674 BINDING SITE, designated SEQ ID:34115, to the nucleotide sequence of VGAM2636 RNA, herein designated VGAM RNA, also designated SEQ ID:5347.

[88766] Another function of VGAM2636 is therefore inhibition of KIAA1674 (Accession XM_044065). Accordingly, utilities of VGAM2636 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1674. LOC51125 (Accession NM_016099) is another VGAM2636 host target gene. LOC51125 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51125, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51125 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of VGAM2636 RNA, herein designated VGAM RNA, also designated SEQ ID:5347.

[88767] Another function of VGAM2636 is therefore inhibition of LOC51125 (Accession NM_016099). Accordingly, utilities of VGAM2636 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51125. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2637 (VGAM2637) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88768] VGAM2637 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2637 was detected is described hereinabove with reference to Figs. 1-8.

[88769] VGAM2637 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2637 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88770] VGAM2637 gene encodes a VGAM2637 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2637 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2637 precursor RNA is designated SEQ ID:2623, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2623 is located at position 24739 relative to the genome of Goatpox Virus.

[88771] VGAM2637 precursor RNA folds onto itself, forming VGAM2637 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[88772] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2637 folded precursor RNA into VGAM2637 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2637 RNA is designated SEQ ID:5348, and is provided hereinbelow with reference to the sequence listing part.

[88773] VGAM2637 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2637 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88774] VGAM2637 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2637 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2637 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2637 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88775] The complementary binding of VGAM2637 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2637 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2637 host target RNA into VGAM2637 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88776] It is appreciated that VGAM2637 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2637 host target genes. The mRNA of each one of this plurality of VGAM2637 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2637 RNA, herein designated VGAM RNA, and which when bound by VGAM2637 RNA causes inhibition of translation of respective one or more VGAM2637 host target proteins.

[88777] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2637 gene, herein designated VGAM GENE, on one or more VGAM2637 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88778] It is yet further appreciated that a function of VGAM2637 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2637 correlate with, and may be deduced from, the identity of the host target genes which VGAM2637 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88779] Nucleotide sequences of the VGAM2637 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2637 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2637 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2637 are further described hereinbelow with reference to Table 1.

[88780] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2637 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2637 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88781] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2637 gene, herein designated VGAM is inhibition of expression of VGAM2637 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2637 correlate with, and may be deduced from, the identity of the target genes which VGAM2637 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88782] Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_000962) is a VGAM2637 host target gene. PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTGS1, corresponding to HOST TARGET bind-

ing sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2, designated SEQ ID:6671 and SEQ ID:27892 respectively, to the nucleotide sequence of VGAM2637 RNA, herein designated VGAM RNA, also designated SEQ ID:5348.

[88783] A function of VGAM2637 is therefore inhibition of Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_000962), a gene which may play an important role in regulating or promoting cell proliferation in some normal and neoplastically transformed cells. Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS1. The function of PTGS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1224.Von Hippel-Lindau Binding Protein 1 (VBP1, Accession NM_003372) is another VGAM2637 host target gene. VBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VBP1, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VBP1 BINDING SITE, designated SEQ ID:9398, to the nucleotide sequence of VGAM2637 RNA, herein designated VGAM RNA, also designated SEQ ID:5348.

[88784] Another function of VGAM2637 is therefore inhibition of Von Hippel-Lindau Binding Protein 1 (VBP1, Accession NM_003372), a gene which binds specifically to cytosolic chaperonin (c-cpn) and transfers target proteins to it. Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VBP1. The function of VBP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM945.Ras Homolog Gene Family, Member E (ARHE, Accession NM_005168) is another VGAM2637 host target gene. ARHE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHE BIND-

ING SITE, designated SEQ ID:11667, to the nucleotide sequence of VGAM2637 RNA, herein designated VGAM RNA, also designated SEQ ID:5348.

[88785] Another function of VGAM2637 is therefore inhibition of Ras Homolog Gene Family, Member E (ARHE, Accession NM_005168). Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHE. FLJ10139 (Accession NM_018005) is another VGAM2637 host target gene. FLJ10139 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10139 BINDING SITE, designated SEQ ID:19734, to the nucleotide sequence of VGAM2637 RNA, herein designated VGAM RNA, also designated SEQ ID:5348.

[88786] Another function of VGAM2637 is therefore inhibition of FLJ10139 (Accession NM_018005). Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10139. KIAA1655 (Accession XM_039442) is another

VGAM2637 host target gene. KIAA1655 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1655, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1655 BINDING SITE, designated SEQ ID:33090, to the nucleotide sequence of VGAM2637 RNA, herein designated VGAM RNA, also designated SEQ ID:5348.

[88787] Another function of VGAM2637 is therefore inhibition of KIAA1655 (Accession XM_039442). Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1655. NY-REN-25 (Accession XM_027116) is another VGAM2637 host target gene. NY-REN-25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NY-REN-25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NY-REN-25 BINDING SITE, designated SEQ ID:30414, to the nucleotide sequence of VGAM2637 RNA, herein designated VGAM RNA, also designated SEQ ID:5348.

[88788] Another function of VGAM2637 is therefore inhibition of NY-REN-25 (Accession XM_027116). Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NY-REN-25. RoXaN (Accession NM_025013) is another VGAM2637 host target gene. RoXaN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RoXaN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RoXaN BINDING SITE, designated SEQ ID:24599, to the nucleotide sequence of VGAM2637 RNA, herein designated VGAM RNA, also designated SEQ ID:5348.

[88789] Another function of VGAM2637 is therefore inhibition of RoXaN (Accession NM_025013). Accordingly, utilities of VGAM2637 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RoXaN. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2638 (VGAM2638) viral gene, which modulates expression of respective host target genes thereof, the function and

utility of which host target genes is known in the art.

[88790] VGAM2638 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2638 was detected is described hereinabove with reference to Figs. 1-8.

[88791] VGAM2638 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth Disease Virus O. VGAM2638 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88792] VGAM2638 gene encodes a VGAM2638 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2638 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2638 precursor RNA is designated SEQ ID:2624, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2624 is located at position 3143 relative to the genome of Foot-and-mouth Disease Virus O.

[88793] VGAM2638 precursor RNA folds onto itself, forming VGAM2638 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88794] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2638 folded precursor RNA into VGAM2638 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2638 RNA is designated SEQ ID:5349, and is provided hereinbelow with reference to the sequence listing part.

[88795] VGAM2638 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2638 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88796] VGAM2638 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2638 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2638 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[88797] The complementary binding of VGAM2638 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2638 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2638 host target RNA into VGAM2638 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88798] It is appreciated that VGAM2638 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2638 host target genes. The mRNA of each one of this plurality of VGAM2638 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2638 RNA, herein designated VGAM RNA, and which when bound by VGAM2638 RNA causes inhibition of translation of respective one or more VGAM2638 host target proteins.

[88799] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2638 gene, herein designated VGAM GENE, on one

or more VGAM2638 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88800] It is yet further appreciated that a function of VGAM2638 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2638 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus O. Specific functions, and accordingly utilities, of VGAM2638 correlate with, and may be deduced from, the identity of the host target genes which VGAM2638 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88801] Nucleotide sequences of the VGAM2638 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2638 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2638 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2638 are further described hereinbelow with reference to Table 1.

[88802] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2638 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2638 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88803] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2638 gene, herein designated VGAM is inhibition of expression of VGAM2638 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2638 correlate with, and may be deduced from, the identity of the target genes which VGAM2638 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88804] Forkhead Box O1A (rhabdomyosarcoma) (FOXO1A, Acces-

sion NM_002015) is a VGAM2638 host target gene. FOXO1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FOXO1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXO1A BINDING SITE, designated SEQ ID:7756, to the nucleotide sequence of VGAM2638 RNA, herein designated VGAM RNA, also designated SEQ ID:5349.

[88805] A function of VGAM2638 is therefore inhibition of Forkhead Box O1A (rhabdomyosarcoma) (FOXO1A, Accession NM_002015), a gene which is a probable transcription factor. Accordingly, utilities of VGAM2638 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXO1A. The function of FOXO1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM228.Retinoschisis (X-linked, juvenile) 1 (RS1, Accession NM_000330) is another VGAM2638 host target gene. RS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RS1, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RS1 BINDING SITE, designated SEQ ID:5873, to the nucleotide sequence of VGAM2638 RNA, herein designated VGAM RNA, also designated SEQ ID:5349.

[88806] Another function of VGAM2638 is therefore inhibition of Retinoschisis (X-linked, juvenile) 1 (RS1, Accession NM_000330). Accordingly, utilities of VGAM2638 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RS1. Cadherin-like 26 (CDH26, Accession NM_021810) is another VGAM2638 host target gene. CDH26 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CDH26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH26 BINDING SITE, designated SEQ ID:22370, to the nucleotide sequence of VGAM2638 RNA, herein designated VGAM RNA, also designated SEQ ID:5349.

[88807] Another function of VGAM2638 is therefore inhibition of Cadherin-like 26 (CDH26, Accession NM_021810). Ac-

cordingly, utilities of VGAM2638 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH26. ZER6 (Accession XM_032742) is another VGAM2638 host target gene. ZER6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZER6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZER6 BINDING SITE, designated SEQ ID:31747, to the nucleotide sequence of VGAM2638 RNA, herein designated VGAM RNA, also designated SEQ ID:5349.

[88808] Another function of VGAM2638 is therefore inhibition of ZER6 (Accession XM_032742). Accordingly, utilities of VGAM2638 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZER6. LOC196527 (Accession XM_113743) is another VGAM2638 host target gene. LOC196527 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC196527 BINDING SITE, designated SEQ ID:42397, to the nucleotide sequence of VGAM2638 RNA, herein designated VGAM RNA, also designated SEQ ID:5349.

[88809] Another function of VGAM2638 is therefore inhibition of LOC196527 (Accession XM_113743). Accordingly, utilities of VGAM2638 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196527. LOC220954 (Accession XM_167628) is another VGAM2638 host target gene. LOC220954 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220954, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220954 BINDING SITE, designated SEQ ID:44736, to the nucleotide sequence of VGAM2638 RNA, herein designated VGAM RNA, also designated SEQ ID:5349.

[88810] Another function of VGAM2638 is therefore inhibition of LOC220954 (Accession XM_167628). Accordingly, utilities of VGAM2638 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220954. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2639 (VGAM2639) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88811] VGAM2639 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2639 was detected is described hereinabove with reference to Figs. 1-8.

[88812] VGAM2639 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth Disease Virus O. VGAM2639 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88813] VGAM2639 gene encodes a VGAM2639 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2639 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2639 precursor RNA is designated SEQ ID:2625, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2625 is located at position 2526 relative to the

genome of Foot-and-mouth Disease Virus O.

[88814] VGAM2639 precursor RNA folds onto itself, forming VGAM2639 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88815] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2639 folded precursor RNA into VGAM2639 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2639 RNA is designated SEQ ID:5350, and is provided hereinbelow with reference to the sequence listing part.

[88816] VGAM2639 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2639 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88817] VGAM2639 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2639 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2639 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88818] The complementary binding of VGAM2639 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2639 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2639 host target RNA into VGAM2639 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88819] It is appreciated that VGAM2639 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2639 host target genes. The mRNA of each one of this plurality of VGAM2639 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2639 RNA, herein designated VGAM RNA, and which when bound by VGAM2639 RNA causes inhibition of translation of respective one or more VGAM2639 host target proteins.

[88820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2639 gene, herein designated VGAM GENE, on one or more VGAM2639 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88821] It is yet further appreciated that a function of VGAM2639 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus O. Specific functions, and accordingly utilities, of

VGAM2639 correlate with, and may be deduced from, the identity of the host target genes which VGAM2639 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88822] Nucleotide sequences of the VGAM2639 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2639 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2639 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2639 are further described hereinbelow with reference to Table 1.

[88823] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2639 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2639 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88824] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2639 gene, herein designated VGAM is inhibition of expression of VGAM2639 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2639 correlate with, and may be deduced

from, the identity of the target genes which VGAM2639 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88825] A Disintegrin and Metalloproteinase Domain 11 (ADAM11, Accession NM_021612) is a VGAM2639 host target gene. ADAM11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAM11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM11 BINDING SITE, designated SEQ ID:22241, to the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, also designated SEQ ID:5350.

[88826] A function of VGAM2639 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 11 (ADAM11, Accession NM_021612), a gene which Member of the ADAM family of zinc metalloproteases. Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM11. The function of ADAM11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM387.BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 1 (BACH1, Accession NM_001186) is another VGAM2639 host target gene. BACH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BACH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BACH1 BINDING SITE, designated SEQ ID:6857, to the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, also designated SEQ ID:5350.

[88827] Another function of VGAM2639 is therefore inhibition of BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 1 (BACH1, Accession NM_001186), a gene which acts as repressor or activator, binds to nf-e2 binding sites. Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BACH1. The function of BACH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM724.Carnitine Acetyltransferase (CRAT, Accession NM_004003) is an-

other VGAM2639 host target gene. CRAT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CRAT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRAT BINDING SITE, designated SEQ ID:10151, to the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, also designated SEQ ID:5350.

[88828] Another function of VGAM2639 is therefore inhibition of Carnitine Acetyltransferase (CRAT, Accession NM_004003), a gene which catalyzes the reversible transfer of acyl groups from an acyl-CoA thioester to carnitine. Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRAT. The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1189.Potassium Voltage-gated Channel, Shal-related Subfamily, Member 2 (KCND2, Accession NM_012281) is another VGAM2639 host target gene. KCND2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by KCND2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCND2 BINDING SITE, designated SEQ ID:14607, to the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, also designated SEQ ID:5350.

[88829] Another function of VGAM2639 is therefore inhibition of Potassium Voltage-gated Channel, Shal-related Subfamily, Member 2 (KCND2, Accession NM_012281), a gene which is prominent in the repolarization phase of the action potential. Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCND2. The function of KCND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM449.Transforming Growth Factor, Beta Receptor II (70/80kDa) (TGFBR2, Accession NM_003242) is another VGAM2639 host target gene. TGFBR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TGFBR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGFBR2 BINDING SITE, designated SEQ ID:9237, to the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, also designated SEQ ID:5350.

[88830] Another function of VGAM2639 is therefore inhibition of Transforming Growth Factor, Beta Receptor II (70/80kDa) (TGFBR2, Accession NM_003242). Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFBR2. KIAA0628 (Accession NM_014789) is another VGAM2639 host target gene. KIAA0628 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0628, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0628 BINDING SITE, designated SEQ ID:16674, to the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, also designated SEQ ID:5350.

[88831] Another function of VGAM2639 is therefore inhibition of KIAA0628 (Accession NM_014789). Accordingly, utilities of VGAM2639 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0628. KIAA0960 (Accession XM_166543) is another VGAM2639 host target gene. KIAA0960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0960 BINDING SITE, designated SEQ ID:44516, to the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, also designated SEQ ID:5350.

[88832] Another function of VGAM2639 is therefore inhibition of KIAA0960 (Accession XM_166543). Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0960. LOC150776 (Accession XM_032542) is another VGAM2639 host target gene. LOC150776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150776 BINDING SITE, designated SEQ ID:31672, to

the nucleotide sequence of VGAM2639 RNA, herein designated VGAM RNA, also designated SEQ ID:5350.

[88833] Another function of VGAM2639 is therefore inhibition of LOC150776 (Accession XM_032542). Accordingly, utilities of VGAM2639 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150776. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2640 (VGAM2640) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88834] VGAM2640 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2640 was detected is described hereinabove with reference to Figs. 1-8.

[88835] VGAM2640 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth Disease Virus O. VGAM2640 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88836] VGAM2640 gene encodes a VGAM2640 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2640 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2640 precursor RNA is designated SEQ ID:2626, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2626 is located at position 4136 relative to the genome of Foot-and-mouth Disease Virus O.

[88837] VGAM2640 precursor RNA folds onto itself, forming VGAM2640 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88838] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2640 folded precursor RNA into VGAM2640 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2640 RNA is designated SEQ ID:5351, and is provided hereinbelow with reference to the sequence listing part.

[88839] VGAM2640 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2640 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88840] VGAM2640 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2640 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2640 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88841] The complementary binding of VGAM2640 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2640 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2640 host target RNA into VGAM2640 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88842] It is appreciated that VGAM2640 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2640 host target genes. The mRNA of each one of this plurality of VGAM2640 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2640 RNA, herein designated VGAM RNA, and which when bound by VGAM2640 RNA causes inhibition of translation of respective one or more VGAM2640 host target proteins.

[88843] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2640 gene, herein designated VGAM GENE, on one or more VGAM2640 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88844] It is yet further appreciated that a function of VGAM2640 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus O. Specific functions, and accordingly utilities, of VGAM2640 correlate with, and may be deduced from, the identity of the host target genes which VGAM2640 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88845] Nucleotide sequences of the VGAM2640 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2640 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2640 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2640 are further described hereinbelow with reference to Table 1.

[88846] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2640 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2640 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88847] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2640 gene, herein designated VGAM is inhibition of expression of VGAM2640 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2640 correlate with, and may be deduced from, the identity of the target genes which VGAM2640 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88848] B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898) is a VGAM2640 host target gene. BCL11B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL11B BINDING SITE, designated SEQ ID:23168, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88849] A function of VGAM2640 is therefore inhibition of B-cell

CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL11B. Developmentally Regulated GTP Binding Protein 2 (DRG2, Accession NM_001388) is another VGAM2640 host target gene. DRG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DRG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DRG2 BINDING SITE, designated SEQ ID:7075, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88850] Another function of VGAM2640 is therefore inhibition of Developmentally Regulated GTP Binding Protein 2 (DRG2, Accession NM_001388), a gene which may play a role in cell proliferation, differentiation and death. Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRG2. The function of DRG2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to VGAM2003.LFG (Accession XM_084780) is another VGAM2640 host target gene. LFG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LFG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LFG BINDING SITE, designated SEQ ID:37694, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88851] Another function of VGAM2640 is therefore inhibition of LFG (Accession XM_084780). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LFG. Neogenin Homolog 1 (chicken) (NEO1, Accession NM_002499) is another VGAM2640 host target gene. NEO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NEO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NEO1 BINDING SITE, designated SEQ ID:8318, to the nucleotide sequence of VGAM2640 RNA, herein

designated VGAM RNA, also designated SEQ ID:5351.

[88852] Another function of VGAM2640 is therefore inhibition of Neogenin Homolog 1 (chicken) (NEO1, Accession NM_002499), a gene which regulates the transition of undifferentiated proliferating cells to their differentiated state. Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEO1. The function of NEO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM329.RAP1, GTPase Activating Protein 1 (RAP1GA1, Accession NM_002885) is another VGAM2640 host target gene. RAP1GA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAP1GA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP1GA1 BINDING SITE, designated SEQ ID:8799, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88853] Another function of VGAM2640 is therefore inhibition of

RAP1, GTPase Activating Protein 1 (RAP1GA1, Accession NM_002885). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP1GA1. Solute Carrier Family 19 (folate transporter), Member 1 (SLC19A1, Accession NM_003056) is another VGAM2640 host target gene. SLC19A1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC19A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC19A1 BINDING SITE, designated SEQ ID:9024, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88854] Another function of VGAM2640 is therefore inhibition of Solute Carrier Family 19 (folate transporter), Member 1 (SLC19A1, Accession NM_003056). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC19A1. SRY (sex determining region Y)-box 15 (SOX15, Accession NM_006942) is another VGAM2640 host target gene. SOX15 BINDING SITE is HOST TARGET binding site

found in the 5` untranslated region of mRNA encoded by SOX15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX15 BINDING SITE, designated SEQ ID:13827, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88855] Another function of VGAM2640 is therefore inhibition of SRY (sex determining region Y)-box 15 (SOX15, Accession NM_006942), a gene which is a member of the SOX gene family. Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX15. The function of SOX15 has been established by previous studies. The testis-determining gene SRY (OMIM Ref. No. 480000) encodes a transcription factor characterized by a DNA-binding motif known as the HMG domain. The SOX gene family consists of genes related to SRY, with a sequence identity of more than 60% to the SRY HMG box. Other members of the SOX gene family are assumed to play a role in gonadal function: the murine Sox5 gene is expressed exclusively in post-meiotic germ cells. SOX4 (OMIM Ref. No. 184430) is

expressed in brain, heart, and testis. Mutations in the human SOX9 gene (OMIM Ref. No. 114290) cause a skeletal dysplasia, campomelic dysplasia associated with autosomal sex reversal. By use of a SOX9 cDNA as a hybridization probe, Meyer et al. (1996) discovered a new member of the SOX gene family, designated SOX20. They found that SOX20 has a high similarity to the deduced amino acid sequence of human SOX12 and murine Sox16 HMG domains. By fluorescence in situ hybridization (FISH), Meyer et al. (1996) mapped the SOX20 gene to 17p13. Critcher et al. (1998) used FISH to refine the localization to 17p12.3. Vujic et al. (1998) assigned the SOX20 gene to 17p13.1 by the study of a radiation hybrid panel.

[88856] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[88857] Meyer, J.; Wirth, J.; Held, M.; Schempp, W.; Scherer, G. : SOX20, a new member of the SOX gene family, is located on chromosome 17p13. Cytogenet. Cell Genet. 72: 246-249, 1996. ; and

[88858] Vujic, M.; Rajic, T.; Goodfellow, P. N.; Stevanovic, M. : cDNA characterization and high resolution mapping of the human SOX20 gene. Mammalian Genome 9: 1059-1061,

1998.

[88859] Further studies establishing the function and utilities of SOX15 are found in John Hopkins OMIM database record ID 601297, and in sited publications numbered 12406-6897 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Tumor Necrosis Factor Receptor Superfamily, Member 8 (TNFRSF8, Accession NM_001243) is another VGAM2640 host target gene. TNFRSF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF8 BINDING SITE, designated SEQ ID:6910, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88860] Another function of VGAM2640 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 8 (TNFRSF8, Accession NM_001243), a gene which regulates gene expression through activation of nf-kappab. Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with TNFRSF8. The function of TNFRSF8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM154.Ubiquitin-conjugating Enzyme E2 Variant 1 (UBE2V1, Accession NM_003349) is another VGAM2640 host target gene. UBE2V1 BINDING SITE1 through UBE2V1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by UBE2V1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2V1 BINDING SITE1 through UBE2V1 BINDING SITE3, designated SEQ ID:9373, SEQ ID:22772 and SEQ ID:22525 respectively, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88861] Another function of VGAM2640 is therefore inhibition of Ubiquitin-conjugating Enzyme E2 Variant 1 (UBE2V1, Accession NM_003349), a gene which may play a role in signaling for DNA repair. Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2V1. The func-

tion of UBE2V1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM155.Chromosome 20 Open Reading Frame 18 (C20orf18, Accession NM_031228) is another VGAM2640 host target gene. C20orf18 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf18 BINDING SITE, designated SEQ ID:25276, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88862] Another function of VGAM2640 is therefore inhibition of Chromosome 20 Open Reading Frame 18 (C20orf18, Accession NM_031228). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf18. CDT1 (Accession XM_085327) is another VGAM2640 host target gene. CDT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CDT1, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDT1 BINDING SITE, designated SEQ ID:38067, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88863] Another function of VGAM2640 is therefore inhibition of CDT1 (Accession XM_085327). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDT1. Cat Eye Syndrome Chromosome Region, Candidate 7 (CECR7, Accession XM_086803) is another VGAM2640 host target gene. CECR7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CECR7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CECR7 BINDING SITE, designated SEQ ID:38880, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88864] Another function of VGAM2640 is therefore inhibition of Cat Eye Syndrome Chromosome Region, Candidate 7 (CECR7, Accession XM_086803). Accordingly, utilities of

VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR7. Carbohydrate (N-acetylgalactosamine 4-0) Sulfotransferase 8 (CHST8, Accession NM_022467) is another VGAM2640 host target gene. CHST8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CHST8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHST8 BINDING SITE, designated SEQ ID:22818, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88865] Another function of VGAM2640 is therefore inhibition of Carbohydrate (N-acetylgalactosamine 4-0) Sulfotransferase 8 (CHST8, Accession NM_022467). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST8. DKFZP434H132 (Accession XM_057020) is another VGAM2640 host target gene. DKFZP434H132 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434H132, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434H132 BINDING SITE, designated SEQ ID:36450, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88866] Another function of VGAM2640 is therefore inhibition of DKFZP434H132 (Accession XM_057020). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H132. Delta-like 1 (Drosophila) (DLL1, Accession NM_005618) is another VGAM2640 host target gene. DLL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DLL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLL1 BINDING SITE, designated SEQ ID:12134, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88867] Another function of VGAM2640 is therefore inhibition of Delta-like 1 (Drosophila) (DLL1, Accession NM_005618). Accordingly, utilities of VGAM2640 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with DLL1. FLJ10242 (Accession NM_018036) is another VGAM2640 host target gene. FLJ10242 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10242, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10242 BINDING SITE, designated SEQ ID:19776, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88868] Another function of VGAM2640 is therefore inhibition of FLJ10242 (Accession NM_018036). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10242. FLJ12076 (Accession NM_025187) is another VGAM2640 host target gene. FLJ12076 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12076, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12076

BINDING SITE, designated SEQ ID:24826, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88869] Another function of VGAM2640 is therefore inhibition of FLJ12076 (Accession NM_025187). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12076. Myelin Transcription Factor 1 (MYT1, Accession NM_004535) is another VGAM2640 host target gene. MYT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYT1 BINDING SITE, designated SEQ ID:10877, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88870] Another function of VGAM2640 is therefore inhibition of Myelin Transcription Factor 1 (MYT1, Accession NM_004535). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYT1. TAO1 (Accession NM_004783) is another VGAM2640 host target gene.

TAO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAO1 BINDING SITE, designated SEQ ID:11191, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88871] Another function of VGAM2640 is therefore inhibition of TAO1 (Accession NM_004783). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAO1. Zinc Finger Protein 282 (ZNF282, Accession XM_114578) is another VGAM2640 host target gene. ZNF282 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF282, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF282 BINDING SITE, designated SEQ ID:42992, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88872] Another function of VGAM2640 is therefore inhibition of

Zinc Finger Protein 282 (ZNF282, Accession XM_114578). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF282. LOC112868 (Accession XM_053402) is another VGAM2640 host target gene. LOC112868 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112868, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112868 BINDING SITE, designated SEQ ID:36083, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88873] Another function of VGAM2640 is therefore inhibition of LOC112868 (Accession XM_053402). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112868. LOC126661 (Accession XM_059061) is another VGAM2640 host target gene. LOC126661 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126661, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126661 BINDING SITE, designated SEQ ID:36850, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88874] Another function of VGAM2640 is therefore inhibition of LOC126661 (Accession XM_059061). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126661. LOC130470 (Accession XM_059437) is another VGAM2640 host target gene. LOC130470 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC130470, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130470 BINDING SITE, designated SEQ ID:36990, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88875] Another function of VGAM2640 is therefore inhibition of LOC130470 (Accession XM_059437). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC130470. LOC150095 (Accession XM_097805) is another VGAM2640 host target gene. LOC150095 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150095, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150095 BINDING SITE, designated SEQ ID:41130, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88876] Another function of VGAM2640 is therefore inhibition of LOC150095 (Accession XM_097805). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150095. LOC158267 (Accession XM_088528) is another VGAM2640 host target gene. LOC158267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158267 BINDING SITE, designated SEQ ID:39794, to the nucleotide sequence of VGAM2640 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5351.

[88877] Another function of VGAM2640 is therefore inhibition of LOC158267 (Accession XM_088528). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158267. LOC163682 (Accession XM_099402) is another VGAM2640 host target gene. LOC163682 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC163682, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163682 BINDING SITE, designated SEQ ID:42097, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88878] Another function of VGAM2640 is therefore inhibition of LOC163682 (Accession XM_099402). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163682. LOC204804 (Accession XM_115599) is another VGAM2640 host target gene. LOC204804 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC204804, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC204804 BINDING SITE, designated SEQ ID:43100, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88879] Another function of VGAM2640 is therefore inhibition of LOC204804 (Accession XM_115599). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC204804. LOC256933 (Accession XM_172970) is another VGAM2640 host target gene. LOC256933 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256933, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256933 BINDING SITE, designated SEQ ID:46226, to the nucleotide sequence of VGAM2640 RNA, herein designated VGAM RNA, also designated SEQ ID:5351.

[88880] Another function of VGAM2640 is therefore inhibition of LOC256933 (Accession XM_172970). Accordingly, utilities of VGAM2640 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC256933. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2641 (VGAM2641) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88881] VGAM2641 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2641 was detected is described hereinabove with reference to Figs. 1-8.

[88882] VGAM2641 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth Disease Virus O. VGAM2641 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88883] VGAM2641 gene encodes a VGAM2641 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2641 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2641 precursor RNA is desig-

nated SEQ ID:2627, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2627 is located at position 1368 relative to the genome of Foot-and-mouth Disease Virus O.

[88884] VGAM2641 precursor RNA folds onto itself, forming VGAM2641 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88885] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2641 folded precursor RNA into VGAM2641 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2641 RNA is designated SEQ ID:5352, and is provided hereinbelow with reference to the sequence

listing part.

[88886] VGAM2641 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2641 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88887] VGAM2641 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2641 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2641 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88888] The complementary binding of VGAM2641 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2641 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2641 host target RNA into VGAM2641 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88889] It is appreciated that VGAM2641 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2641 host target genes. The mRNA of each one of this plurality of VGAM2641 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2641 RNA, herein designated VGAM

RNA, and which when bound by VGAM2641 RNA causes inhibition of translation of respective one or more VGAM2641 host target proteins.

[88890] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2641 gene, herein designated VGAM GENE, on one or more VGAM2641 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88891] It is yet further appreciated that a function of VGAM2641 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2641 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus O. Specific functions, and accordingly utilities, of VGAM2641 correlate with, and may be deduced from, the identity of the host target genes which VGAM2641 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88892] Nucleotide sequences of the VGAM2641 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2641 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2641 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2641 are further described hereinbelow with reference to Table 1.

[88893] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2641 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2641 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88894] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2641 gene, herein designated VGAM is

inhibition of expression of VGAM2641 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2641 correlate with, and may be deduced from, the identity of the target genes which VGAM2641 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88895] Axin 1 (AXIN1, Accession XM_027520) is a VGAM2641 host target gene. AXIN1 BINDING SITE1 and AXIN1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AXIN1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AXIN1 BINDING SITE1 and AXIN1 BINDING SITE2, designated SEQ ID:30512 and SEQ ID:30516 respectively, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88896] A function of VGAM2641 is therefore inhibition of Axin 1 (AXIN1, Accession XM_027520). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXIN1. Fibroblast Growth Factor 5 (FGF5, Accession NM_004464) is another VGAM2641 host target gene. FGF5 BINDING

SITE1 and FGF5 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FGF5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE1 and FGF5 BINDING SITE2, designated SEQ ID:10775 and SEQ ID:7884 respectively, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88897] Another function of VGAM2641 is therefore inhibition of Fibroblast Growth Factor 5 (FGF5, Accession NM_004464), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5. The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM276.Trichorhinophalangeal Syndrome I (TRPS1, Accession NM_014112) is another VGAM2641 host target gene. TRPS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRPS1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPS1 BINDING SITE, designated SEQ ID:15353, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88898] Another function of VGAM2641 is therefore inhibition of Trichorhinophalangeal Syndrome I (TRPS1, Accession NM_014112), a gene which may function as a transcriptional activator protein. Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPS1. The function of TRPS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_014919) is another VGAM2641 host target gene. WHSC1 BINDING SITE1 through WHSC1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WHSC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

WHSC1 BINDING SITE1 through WHSC1 BINDING SITE3, designated SEQ ID:17187, SEQ ID:28451 and SEQ ID:28468 respectively, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88899] Another function of VGAM2641 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_014919), a gene which binds covalently to and repairs g/t mismatches. Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1. The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Caspase Recruitment Domain Family, Member 9 (CARD9, Accession NM_022352) is another VGAM2641 host target gene. CARD9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CARD9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARD9 BINDING SITE, designated SEQ ID:22747, to the nucleotide se-

quence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88900] Another function of VGAM2641 is therefore inhibition of Caspase Recruitment Domain Family, Member 9 (CARD9, Accession NM_022352). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD9. Catenin, Beta Interacting Protein 1 (CTNNBIP1, Accession NM_020248) is another VGAM2641 host target gene. CTNNBIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTNNBIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTNNBIP1 BINDING SITE, designated SEQ ID:21545, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88901] Another function of VGAM2641 is therefore inhibition of Catenin, Beta Interacting Protein 1 (CTNNBIP1, Accession NM_020248). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNNBIP1. FLJ12960

(Accession NM_024638) is another VGAM2641 host target gene. FLJ12960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12960 BINDING SITE, designated SEQ ID:23918, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88902] Another function of VGAM2641 is therefore inhibition of FLJ12960 (Accession NM_024638). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12960. FLJ13441 (Accession NM_023924) is another VGAM2641 host target gene. FLJ13441 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13441 BINDING SITE, designated SEQ ID:23396, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM

RNA, also designated SEQ ID:5352.

[88903] Another function of VGAM2641 is therefore inhibition of FLJ13441 (Accession NM_023924). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13441. FLJ20452 (Accession NM_017828) is another VGAM2641 host target gene. FLJ20452 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20452, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20452 BINDING SITE, designated SEQ ID:19489, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88904] Another function of VGAM2641 is therefore inhibition of FLJ20452 (Accession NM_017828). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20452. KIAA0329 (Accession NM_014844) is another VGAM2641 host target gene. KIAA0329 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0329, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0329 BINDING SITE, designated SEQ ID:16875, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88905] Another function of VGAM2641 is therefore inhibition of KIAA0329 (Accession NM_014844). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0329. KIAA1126 (Accession XM_050325) is another VGAM2641 host target gene. KIAA1126 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1126, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1126 BINDING SITE, designated SEQ ID:35608, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88906] Another function of VGAM2641 is therefore inhibition of KIAA1126 (Accession XM_050325). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1126. KIAA1550 (Accession XM_039393) is another VGAM2641 host target gene. KIAA1550 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1550, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1550 BINDING SITE, designated SEQ ID:33065, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88907] Another function of VGAM2641 is therefore inhibition of KIAA1550 (Accession XM_039393). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1550. KIAA1918 (Accession XM_054951) is another VGAM2641 host target gene. KIAA1918 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1918 BINDING SITE, designated SEQ ID:36216, to the

nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88908] Another function of VGAM2641 is therefore inhibition of KIAA1918 (Accession XM_054951). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1918. KIAA1970 (Accession XM_058808) is another VGAM2641 host target gene. KIAA1970 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1970, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1970 BINDING SITE, designated SEQ ID:36754, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88909] Another function of VGAM2641 is therefore inhibition of KIAA1970 (Accession XM_058808). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1970. RNA Binding Protein S1, Serine-rich Domain (RNPS1, Accession NM_080594) is another VGAM2641 host target gene. RNPS1 BINDING SITE1 and RNPS1 BIND-

ING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RNPS1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNPS1 BINDING SITE1 and RNPS1 BINDING SITE2, designated SEQ ID:27903 and SEQ ID:13538 respectively, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88910] Another function of VGAM2641 is therefore inhibition of RNA Binding Protein S1, Serine-rich Domain (RNPS1, Accession NM_080594). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNPS1. LOC147054 (Accession XM_097172) is another VGAM2641 host target gene. LOC147054 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147054 BINDING SITE, designated SEQ ID:40791, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5352.

[88911] Another function of VGAM2641 is therefore inhibition of LOC147054 (Accession XM_097172). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147054. LOC147817 (Accession XM_085903) is another VGAM2641 host target gene. LOC147817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE, designated SEQ ID:38386, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88912] Another function of VGAM2641 is therefore inhibition of LOC147817 (Accession XM_085903). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817. LOC149345 (Accession XM_086502) is another VGAM2641 host target gene. LOC149345 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149345, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149345 BINDING SITE, designated SEQ ID:38714, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88913] Another function of VGAM2641 is therefore inhibition of LOC149345 (Accession XM_086502). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149345. LOC153346 (Accession XM_098364) is another VGAM2641 host target gene. LOC153346 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153346, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153346 BINDING SITE, designated SEQ ID:41617, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88914] Another function of VGAM2641 is therefore inhibition of LOC153346 (Accession XM_098364). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC153346. LOC220018 (Accession XM_167816) is another VGAM2641 host target gene. LOC220018 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220018, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220018 BINDING SITE, designated SEQ ID:44855, to the nucleotide sequence of VGAM2641 RNA, herein designated VGAM RNA, also designated SEQ ID:5352.

[88915] Another function of VGAM2641 is therefore inhibition of LOC220018 (Accession XM_167816). Accordingly, utilities of VGAM2641 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220018. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2642 (VGAM2642) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88916] VGAM2642 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2642 was detected is described hereinabove with reference to Figs. 1-8.

[88917] VGAM2642 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Foot-and-mouth Disease Virus O. VGAM2642 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88918] VGAM2642 gene encodes a VGAM2642 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2642 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2642 precursor RNA is designated SEQ ID:2628, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2628 is located at position 1959 relative to the genome of Foot-and-mouth Disease Virus O.

[88919] VGAM2642 precursor RNA folds onto itself, forming VGAM2642 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88920] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2642 folded precursor RNA into VGAM2642 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of VGAM2642 RNA is designated SEQ ID:5353, and is provided hereinbelow with reference to the sequence listing part.

[88921] VGAM2642 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2642 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88922] VGAM2642 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2642 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2642 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88923] The complementary binding of VGAM2642 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2642 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2642 host target RNA into VGAM2642 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88924] It is appreciated that VGAM2642 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2642 host target genes. The mRNA of each one of this plurality of VGAM2642 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2642 RNA, herein designated VGAM RNA, and which when bound by VGAM2642 RNA causes inhibition of translation of respective one or more VGAM2642 host target proteins.

[88925] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2642 gene, herein designated VGAM GENE, on one or more VGAM2642 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88926] It is yet further appreciated that a function of VGAM2642 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus O. Specific functions, and accordingly utilities, of VGAM2642 correlate with, and may be deduced from, the identity of the host target genes which VGAM2642 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88927] Nucleotide sequences of the VGAM2642 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2642 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2642 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2642 are further described hereinbelow with reference to Table 1.

[88928] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2642 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2642 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88929] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2642 gene, herein designated VGAM is inhibition of expression of VGAM2642 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2642 correlate with, and may be deduced from, the identity of the target genes which VGAM2642 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88930] Cytoplasmic Linker 2 (CYLN2, Accession NM_003388) is a VGAM2642 host target gene. CYLN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by CYLN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYLN2 BINDING SITE, designated SEQ ID:9425, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88931] A function of VGAM2642 is therefore inhibition of Cytoplasmic Linker 2 (CYLN2, Accession NM_003388), a gene which associates with microtubules and dendritic lamellar bodies. Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYLN2. The function of CYLN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM94.Transient Receptor Potential Cation Channel, Subfamily M, Member 2 (TRPM2, Accession NM_003307) is another VGAM2642 host target gene. TRPM2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of TRPM2 BINDING SITE, designated SEQ ID:9312, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88932] Another function of VGAM2642 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily M, Member 2 (TRPM2, Accession NM_003307), a gene which may be a calcium channel. Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPM2. The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1928.Unc-5 Homolog B (C. elegans) (UNC5C, Accession NM_003728) is another VGAM2642 host target gene. UNC5C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UNC5C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UNC5C BINDING SITE, designated SEQ ID:9820, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ

ID:5353.

[88933] Another function of VGAM2642 is therefore inhibition of Unc-5 Homolog B (C. elegans) (UNC5C, Accession NM_003728), a gene which is a putative receptor for netrin, which is involved in axon guidance. Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC5C. The function of UNC5C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM298.Ankyrin Repeat and BTB (POZ) Domain Containing 1 (ABTB1, Accession NM_032548) is another VGAM2642 host target gene. ABTB1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ABTB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABTB1 BINDING SITE, designated SEQ ID:26272, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88934] Another function of VGAM2642 is therefore inhibition of Ankyrin Repeat and BTB (POZ) Domain Containing 1

(ABTB1, Accession NM_032548). Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABTB1. ADP-ribosylation Factor Domain Protein 1, 64kDa (ARFD1, Accession NM_001656) is another VGAM2642 host target gene. ARFD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARFD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARFD1 BINDING SITE, designated SEQ ID:7371, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88935] Another function of VGAM2642 is therefore inhibition of ADP-ribosylation Factor Domain Protein 1, 64kDa (ARFD1, Accession NM_001656). Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARFD1. Chromosome 20 Open Reading Frame 59 (C20orf59, Accession NM_022082) is another VGAM2642 host target gene. C20orf59 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by C20orf59, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf59 BINDING SITE, designated SEQ ID:22625, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88936] Another function of VGAM2642 is therefore inhibition of Chromosome 20 Open Reading Frame 59 (C20orf59, Accession NM_022082). Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf59. DKFZp566H0824 (Accession NM_017535) is another VGAM2642 host target gene. DKFZp566H0824 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp566H0824, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp566H0824 BINDING SITE, designated SEQ ID:18974, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88937] Another function of VGAM2642 is therefore inhibition of DKFZp566H0824 (Accession NM_017535). Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp566H0824. KIAA0173 (Accession NM_014640) is another VGAM2642 host target gene. KIAA0173 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0173 BINDING SITE, designated SEQ ID:16040, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88938] Another function of VGAM2642 is therefore inhibition of KIAA0173 (Accession NM_014640). Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0173. MNAB (Accession NM_018835) is another VGAM2642 host target gene. MNAB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MNAB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MNAB BINDING SITE, designated SEQ ID:20821, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88939] Another function of VGAM2642 is therefore inhibition of MNAB (Accession NM_018835). Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MNAB. LOC125268 (Accession XM_071960) is another VGAM2642 host target gene. LOC125268 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC125268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC125268 BINDING SITE, designated SEQ ID:37451, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88940] Another function of VGAM2642 is therefore inhibition of LOC125268 (Accession XM_071960). Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC125268. LOC256158 (Accession XM_175125) is another VGAM2642 host target gene. LOC256158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256158 BINDING SITE, designated SEQ ID:46626, to the nucleotide sequence of VGAM2642 RNA, herein designated VGAM RNA, also designated SEQ ID:5353.

[88941] Another function of VGAM2642 is therefore inhibition of LOC256158 (Accession XM_175125). Accordingly, utilities of VGAM2642 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256158. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2643 (VGAM2643) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88942] VGAM2643 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2643 was detected is described hereinabove with reference to Figs. 1-8.

[88943] VGAM2643 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea Aphid-borne Mosaic Virus. VGAM2643 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88944] VGAM2643 gene encodes a VGAM2643 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2643 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2643 precursor RNA is designated SEQ ID:2629, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2629 is located at position 4628 relative to the genome of Cowpea Aphid-borne Mosaic Virus.

[88945] VGAM2643 precursor RNA folds onto itself, forming VGAM2643 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88946] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2643 folded precursor RNA into VGAM2643 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2643 RNA is designated SEQ ID:5354, and is provided hereinbelow with reference to the sequence listing part.

[88947] VGAM2643 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2643 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88948] VGAM2643 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2643 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2643 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88949] The complementary binding of VGAM2643 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2643 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2643 host target RNA into VGAM2643 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88950] It is appreciated that VGAM2643 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2643 host target genes. The mRNA of each one of this plurality of VGAM2643 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2643 RNA, herein designated VGAM RNA, and which when bound by VGAM2643 RNA causes inhibition of translation of respective one or more VGAM2643 host target proteins.

[88951] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2643 gene, herein designated VGAM GENE, on one or more VGAM2643 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88952] It is yet further appreciated that a function of VGAM2643 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2643 correlate with, and may be deduced from, the identity of the host target genes which VGAM2643 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88953] Nucleotide sequences of the VGAM2643 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2643 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2643 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2643 are further described hereinbelow with reference to Table 1.

[88954] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2643 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2643 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88955] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2643 gene, herein designated VGAM is inhibition of expression of VGAM2643 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2643 correlate with, and may be deduced from, the identity of the target genes which VGAM2643 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88956] ACATN (Accession NM_004733) is a VGAM2643 host target gene. ACATN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACATN, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACATN BINDING SITE, designated SEQ ID:11109, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88957] A function of VGAM2643 is therefore inhibition of ACATN (Accession NM_004733), a gene which Putative acetyl-Coenzyme A transporter; required for the formation of O-acetylated gangliosides. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACATN. The function of ACATN has been established by previous studies. The structural diversity and complexity of sugar chains in membrane gangliosides are caused in part by the occurrence of several different species of sialic acid molecules, including O-acetylated forms. Acetylation of sialic acid residues of glycoproteins and gangliosides occurs in the lumen of the Golgi apparatus, using acetyl-CoA as the acetate donor. By expression cloning, Kanamori et al. (1997) isolated a human melanoma cell line cDNA encoding AT1, a protein that directed the formation of 9-O-acetylated ganglioside GD3 in mammalian

cells. The predicted 549-amino acid protein contained 6 to 10 transmembrane domains and a leucine zipper motif in transmembrane domain III. Immunofluorescence experiments indicated that the 58-kD protein is localized to the cytoplasm. Using in vitro assays with semi-intact cells, Kanamori et al. (1997) demonstrated that the AT1 protein functioned as an acetyl-CoA transporter. Northern blot analysis revealed that AT1 was expressed as 3.3- and 4.3-kb mRNAs in all tissues tested. Kanamori et al. (1997) concluded that AT1 is an acetyl-CoA transporter that is involved in the process of O-acetylation. Bora et al. (1998) stated that nucleotide sequences of the mouse and human ACATN genes are 87% identical. By fluorescence in situ hybridization, Bora et al. (1998) mapped the Acatn gene to mouse chromosome 3E1-E3.

[88958] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[88959] Bora, R. S.; Kanamori, A.; Hirabayashi, Y. : Assignment of a putative acetyl-CoA transporter gene (Acatn) to mouse chromosome band 3E1-E3 by in situ hybridization. Cytogenet. Cell Genet. 83: 78-79, 1998. ; and

[88960] Kanamori, A.; Nakayama, J.; Fukuda, M. N.; Stallcup, W. B.;

Sasaki, K.; Fukuda, M.; Hirabayashi, Y. : Expression cloning and characterization of a cDNA encoding a novel membrane protein.

[88961] Further studies establishing the function and utilities of ACATN are found in John Hopkins OMIM database record ID 603690, and in sited publications numbered 493 and 4949 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1, Accession NM_053056) is another VGAM2643 host target gene. CCND1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCND1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCND1 BINDING SITE, designated SEQ ID:27603, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88962] Another function of VGAM2643 is therefore inhibition of Cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1, Accession NM_053056), a gene which is involved in the control of cell cycle and is required for Schwann cell pro-

liferation to proceed normally during Wallerian degeneration. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCND1. The function of CCND1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM220.CD4 Antigen (p55) (CD4, Accession NM_000616) is another VGAM2643 host target gene. CD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD4 BINDING SITE, designated SEQ ID:6219, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88963] Another function of VGAM2643 is therefore inhibition of CD4 Antigen (p55) (CD4, Accession NM_000616), a gene which is T-cell surface glycoprotein and has role in cell-cell interactions and may act in signal transduction. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with CD4. The function of CD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Development and Differentiation Enhancing Factor 2 (DDEF2, Accession NM_003887) is another VGAM2643 host target gene. DDEF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDEF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDEF2 BINDING SITE, designated SEQ ID:9970, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88964] Another function of VGAM2643 is therefore inhibition of Development and Differentiation Enhancing Factor 2 (DDEF2, Accession NM_003887), a gene which interacts with members of the Arf and Src family. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDEF2. The function of DDEF2 and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM464.G Protein-coupled Receptor 87 (GPR87, Accession NM_023915) is another VGAM2643 host target gene. GPR87 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GPR87, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR87 BINDING SITE, designated SEQ ID:23388, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88965] Another function of VGAM2643 is therefore inhibition of G Protein-coupled Receptor 87 (GPR87, Accession NM_023915), a gene which plays a role in cell communication. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR87. The function of GPR87 has been established by previous studies. By batch EST database searching, Wittenberger et al. (2001) identified a cDNA encoding GPR87. The deduced 358-amino acid protein, which is 89% identical to the mouse protein, lacks a leader peptide but possesses a C-terminal PDZ domain-

binding site. Northern blot analysis revealed expression of a 1.6-kb GPR87 transcript in placenta, with weaker expression in thymus. Lee et al. (2001) identified GPR87, which they called GPR95, in a genomic database using sequences of related GPRs as query. They cloned partial GPR87 sequences from ESTs of a human testis library and a human bladder cell library. Analysis of overlapping regions confirmed identity. The deduced 358-amino acid protein shares highest identity (OMIM Ref. No. 51-62%) in the transmembrane regions with the UDP-glucose receptor, the platelet ADP receptor, P2Y12 (OMIM Ref. No. 600515), and GPR86 (OMIM Ref. No. 606380). Northern blot analysis detected a 1.8-kb transcript at high levels in prostate and at lower levels in uterus and testis. Little expression was detected in thymus, colon, small intestine, and peripheral blood leukocytes.

[88966] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[88967] Lee, D. K.; Nguyen, T.; Lynch, K. R.; Cheng, R.; Vanti, W. B.; Arkhitko, O.; Lewis, T.; Evans, J. F.; George, S. R.; O'Dowd, B. F. : Discovery and mapping of ten novel G protein-coupled receptor genes. Gene 275: 83-91, 2001. ;

and

[88968] Wittenberger, T.; Schaller, H. C.; Hellebrand, S. : An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors. J. Molec. Biol.

[88969] Further studies establishing the function and utilities of GPR87 are found in John Hopkins OMIM database record ID 606379, and in sited publications numbered 10637 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Karyopherin Alpha 1 (importin alpha 5) (KPNA1, Accession XM_087256) is another VGAM2643 host target gene. KPNA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KPNA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KPNA1 BINDING SITE, designated SEQ ID:39151, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88970] Another function of VGAM2643 is therefore inhibition of Karyopherin Alpha 1 (importin alpha 5) (KPNA1, Accession XM_087256), a gene which promotes docking of import

substrates to the nuclear pore complex. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KPNA1. The function of KPNA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM859.Nuclear Factor of Activated T-cells, Cytoplasmic, Calcineurin-dependent 1 (NFATC1, Accession NM_006162) is another VGAM2643 host target gene. NFATC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NFATC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFATC1 BINDING SITE, designated SEQ ID:12817, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88971] Another function of VGAM2643 is therefore inhibition of Nuclear Factor of Activated T-cells, Cytoplasmic, Calcineurin-dependent 1 (NFATC1, Accession NM_006162), a gene which regulates he activation,proliferation,differentiation and programmed death of

ymphoid and nonlymphoid cells. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFATC1. The function of NFATC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM123.RPP30 (Accession NM_006413) is another VGAM2643 host target gene. RPP30 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPP30, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPP30 BINDING SITE, designated SEQ ID:13123, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88972] Another function of VGAM2643 is therefore inhibition of RPP30 (Accession NM_006413), a gene which is a component of ribonuclease p that processes 5' ends of precursor tRNAs. Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPP30. The function of RPP30 and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM230.Spastic Ataxia of Charlevoix-Saguenay (sacsin) (SACS, Accession XM_170738) is another VGAM2643 host target gene. SACS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SACS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SACS BINDING SITE, designated SEQ ID:45497, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88973] Another function of VGAM2643 is therefore inhibition of Spastic Ataxia of Charlevoix-Saguenay (sacsin) (SACS, Accession XM_170738). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SACS. Ras Homolog Gene Family, Member U (ARHU, Accession NM_021205) is another VGAM2643 host target gene. ARHU BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHU, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ARHU BINDING SITE, designated SEQ ID:22182, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88974] Another function of VGAM2643 is therefore inhibition of Ras Homolog Gene Family, Member U (ARHU, Accession NM_021205). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHU. Baculoviral IAP Repeat-containing 1 (BIRC1, Accession NM_004536) is another VGAM2643 host target gene. BIRC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIRC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIRC1 BINDING SITE, designated SEQ ID:10888, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88975] Another function of VGAM2643 is therefore inhibition of Baculoviral IAP Repeat-containing 1 (BIRC1, Accession NM_004536). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with BIRC1. Cat Eye Syndrome Chromosome Region, Candidate 1 (CECR1, Accession NM_017424) is another VGAM2643 host target gene. CECR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CECR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE, designated SEQ ID:18887, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88976] Another function of VGAM2643 is therefore inhibition of Cat Eye Syndrome Chromosome Region, Candidate 1 (CECR1, Accession NM_017424). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1. FLJ14437 (Accession NM_032578) is another VGAM2643 host target gene. FLJ14437 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14437, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of FLJ14437 BINDING SITE, designated SEQ ID:26312, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88977] Another function of VGAM2643 is therefore inhibition of FLJ14437 (Accession NM_032578). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14437. KIAA1940 (Accession XM_086981) is another VGAM2643 host target gene. KIAA1940 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1940 BINDING SITE, designated SEQ ID:39011, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88978] Another function of VGAM2643 is therefore inhibition of KIAA1940 (Accession XM_086981). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1940. ODZ2 (Accession XM_047995) is another

VGAM2643 host target gene. ODZ2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ODZ2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ODZ2 BINDING SITE, designated SEQ ID:35096, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88979] Another function of VGAM2643 is therefore inhibition of ODZ2 (Accession XM_047995). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ODZ2. Peptidylprolyl Isomerase (cyclophilin)-like 2 (PPIL2, Accession NM_014337) is another VGAM2643 host target gene. PPIL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPIL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPIL2 BINDING SITE, designated SEQ ID:15651, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88980] Another function of VGAM2643 is therefore inhibition of Peptidylprolyl Isomerase (cyclophilin)-like 2 (PPIL2, Accession NM_014337). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPIL2. LOC121441 (Accession XM_058561) is another VGAM2643 host target gene. LOC121441 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC121441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121441 BINDING SITE, designated SEQ ID:36660, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88981] Another function of VGAM2643 is therefore inhibition of LOC121441 (Accession XM_058561). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121441. LOC145945 (Accession XM_096908) is another VGAM2643 host target gene. LOC145945 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145945, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145945 BINDING SITE, designated SEQ ID:40631, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88982] Another function of VGAM2643 is therefore inhibition of LOC145945 (Accession XM_096908). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145945. LOC222008 (Accession XM_168361) is another VGAM2643 host target gene. LOC222008 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222008, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222008 BINDING SITE, designated SEQ ID:45128, to the nucleotide sequence of VGAM2643 RNA, herein designated VGAM RNA, also designated SEQ ID:5354.

[88983] Another function of VGAM2643 is therefore inhibition of LOC222008 (Accession XM_168361). Accordingly, utilities of VGAM2643 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC222008. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2644 (VGAM2644) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[88984] VGAM2644 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2644 was detected is described hereinabove with reference to Figs. 1-8.

[88985] VGAM2644 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea Aphid-borne Mosaic Virus. VGAM2644 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[88986] VGAM2644 gene encodes a VGAM2644 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2644 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2644 precursor RNA is desig-

nated SEQ ID:2630, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2630 is located at position 5711 relative to the genome of Cowpea Aphid-borne Mosaic Virus.

[88987] VGAM2644 precursor RNA folds onto itself, forming VGAM2644 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[88988] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2644 folded precursor RNA into VGAM2644 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2644 RNA is designated SEQ ID:5355, and is provided hereinbelow with reference to the sequence

listing part.

[88989] VGAM2644 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2644 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[88990] VGAM2644 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2644 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2644 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[88991] The complementary binding of VGAM2644 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2644 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2644 host target RNA into VGAM2644 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[88992] It is appreciated that VGAM2644 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2644 host target genes. The mRNA of each one of this plurality of VGAM2644 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2644 RNA, herein designated VGAM

RNA, and which when bound by VGAM2644 RNA causes inhibition of translation of respective one or more VGAM2644 host target proteins.

[88993] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2644 gene, herein designated VGAM GENE, on one or more VGAM2644 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[88994] It is yet further appreciated that a function of VGAM2644 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2644 include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2644 correlate with, and may be deduced from, the identity of the host target genes which VGAM2644 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[88995] Nucleotide sequences of the VGAM2644 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2644 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2644 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2644 are further described hereinbelow with reference to Table 1.

[88996] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2644 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2644 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[88997] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2644 gene, herein designated VGAM is

inhibition of expression of VGAM2644 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2644 correlate with, and may be deduced from, the identity of the target genes which VGAM2644 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[88998] Adenylate Kinase 3 (AK3, Accession NM_013410) is a VGAM2644 host target gene. AK3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AK3 BINDING SITE, designated SEQ ID:15072, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[88999] A function of VGAM2644 is therefore inhibition of Adenylate Kinase 3 (AK3, Accession NM_013410), a gene which Adenylate kinase 3; strongly similar to murine Ak4. Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AK3. The function of AK3 and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM135.ALEX3 (Accession NM_016607) is another VGAM2644 host target gene. ALEX3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ALEX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALEX3 BINDING SITE, designated SEQ ID:18712, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89000] Another function of VGAM2644 is therefore inhibition of ALEX3 (Accession NM_016607). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALEX3. EH-domain Containing 2 (EHD2, Accession NM_014601) is another VGAM2644 host target gene. EHD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EHD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EHD2 BIND-

ING SITE, designated SEQ ID:15965, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89001] Another function of VGAM2644 is therefore inhibition of EH-domain Containing 2 (EHD2, Accession NM_014601). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD2. Leukocyte Immunoglobulin-like Receptor, Subfamily B (with TM and ITIM domains), Member 4 (LILRB4, Accession NM_006847) is another VGAM2644 host target gene. LILRB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LILRB4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LILRB4 BINDING SITE, designated SEQ ID:13715, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89002] Another function of VGAM2644 is therefore inhibition of Leukocyte Immunoglobulin-like Receptor, Subfamily B (with TM and ITIM domains), Member 4 (LILRB4, Accession NM_006847). Accordingly, utilities of VGAM2644 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with LILRB4. Nuclear RNA Export Factor 2 (NXF2, Accession NM_022053) is another VGAM2644 host target gene. NXF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NXF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXF2 BINDING SITE, designated SEQ ID:22589, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89003] Another function of VGAM2644 is therefore inhibition of Nuclear RNA Export Factor 2 (NXF2, Accession NM_022053), a gene which is involved in the export of mrna from the nucleus to the cytoplasm. Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXF2. The function of NXF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM595.Tumor Protein P53 Binding Protein, 2 (TP53BP2, Accession NM_005426) is another VGAM2644

host target gene. TP53BP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TP53BP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP53BP2 BINDING SITE, designated SEQ ID:11894, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89004] Another function of VGAM2644 is therefore inhibition of Tumor Protein P53 Binding Protein, 2 (TP53BP2, Accession NM_005426), a gene which bindes p53. enhances the trans-activation function of p53 and induces the expression of p21. Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53BP2. The function of TP53BP2 has been established by previous studies. By immunoblot analysis, Iwabuchi et al. (1998) showed that expression of TP53BP2 or TP53BP1 (OMIM Ref. No. 605230) enhances the trans-activation function of p53 and induces the expression of p21 (CDKN1A; 116899). Immunofluorescence microscopy demonstrated that TP53BP2 is present only in the cytoplasm, regardless of p53 expres-

sion. Western blot analysis of fractionated cells confirmed that whereas p53 is found in both nuclear and cytosolic fractions, TP53BP2 is found only in the cytosol. Samuels-Lev et al. (2001) determined that the ASPP proteins interact with p53 (OMIM Ref. No. 191170) and specifically enhance p53-induced apoptosis but not cell cycle arrest. Inhibition of endogenous ASPP function suppressed the apoptotic function of endogenous p53 in response to apoptotic stimuli. ASPPs enhanced the DNA binding and transactivation function of p53 on the promoters of proapoptotic genes in vivo. Two tumor-derived p53 mutants with reduced apoptotic function were defective in cooperating with ASPP in apoptosis induction. Expression of the ASPPs was frequently downregulated in human breast carcinomas expressing wildtype p53 but not in those expressing mutant p53. Samuels-Lev et al. (2001) concluded that ASPPs regulate the tumor suppression function of p53 in vivo.

[89005] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[89006] Iwabuchi, K.; Li, B.; Massa, H. F.; Trask, B. J.; Date, T.; Fields, S. : Stimulation of p53-mediated transcriptional

activation by the p53-binding proteins, 53BP1 and 53BP2. J. Biol. Chem. 273: 26061-26068, 1998. ; and

[89007] Samuels-Lev, Y.; O'Connor, D. J.; Bergamaschi, D.; Trigiante, G.; Hsieh, J.-K.; Zhong, S.; Campargue, I.; Naumovski, L.; Crook, T.; Lu, X. : ASPP proteins specifically stimulate the apoptot.

[89008] Further studies establishing the function and utilities of TP53BP2 are found in John Hopkins OMIM database record ID 602143, and in sited publications numbered 5969-5973 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Cysteine and Tyrosine-rich 1 (CYYR1, Accession NM_052954) is another VGAM2644 host target gene. CYYR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYYR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYYR1 BINDING SITE, designated SEQ ID:27511, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89009] Another function of VGAM2644 is therefore inhibition of Cysteine and Tyrosine-rich 1 (CYYR1, Accession

NM_052954). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYYR1. FLJ20507 (Accession XM_012558) is another VGAM2644 host target gene. FLJ20507 BINDING SITE1 and FLJ20507 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ20507, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20507 BINDING SITE1 and FLJ20507 BINDING SITE2, designated SEQ ID:30221 and SEQ ID:19513 respectively, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89010] Another function of VGAM2644 is therefore inhibition of FLJ20507 (Accession XM_012558). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20507. KIAA0247 (Accession NM_014734) is another VGAM2644 host target gene. KIAA0247 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0247, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0247 BINDING SITE, designated SEQ ID:16370, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89011] Another function of VGAM2644 is therefore inhibition of KIAA0247 (Accession NM_014734). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0247. KIAA0453 (Accession XM_044546) is another VGAM2644 host target gene. KIAA0453 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0453, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0453 BINDING SITE, designated SEQ ID:34227, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89012] Another function of VGAM2644 is therefore inhibition of KIAA0453 (Accession XM_044546). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0453. KIAA0574 (Accession XM_045076) is another VGAM2644 host target gene. KIAA0574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0574, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0574 BINDING SITE, designated SEQ ID:34345, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89013] Another function of VGAM2644 is therefore inhibition of KIAA0574 (Accession XM_045076). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0574. KIAA0711 (Accession NM_014867) is another VGAM2644 host target gene. KIAA0711 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0711, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0711 BINDING SITE, designated SEQ ID:16958, to the nucleotide sequence of VGAM2644 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5355.

[89014] Another function of VGAM2644 is therefore inhibition of KIAA0711 (Accession NM_014867). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0711. KIAA1786 (Accession XM_038436) is another VGAM2644 host target gene. KIAA1786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1786 BINDING SITE, designated SEQ ID:32843, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89015] Another function of VGAM2644 is therefore inhibition of KIAA1786 (Accession XM_038436). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1786. poly(A) Binding Protein, Cytoplasmic 5 (PABPC5, Accession NM_080832) is another VGAM2644 host target gene. PABPC5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by PABPC5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PABPC5 BINDING SITE, designated SEQ ID:28095, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89016] Another function of VGAM2644 is therefore inhibition of poly(A) Binding Protein, Cytoplasmic 5 (PABPC5, Accession NM_080832). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PABPC5. PR Domain Containing 10 (PRDM10, Accession NM_020228) is another VGAM2644 host target gene. PRDM10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRDM10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM10 BINDING SITE, designated SEQ ID:21494, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89017] Another function of VGAM2644 is therefore inhibition of

PR Domain Containing 10 (PRDM10, Accession NM_020228). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM10. PRO1617 (Accession NM_018587) is another VGAM2644 host target gene. PRO1617 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1617, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1617 BINDING SITE, designated SEQ ID:20663, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89018] Another function of VGAM2644 is therefore inhibition of PRO1617 (Accession NM_018587). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1617. Protein Tyrosine Phosphatase, Receptor Type, U (PTPRU, Accession NM_133177) is another VGAM2644 host target gene. PTPRU BINDING SITE1 through PTPRU BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPRU, corre-

sponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRU BINDING SITE1 through PTPRU BINDING SITE3, designated SEQ ID:28400, SEQ ID:28405 and SEQ ID:12255 respectively, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89019] Another function of VGAM2644 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, U (PTPRU, Accession NM_133177). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRU. Ring Finger Protein 38 (RNF38, Accession NM_022781) is another VGAM2644 host target gene. RNF38 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF38, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF38 BINDING SITE, designated SEQ ID:23062, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89020] Another function of VGAM2644 is therefore inhibition of Ring Finger Protein 38 (RNF38, Accession NM_022781). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF38. LOC144347 (Accession XM_084832) is another VGAM2644 host target gene. LOC144347 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144347, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144347 BINDING SITE, designated SEQ ID:37723, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89021] Another function of VGAM2644 is therefore inhibition of LOC144347 (Accession XM_084832). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144347. LOC148581 (Accession XM_086243) is another VGAM2644 host target gene. LOC148581 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148581, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148581 BINDING SITE, designated SEQ ID:38567, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89022] Another function of VGAM2644 is therefore inhibition of LOC148581 (Accession XM_086243). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148581. LOC197259 (Accession XM_113849) is another VGAM2644 host target gene. LOC197259 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197259 BINDING SITE, designated SEQ ID:42470, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89023] Another function of VGAM2644 is therefore inhibition of LOC197259 (Accession XM_113849). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC197259. LOC93268 (Accession XM_050158) is another VGAM2644 host target gene. LOC93268 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93268 BINDING SITE, designated SEQ ID:35586, to the nucleotide sequence of VGAM2644 RNA, herein designated VGAM RNA, also designated SEQ ID:5355.

[89024] Another function of VGAM2644 is therefore inhibition of LOC93268 (Accession XM_050158). Accordingly, utilities of VGAM2644 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93268. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2645 (VGAM2645) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89025] VGAM2645 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2645 was detected is described hereinabove with reference to Figs. 1-8.

[89026] VGAM2645 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea Aphid-borne Mosaic Virus. VGAM2645 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89027] VGAM2645 gene encodes a VGAM2645 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2645 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2645 precursor RNA is designated SEQ ID:2631, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2631 is located at position 2957 relative to the genome of Cowpea Aphid-borne Mosaic Virus.

[89028] VGAM2645 precursor RNA folds onto itself, forming VGAM2645 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89029] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2645 folded precursor RNA into VGAM2645 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2645 RNA is designated SEQ ID:5356, and is provided hereinbelow with reference to the sequence listing part.

[89030] VGAM2645 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2645 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89031] VGAM2645 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2645 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2645 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89032] The complementary binding of VGAM2645 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2645 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2645 host target RNA into VGAM2645 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89033] It is appreciated that VGAM2645 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2645 host target genes. The mRNA of each one of this plurality of VGAM2645 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2645 RNA, herein designated VGAM RNA, and which when bound by VGAM2645 RNA causes inhibition of translation of respective one or more VGAM2645 host target proteins.

[89034] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2645 gene, herein designated VGAM GENE, on one or more VGAM2645 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89035] It is yet further appreciated that a function of VGAM2645 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2645 include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2645 correlate with, and may be deduced from, the identity of the host target genes which VGAM2645 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89036] Nucleotide sequences of the VGAM2645 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2645 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2645 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2645 are further described hereinbelow with reference to Table 1.

[89037] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2645 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2645 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89038] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2645 gene, herein designated VGAM is inhibition of expression of VGAM2645 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2645 correlate with, and may be deduced from, the identity of the target genes which VGAM2645 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89039] Spinocerebellar Ataxia 7 (olivopontocerebellar atrophy with retinal degeneration) (SCA7, Accession NM_000333) is a VGAM2645 host target gene. SCA7 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SCA7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCA7 BINDING SITE, designated SEQ ID:5885, to the nucleotide sequence of VGAM2645 RNA, herein designated VGAM RNA, also designated SEQ ID:5356.

[89040] A function of VGAM2645 is therefore inhibition of Spinocerebellar Ataxia 7 (olivopontocerebellar atrophy with retinal degeneration) (SCA7, Accession NM_000333). Accordingly, utilities of VGAM2645 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCA7. KIAA1028 (Accession XM_166324) is another VGAM2645 host target gene. KIAA1028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1028 BINDING SITE, designated SEQ ID:44156, to the nucleotide sequence of VGAM2645 RNA, herein designated VGAM RNA, also designated SEQ

ID:5356.

[89041] Another function of VGAM2645 is therefore inhibition of KIAA1028 (Accession XM_166324). Accordingly, utilities of VGAM2645 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1028. LOC148254 (Accession XM_086121) is another VGAM2645 host target gene. LOC148254 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148254, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148254 BINDING SITE, designated SEQ ID:38500, to the nucleotide sequence of VGAM2645 RNA, herein designated VGAM RNA, also designated SEQ ID:5356.

[89042] Another function of VGAM2645 is therefore inhibition of LOC148254 (Accession XM_086121). Accordingly, utilities of VGAM2645 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148254. LOC256306 (Accession XM_172976) is another VGAM2645 host target gene. LOC256306 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256306, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256306 BINDING SITE, designated SEQ ID:46234, to the nucleotide sequence of VGAM2645 RNA, herein designated VGAM RNA, also designated SEQ ID:5356.

[89043] Another function of VGAM2645 is therefore inhibition of LOC256306 (Accession XM_172976). Accordingly, utilities of VGAM2645 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256306. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2646 (VGAM2646) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89044] VGAM2646 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2646 was detected is described hereinabove with reference to Figs. 1-8.

[89045] VGAM2646 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea Aphid-borne

Mosaic Virus. VGAM2646 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89046] VGAM2646 gene encodes a VGAM2646 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2646 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2646 precursor RNA is designated SEQ ID:2632, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2632 is located at position 1728 relative to the genome of Cowpea Aphid-borne Mosaic Virus.

[89047] VGAM2646 precursor RNA folds onto itself, forming VGAM2646 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89048] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2646 folded precursor RNA into VGAM2646 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2646 RNA is designated SEQ ID:5357, and is provided hereinbelow with reference to the sequence listing part.

[89049] VGAM2646 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2646 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89050] VGAM2646 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2646 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2646 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89051] The complementary binding of VGAM2646 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2646 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2646 host target RNA into VGAM2646 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89052] It is appreciated that VGAM2646 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2646 host target genes. The mRNA of each one of this plurality of VGAM2646 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2646 RNA, herein designated VGAM RNA, and which when bound by VGAM2646 RNA causes inhibition of translation of respective one or more VGAM2646 host target proteins.

[89053] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2646 gene, herein designated VGAM GENE, on one or more VGAM2646 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89054] It is yet further appreciated that a function of VGAM2646 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2646 correlate with, and may be deduced from, the identity of the host target genes which VGAM2646 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89055] Nucleotide sequences of the VGAM2646 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2646 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2646 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2646 are further described hereinbelow with reference to Table 1.

[89056] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2646 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2646 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89057] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2646 gene, herein designated VGAM is inhibition of expression of VGAM2646 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2646 correlate with, and may be deduced from, the identity of the target genes which VGAM2646 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89058] Astrotactin (ASTN, Accession XM_045113) is a VGAM2646 host target gene. ASTN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ASTN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASTN BINDING SITE, designated SEQ ID:34362, to the nucleotide sequence of

VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89059] A function of VGAM2646 is therefore inhibition of Astrotactin (ASTN, Accession XM_045113). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASTN. UDP-
N-
acetyl-al-
pha-
D-galac-
tosamine:(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (GalNAc-T) (GALGT, Accession NM_001478) is another VGAM2646 host target gene. GALGT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GALGT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALGT BINDING SITE, designated SEQ ID:7213, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89060] Another function of VGAM2646 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (GalNAc-T) (GALGT, Accession NM_001478), a gene which is involved in the biosynthesis of gangliosides gm2, gd2 and ga2. Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALGT. The function of GALGT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM179.KIAA0442 (Accession NM_015570) is another VGAM2646 host target gene. KIAA0442 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0442, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0442 BINDING SITE, designated SEQ

ID:17841, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89061] Another function of VGAM2646 is therefore inhibition of KIAA0442 (Accession NM_015570). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0442. Leucine-zipper-like Transcriptional Regulator, 1 (LZTR1, Accession NM_006767) is another VGAM2646 host target gene. LZTR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LZTR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LZTR1 BINDING SITE, designated SEQ ID:13639, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89062] Another function of VGAM2646 is therefore inhibition of Leucine-zipper-like Transcriptional Regulator, 1 (LZTR1, Accession NM_006767). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTR1.

Nitric Oxide Synthase 1 (neuronal) (NOS1, Accession NM_000620) is another VGAM2646 host target gene. NOS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NOS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NOS1 BINDING SITE, designated SEQ ID:6232, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89063] Another function of VGAM2646 is therefore inhibition of Nitric Oxide Synthase 1 (neuronal) (NOS1, Accession NM_000620), a gene which produces nitric oxide (no) which is a messenger molecule with diverse functions throughout the body. Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOS1. The function of NOS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.Protocadherin 11 X-linked (PCDH11X, Accession NM_032968) is another VGAM2646 host target gene. PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2 are

HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDH11X, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2, designated SEQ ID:26797 and SEQ ID:26812 respectively, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89064] Another function of VGAM2646 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032968), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.SMAC (Accession NM_138930) is another VGAM2646 host target gene. SMAC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region

of mRNA encoded by SMAC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMAC BINDING SITE, designated SEQ ID:29048, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89065] Another function of VGAM2646 is therefore inhibition of SMAC (Accession NM_138930), a gene which promotes apoptosis via caspase activation. Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAC. The function of SMAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.UV Radiation Resistance Associated Gene (UVRAG, Accession NM_003369) is another VGAM2646 host target gene. UVRAG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UVRAG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UVRAG BINDING SITE, des-

ignated SEQ ID:9395, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89066] Another function of VGAM2646 is therefore inhibition of UV Radiation Resistance Associated Gene (UVRAG, Accession NM_003369). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UVRAG. A Disintegrin and Metalloproteinase Domain 9 (meltrin gamma) (ADAM9, Accession NM_003816) is another VGAM2646 host target gene. ADAM9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAM9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM9 BINDING SITE, designated SEQ ID:9907, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89067] Another function of VGAM2646 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 9 (meltrin gamma) (ADAM9, Accession NM_003816). Accordingly, utilities of VGAM2646 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with ADAM9. Adaptor-related Protein Complex 3, Mu 1 Subunit (AP3M1, Accession NM_012095) is another VGAM2646 host target gene. AP3M1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP3M1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP3M1 BINDING SITE, designated SEQ ID:14396, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89068] Another function of VGAM2646 is therefore inhibition of Adaptor-related Protein Complex 3, Mu 1 Subunit (AP3M1, Accession NM_012095). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3M1. Aquaporin 10 (AQP10, Accession NM_080429) is another VGAM2646 host target gene. AQP10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AQP10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of AQP10 BINDING SITE, designated SEQ ID:27841, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89069] Another function of VGAM2646 is therefore inhibition of Aquaporin 10 (AQP10, Accession NM_080429). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP10. CDT1 (Accession XM_085327) is another VGAM2646 host target gene. CDT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CDT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDT1 BINDING SITE, designated SEQ ID:38070, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89070] Another function of VGAM2646 is therefore inhibition of CDT1 (Accession XM_085327). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDT1. Carbohydrate (chondroitin) Synthase 1 (CHSY1, Accession

NM_014918) is another VGAM2646 host target gene. CHSY1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHSY1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHSY1 BINDING SITE, designated SEQ ID:17172, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89071] Another function of VGAM2646 is therefore inhibition of Carbohydrate (chondroitin) Synthase 1 (CHSY1, Accession NM_014918). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHSY1. DKFZp434E2220 (Accession NM_017612) is another VGAM2646 host target gene. DKFZp434E2220 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434E2220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434E2220 BINDING SITE, designated SEQ ID:19113, to the nucleotide

sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89072] Another function of VGAM2646 is therefore inhibition of DKFZp434E2220 (Accession NM_017612). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2220. DKFZP434L1435 (Accession XM_166401) is another VGAM2646 host target gene. DKFZP434L1435 BINDING SITE1 through DKFZP434L1435 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DKFZP434L1435, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L1435 BINDING SITE1 through DKFZP434L1435 BINDING SITE3, designated SEQ ID:44265, SEQ ID:46701 and SEQ ID:46663 respectively, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89073] Another function of VGAM2646 is therefore inhibition of DKFZP434L1435 (Accession XM_166401). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP434L1435. FLJ13195 (Accession NM_022906) is another VGAM2646 host target gene. FLJ13195 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13195 BINDING SITE, designated SEQ ID:23204, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89074] Another function of VGAM2646 is therefore inhibition of FLJ13195 (Accession NM_022906). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13195. FLJ14547 (Accession NM_032804) is another VGAM2646 host target gene. FLJ14547 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14547, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14547 BINDING SITE, designated SEQ ID:26560, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM

RNA, also designated SEQ ID:5357.

[89075] Another function of VGAM2646 is therefore inhibition of FLJ14547 (Accession NM_032804). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14547. FLJ20079 (Accession NM_017656) is another VGAM2646 host target gene. FLJ20079 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20079, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20079 BINDING SITE, designated SEQ ID:19166, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89076] Another function of VGAM2646 is therefore inhibition of FLJ20079 (Accession NM_017656). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20079. FLJ20342 (Accession NM_017774) is another VGAM2646 host target gene. FLJ20342 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20342, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20342 BINDING SITE, designated SEQ ID:19397, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89077] Another function of VGAM2646 is therefore inhibition of FLJ20342 (Accession NM_017774). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20342. FLJ20519 (Accession NM_017860) is another VGAM2646 host target gene. FLJ20519 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20519 BINDING SITE, designated SEQ ID:19538, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89078] Another function of VGAM2646 is therefore inhibition of FLJ20519 (Accession NM_017860). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20519. FLJ22169 (Accession NM_024085) is another VGAM2646 host target gene. FLJ22169 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22169, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22169 BINDING SITE, designated SEQ ID:23526, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89079] Another function of VGAM2646 is therefore inhibition of FLJ22169 (Accession NM_024085). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22169. KIAA0561 (Accession XM_038150) is another VGAM2646 host target gene. KIAA0561 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0561, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0561 BINDING SITE, designated SEQ ID:32768, to the

nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89080] Another function of VGAM2646 is therefore inhibition of KIAA0561 (Accession XM_038150). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0561. KIAA0779 (Accession XM_098229) is another VGAM2646 host target gene. KIAA0779 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0779, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0779 BINDING SITE, designated SEQ ID:41502, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89081] Another function of VGAM2646 is therefore inhibition of KIAA0779 (Accession XM_098229). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0779. KIAA1396 (Accession XM_032054) is another VGAM2646 host target gene. KIAA1396 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1396, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1396 BINDING SITE, designated SEQ ID:31544, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89082] Another function of VGAM2646 is therefore inhibition of KIAA1396 (Accession XM_032054). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1396. KIAA1553 (Accession XM_166320) is another VGAM2646 host target gene. KIAA1553 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1553 BINDING SITE, designated SEQ ID:44140, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89083] Another function of VGAM2646 is therefore inhibition of KIAA1553 (Accession XM_166320). Accordingly, utilities

of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1553. KIAA1602 (Accession XM_035497) is another VGAM2646 host target gene. KIAA1602 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1602, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1602 BINDING SITE, designated SEQ ID:32276, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89084] Another function of VGAM2646 is therefore inhibition of KIAA1602 (Accession XM_035497). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1602. LIM and SH3 Protein 1 (LASP1, Accession NM_006148) is another VGAM2646 host target gene. LASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of LASP1 BINDING SITE, designated SEQ ID:12805, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89085] Another function of VGAM2646 is therefore inhibition of LIM and SH3 Protein 1 (LASP1, Accession NM_006148). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LASP1. Mitogen-activated Protein Kinase 8 Interacting Protein 3 (MAPK8IP3, Accession NM_033392) is another VGAM2646 host target gene. MAPK8IP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPK8IP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK8IP3 BINDING SITE, designated SEQ ID:27217, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89086] Another function of VGAM2646 is therefore inhibition of Mitogen-activated Protein Kinase 8 Interacting Protein 3 (MAPK8IP3, Accession NM_033392). Accordingly, utilities

of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK8IP3. Nudix (nucleoside diphosphate linked moiety X)-type Motif 12 (NUDT12, Accession NM_031438) is another VGAM2646 host target gene. NUDT12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUDT12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUDT12 BINDING SITE, designated SEQ ID:25446, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89087] Another function of VGAM2646 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety X)-type Motif 12 (NUDT12, Accession NM_031438). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT12. Paired Mesoderm Homeobox 2b (PMX2B, Accession NM_003924) is another VGAM2646 host target gene. PMX2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PMX2B, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMX2B BINDING SITE, designated SEQ ID:10014, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89088] Another function of VGAM2646 is therefore inhibition of Paired Mesoderm Homeobox 2b (PMX2B, Accession NM_003924). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMX2B. PRO2389 (Accession XM_033334) is another VGAM2646 host target gene. PRO2389 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2389, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2389 BINDING SITE, designated SEQ ID:31879, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89089] Another function of VGAM2646 is therefore inhibition of PRO2389 (Accession XM_033334). Accordingly, utilities of

VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2389. SIMRP7 (Accession XM_166462) is another VGAM2646 host target gene. SIMRP7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIMRP7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIMRP7 BINDING SITE, designated SEQ ID:44369, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89090] Another function of VGAM2646 is therefore inhibition of SIMRP7 (Accession XM_166462). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIMRP7. TCF-3 (Accession NM_031283) is another VGAM2646 host target gene. TCF-3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCF-3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF-3 BINDING SITE, designated SEQ

ID:25307, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89091] Another function of VGAM2646 is therefore inhibition of TCF-3 (Accession NM_031283). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF-3. TUBB5 (Accession NM_006087) is another VGAM2646 host target gene. TUBB5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUBB5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUBB5 BINDING SITE, designated SEQ ID:12732, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89092] Another function of VGAM2646 is therefore inhibition of TUBB5 (Accession NM_006087). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUBB5. Zinc Finger Protein 31 (KOX 29) (ZNF31, Accession XM_036305) is another VGAM2646 host target gene.

ZNF31 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF31 BINDING SITE, designated SEQ ID:32421, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89093] Another function of VGAM2646 is therefore inhibition of Zinc Finger Protein 31 (KOX 29) (ZNF31, Accession XM_036305). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF31. Zinc Finger Protein 317 (ZNF317, Accession XM_050435) is another VGAM2646 host target gene. ZNF317 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF317 BINDING SITE, designated SEQ ID:35634, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM

RNA, also designated SEQ ID:5357.

[89094] Another function of VGAM2646 is therefore inhibition of Zinc Finger Protein 317 (ZNF317, Accession XM_050435). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF317. LOC130644 (Accession XM_065813) is another VGAM2646 host target gene. LOC130644 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130644, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130644 BINDING SITE, designated SEQ ID:37302, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89095] Another function of VGAM2646 is therefore inhibition of LOC130644 (Accession XM_065813). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130644. LOC149650 (Accession XM_086623) is another VGAM2646 host target gene. LOC149650 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC149650, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149650 BINDING SITE, designated SEQ ID:38798, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89096] Another function of VGAM2646 is therefore inhibition of LOC149650 (Accession XM_086623). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149650. LOC150776 (Accession XM_032542) is another VGAM2646 host target gene. LOC150776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150776 BINDING SITE, designated SEQ ID:31674, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89097] Another function of VGAM2646 is therefore inhibition of LOC150776 (Accession XM_032542). Accordingly, utilities

of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150776. LOC256158 (Accession XM_175125) is another VGAM2646 host target gene. LOC256158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256158 BINDING SITE, designated SEQ ID:46630, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89098] Another function of VGAM2646 is therefore inhibition of LOC256158 (Accession XM_175125). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256158. LOC90841 (Accession XM_034427) is another VGAM2646 host target gene. LOC90841 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC90841 BINDING SITE, designated SEQ ID:32112, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89099] Another function of VGAM2646 is therefore inhibition of LOC90841 (Accession XM_034427). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90841. LOC92609 (Accession XM_053074) is another VGAM2646 host target gene. LOC92609 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92609, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92609 BINDING SITE, designated SEQ ID:36060, to the nucleotide sequence of VGAM2646 RNA, herein designated VGAM RNA, also designated SEQ ID:5357.

[89100] Another function of VGAM2646 is therefore inhibition of LOC92609 (Accession XM_053074). Accordingly, utilities of VGAM2646 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92609. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2647 (VGAM2647) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89101] VGAM2647 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2647 was detected is described hereinabove with reference to Figs. 1-8.

[89102] VGAM2647 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea Aphid-borne Mosaic Virus. VGAM2647 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89103] VGAM2647 gene encodes a VGAM2647 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2647 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2647 precursor RNA is designated SEQ ID:2633, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2633 is located at position 7881 relative to the

genome of Cowpea Aphid-borne Mosaic Virus.

[89104] VGAM2647 precursor RNA folds onto itself, forming VGAM2647 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89105] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2647 folded precursor RNA into VGAM2647 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2647 RNA is designated SEQ ID:5358, and is provided hereinbelow with reference to the sequence listing part.

[89106] VGAM2647 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2647 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89107] VGAM2647 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2647 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2647 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89108] The complementary binding of VGAM2647 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2647 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2647 host target RNA into VGAM2647 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89109] It is appreciated that VGAM2647 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2647 host target genes. The mRNA of each one of this plurality of VGAM2647 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2647 RNA, herein designated VGAM RNA, and which when bound by VGAM2647 RNA causes inhibition of translation of respective one or more VGAM2647 host target proteins.

[89110] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2647 gene, herein designated VGAM GENE, on one or more VGAM2647 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89111] It is yet further appreciated that a function of VGAM2647 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2647 include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of

VGAM2647 correlate with, and may be deduced from, the identity of the host target genes which VGAM2647 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89112] Nucleotide sequences of the VGAM2647 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2647 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2647 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2647 are further described hereinbelow with reference to Table 1.

[89113] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2647 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2647 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89114] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2647 gene, herein designated VGAM is inhibition of expression of VGAM2647 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2647 correlate with, and may be deduced

from, the identity of the target genes which VGAM2647 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89115] Nebulin-related Anchoring Protein (NRAP, Accession NM_006175) is a VGAM2647 host target gene. NRAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NRAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRAP BINDING SITE, designated SEQ ID:12832, to the nucleotide sequence of VGAM2647 RNA, herein designated VGAM RNA, also designated SEQ ID:5358.

[89116] A function of VGAM2647 is therefore inhibition of Nebulin-related Anchoring Protein (NRAP, Accession NM_006175), a gene which performs an anchoring function to link the terminal actin filaments of myofibrils to protein complexes located beneath the sarcolemma. Accordingly, utilities of VGAM2647 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRAP. The function of NRAP and its association with various diseases and clinical conditions, has been established by previous studies, as described here-

inabove with reference to VGAM649.LOC115294 (Accession XM_054302) is another VGAM2647 host target gene. LOC115294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115294 BINDING SITE, designated SEQ ID:36144, to the nucleotide sequence of VGAM2647 RNA, herein designated VGAM RNA, also designated SEQ ID:5358.

[89117] Another function of VGAM2647 is therefore inhibition of LOC115294 (Accession XM_054302). Accordingly, utilities of VGAM2647 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115294. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2648 (VGAM2648) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89118] VGAM2648 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2648 was detected is described hereinabove with reference to Figs. 1-8.

[89119] VGAM2648 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea Aphid-borne Mosaic Virus. VGAM2648 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89120] VGAM2648 gene encodes a VGAM2648 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2648 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2648 precursor RNA is designated SEQ ID:2634, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2634 is located at position 7656 relative to the genome of Cowpea Aphid-borne Mosaic Virus.

[89121] VGAM2648 precursor RNA folds onto itself, forming VGAM2648 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89122] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2648 folded precursor RNA into VGAM2648 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2648 RNA is designated SEQ ID:5359, and is provided hereinbelow with reference to the sequence listing part.

[89123] VGAM2648 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2648 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89124] VGAM2648 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2648 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2648 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89125] The complementary binding of VGAM2648 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2648 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2648 host target RNA into VGAM2648 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89126] It is appreciated that VGAM2648 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2648 host target genes. The mRNA of each one of this plurality of VGAM2648 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2648 RNA, herein designated VGAM RNA, and which when bound by VGAM2648 RNA causes inhibition of translation of respective one or more VGAM2648 host target proteins.

[89127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2648 gene, herein designated VGAM GENE, on one or more VGAM2648 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89128] It is yet further appreciated that a function of VGAM2648 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2648 include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2648 correlate with, and may be deduced from, the identity of the host target genes which VGAM2648 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89129] Nucleotide sequences of the VGAM2648 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2648 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2648 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2648 are further described hereinbelow with reference to Table 1.

[89130] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2648 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2648 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89131] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2648 gene, herein designated VGAM is inhibition of expression of VGAM2648 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2648 correlate with, and may be deduced from, the identity of the target genes which VGAM2648 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89132] Prominin-like 1 (mouse) (PROML1, Accession NM_006017) is a VGAM2648 host target gene. PROML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by PROML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PROML1 BINDING SITE, designated SEQ ID:12633, to the nucleotide sequence of VGAM2648 RNA, herein designated VGAM RNA, also designated SEQ ID:5359.

[89133] A function of VGAM2648 is therefore inhibition of Prominin-like 1 (mouse) (PROML1, Accession NM_006017), a gene which is a Transmembrane protein. Accordingly, utilities of VGAM2648 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROML1. The function of PROML1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM905.FLJ13052 (Accession NM_023018) is another VGAM2648 host target gene. FLJ13052 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13052, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13052 BINDING SITE, designated SEQ

ID:23282, to the nucleotide sequence of VGAM2648 RNA, herein designated VGAM RNA, also designated SEQ ID:5359.

[89134] Another function of VGAM2648 is therefore inhibition of FLJ13052 (Accession NM_023018). Accordingly, utilities of VGAM2648 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13052. HSPC063 (Accession NM_014155) is another VGAM2648 host target gene. HSPC063 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSPC063, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPC063 BINDING SITE, designated SEQ ID:15439, to the nucleotide sequence of VGAM2648 RNA, herein designated VGAM RNA, also designated SEQ ID:5359.

[89135] Another function of VGAM2648 is therefore inhibition of HSPC063 (Accession NM_014155). Accordingly, utilities of VGAM2648 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC063. Proteasome (prosome, macropain) 26S Subunit, Non-ATPase, 12 (PSMD12, Accession NM_002816) is an-

other VGAM2648 host target gene. PSMD12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSMD12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSMD12 BINDING SITE, designated SEQ ID:8683, to the nucleotide sequence of VGAM2648 RNA, herein designated VGAM RNA, also designated SEQ ID:5359.

[89136] Another function of VGAM2648 is therefore inhibition of Proteasome (prosome, macropain) 26S Subunit, Non-ATPase, 12 (PSMD12, Accession NM_002816). Accordingly, utilities of VGAM2648 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSMD12. LOC158055 (Accession XM_088453) is another VGAM2648 host target gene. LOC158055 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158055, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158055 BINDING SITE, designated SEQ ID:39702, to the nucleotide sequence of VGAM2648 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5359.

[89137] Another function of VGAM2648 is therefore inhibition of LOC158055 (Accession XM_088453). Accordingly, utilities of VGAM2648 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158055. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2649 (VGAM2649) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89138] VGAM2649 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2649 was detected is described hereinabove with reference to Figs. 1-8.

[89139] VGAM2649 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpea Aphid-borne Mosaic Virus. VGAM2649 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89140] VGAM2649 gene encodes a VGAM2649 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2649 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2649 precursor RNA is designated SEQ ID:2635, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2635 is located at position 2803 relative to the genome of Cowpea Aphid-borne Mosaic Virus.

[89141] VGAM2649 precursor RNA folds onto itself, forming VGAM2649 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89142] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2649 folded precursor RNA into VGAM2649 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2649 RNA is designated SEQ ID:5360, and is provided hereinbelow with reference to the sequence listing part.

[89143] VGAM2649 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2649 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89144] VGAM2649 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2649 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2649 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89145] The complementary binding of VGAM2649 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2649 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2649 host target RNA into VGAM2649 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89146] It is appreciated that VGAM2649 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2649 host target genes. The mRNA of

each one of this plurality of VGAM2649 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2649 RNA, herein designated VGAM RNA, and which when bound by VGAM2649 RNA causes inhibition of translation of respective one or more VGAM2649 host target proteins.

[89147] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2649 gene, herein designated VGAM GENE, on one or more VGAM2649 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[89148] It is yet further appreciated that a function of VGAM2649 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2649 include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2649 correlate with, and may be deduced from, the identity of the host target genes which VGAM2649 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89149] Nucleotide sequences of the VGAM2649 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2649 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2649 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2649 are further described hereinbelow with reference to Table 1.

[89150] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2649 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2649 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89151] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2649 gene, herein designated VGAM is inhibition of expression of VGAM2649 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2649 correlate with, and may be deduced from, the identity of the target genes which VGAM2649 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89152] Protein Kinase C, Beta 1 (PRKCB1, Accession XM_047187) is a VGAM2649 host target gene. PRKCB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKCB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKCB1 BINDING SITE, designated SEQ ID:34902, to the nucleotide sequence of VGAM2649 RNA, herein designated VGAM RNA, also designated SEQ ID:5360.

[89153] A function of VGAM2649 is therefore inhibition of Protein Kinase C, Beta 1 (PRKCB1, Accession XM_047187), a gene which is a calcium-activated, phospholipid-dependent,

serine- and threonine-specific enzyme. Accordingly, utilities of VGAM2649 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKCB1. The function of PRKCB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2065.Solute Carrier Family 16 (monocarboxylic acid transporters), Member 2 (putative transporter) (SLC16A2, Accession NM_006517) is another VGAM2649 host target gene. SLC16A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC16A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC16A2 BINDING SITE, designated SEQ ID:13273, to the nucleotide sequence of VGAM2649 RNA, herein designated VGAM RNA, also designated SEQ ID:5360.

[89154] Another function of VGAM2649 is therefore inhibition of Solute Carrier Family 16 (monocarboxylic acid transporters), Member 2 (putative transporter) (SLC16A2, Accession NM_006517). Accordingly, utilities of VGAM2649 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with SLC16A2. MGC4415 (Accession NM_031484) is another VGAM2649 host target gene. MGC4415 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4415, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4415 BINDING SITE, designated SEQ ID:25573, to the nucleotide sequence of VGAM2649 RNA, herein designated VGAM RNA, also designated SEQ ID:5360.

[89155] Another function of VGAM2649 is therefore inhibition of MGC4415 (Accession NM_031484). Accordingly, utilities of VGAM2649 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4415. LOC126669 (Accession XM_060121) is another VGAM2649 host target gene. LOC126669 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126669, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE, designated SEQ ID:37161, to

the nucleotide sequence of VGAM2649 RNA, herein designated VGAM RNA, also designated SEQ ID:5360.

[89156] Another function of VGAM2649 is therefore inhibition of LOC126669 (Accession XM_060121). Accordingly, utilities of VGAM2649 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669. LOC195977 (Accession XM_113625) is another VGAM2649 host target gene. LOC195977 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC195977, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC195977 BINDING SITE, designated SEQ ID:42299, to the nucleotide sequence of VGAM2649 RNA, herein designated VGAM RNA, also designated SEQ ID:5360.

[89157] Another function of VGAM2649 is therefore inhibition of LOC195977 (Accession XM_113625). Accordingly, utilities of VGAM2649 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC195977. LOC51026 (Accession NM_016072) is another VGAM2649 host target gene. LOC51026 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC51026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51026 BINDING SITE, designated SEQ ID:18143, to the nucleotide sequence of VGAM2649 RNA, herein designated VGAM RNA, also designated SEQ ID:5360.

[89158] Another function of VGAM2649 is therefore inhibition of LOC51026 (Accession NM_016072). Accordingly, utilities of VGAM2649 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51026. LOC91565 (Accession XM_039231) is another VGAM2649 host target gene. LOC91565 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91565 BINDING SITE, designated SEQ ID:33025, to the nucleotide sequence of VGAM2649 RNA, herein designated VGAM RNA, also designated SEQ ID:5360.

[89159] Another function of VGAM2649 is therefore inhibition of LOC91565 (Accession XM_039231). Accordingly, utilities

of VGAM2649 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91565. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2650 (VGAM2650) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89160] VGAM2650 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2650 was detected is described hereinabove with reference to Figs. 1-8.

[89161] VGAM2650 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Trichomonas Vaginalis Virus 3. VGAM2650 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89162] VGAM2650 gene encodes a VGAM2650 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2650 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2650 precursor RNA is designated SEQ ID:2636, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2636 is located at position 2782 relative to the genome of Trichomonas Vaginalis Virus 3.

[89163] VGAM2650 precursor RNA folds onto itself, forming VGAM2650 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89164] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2650 folded precursor RNA into VGAM2650 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2650 RNA is designated SEQ ID:5361, and

is provided hereinbelow with reference to the sequence listing part.

[89165] VGAM2650 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2650 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89166] VGAM2650 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2650 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2650 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89167] The complementary binding of VGAM2650 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2650 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2650 host target RNA into VGAM2650 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89168] It is appreciated that VGAM2650 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2650 host target genes. The mRNA of each one of this plurality of VGAM2650 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2650 RNA, herein designated VGAM RNA, and which when bound by VGAM2650 RNA causes inhibition of translation of respective one or more VGAM2650 host target proteins.

[89169] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2650 gene, herein designated VGAM GENE, on one or more VGAM2650 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89170] It is yet further appreciated that a function of VGAM2650 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2650 include diagnosis, prevention and treatment of viral infection by Trichomonas Vaginalis Virus 3. Specific functions, and accordingly utilities, of VGAM2650 correlate with, and may be deduced from, the identity of the host target genes which VGAM2650 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89171] Nucleotide sequences of the VGAM2650 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2650 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2650 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2650 are further described hereinbelow with reference to Table 1.

[89172] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2650 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2650 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89173] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2650 gene, herein designated VGAM is inhibition of expression of VGAM2650 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2650 correlate with, and may be deduced from, the identity of the target genes which VGAM2650 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89174] MGC10960 (Accession NM_032653) is a VGAM2650 host target gene. MGC10960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10960 BINDING SITE, designated SEQ ID:26386, to the nucleotide sequence of VGAM2650 RNA, herein designated VGAM RNA, also designated SEQ ID:5361.

[89175] A function of VGAM2650 is therefore inhibition of MGC10960 (Accession NM_032653). Accordingly, utilities of VGAM2650 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10960. LOC220514 (Accession XM_017498) is another VGAM2650 host target gene. LOC220514 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220514 BINDING SITE, designated SEQ ID:30324, to the nucleotide sequence of VGAM2650 RNA, herein designated VGAM RNA, also designated SEQ ID:5361.

[89176] Another function of VGAM2650 is therefore inhibition of LOC220514 (Accession XM_017498). Accordingly, utilities of VGAM2650 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220514. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2651 (VGAM2651) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89177] VGAM2651 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2651 was detected is described hereinabove with reference to Figs. 1-8.

[89178] VGAM2651 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Trichomonas Vaginalis Virus 3. VGAM2651 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89179] VGAM2651 gene encodes a VGAM2651 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2651 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2651 precursor RNA is designated SEQ ID:2637, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2637 is located at position 3926 relative to the genome of Trichomonas Vaginalis Virus 3.

[89180] VGAM2651 precursor RNA folds onto itself, forming VGAM2651 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[89181] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2651 folded precursor RNA into VGAM2651 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2651 RNA is designated SEQ ID:5362, and is provided hereinbelow with reference to the sequence listing part.

[89182] VGAM2651 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2651 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89183] VGAM2651 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2651 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2651 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2651 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89184] The complementary binding of VGAM2651 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2651 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2651 host target RNA into VGAM2651 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89185] It is appreciated that VGAM2651 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2651 host target genes. The mRNA of each one of this plurality of VGAM2651 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2651 RNA, herein designated VGAM RNA, and which when bound by VGAM2651 RNA causes inhibition of translation of respective one or more VGAM2651 host target proteins.

[89186] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2651 gene, herein designated VGAM GENE, on one or more VGAM2651 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89187] It is yet further appreciated that a function of VGAM2651 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of viral infection by Trichomonas Vaginalis Virus 3. Specific functions, and accordingly utilities, of VGAM2651 correlate with, and may be deduced from, the identity of the host target genes which VGAM2651 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89188] Nucleotide sequences of the VGAM2651 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2651 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2651 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2651 are further described hereinbelow with reference to Table 1.

[89189] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2651 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2651 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89190] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2651 gene, herein designated VGAM is inhibition of expression of VGAM2651 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2651 correlate with, and may be deduced from, the identity of the target genes which VGAM2651 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89191] Adducin 2 (beta) (ADD2, Accession NM_017485) is a VGAM2651 host target gene. ADD2 BINDING SITE1 through ADD2 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADD2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of ADD2 BINDING SITE1 through ADD2 BINDING SITE4, designated SEQ ID:18942, SEQ ID:18945, SEQ ID:18950 and SEQ ID:18937 respectively, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89192] A function of VGAM2651 is therefore inhibition of Adducin 2 (beta) (ADD2, Accession NM_017485), a gene which membrane-cytoskeleton- protein that promotes the assembly of the spectrin-actin network. Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADD2. The function of ADD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1185.Alpha Thalassemia/mental Retardation Syndrome X-linked (RAD54 homolog, S. cerevisiae) (ATRX, Accession NM_000489) is another VGAM2651 host target gene. ATRX BINDING SITE1 and ATRX BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ATRX, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the comple-

mentarity of the nucleotide sequences of ATRX BINDING SITE1 and ATRX BINDING SITE2, designated SEQ ID:6099 and SEQ ID:8609 respectively, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89193] Another function of VGAM2651 is therefore inhibition of Alpha Thalassemia/mental Retardation Syndrome X-linked (RAD54 homolog, S. cerevisiae) (ATRX, Accession NM_000489). Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATRX. DKFZP434L187 (Accession XM_044070) is another VGAM2651 host target gene. DKFZP434L187 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434L187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L187 BINDING SITE, designated SEQ ID:34128, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89194] Another function of VGAM2651 is therefore inhibition of DKFZP434L187 (Accession XM_044070). Accordingly, util-

ities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434L187. FLJ11506 (Accession NM_024666) is another VGAM2651 host target gene. FLJ11506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11506, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11506 BINDING SITE, designated SEQ ID:23970, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89195] Another function of VGAM2651 is therefore inhibition of FLJ11506 (Accession NM_024666). Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11506. FLJ23878 (Accession NM_144990) is another VGAM2651 host target gene. FLJ23878 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23878, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23878

BINDING SITE, designated SEQ ID:29593, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89196] Another function of VGAM2651 is therefore inhibition of FLJ23878 (Accession NM_144990). Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23878. KIAA0649 (Accession NM_014811) is another VGAM2651 host target gene. KIAA0649 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0649 BINDING SITE, designated SEQ ID:16775, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89197] Another function of VGAM2651 is therefore inhibition of KIAA0649 (Accession NM_014811). Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0649. KIAA1238 (Accession XM_048675) is another VGAM2651 host target gene. KIAA1238 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1238, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1238 BINDING SITE, designated SEQ ID:35217, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89198] Another function of VGAM2651 is therefore inhibition of KIAA1238 (Accession XM_048675). Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1238. Zinc Finger Protein 84 (HPF2) (ZNF84, Accession NM_003428) is another VGAM2651 host target gene. ZNF84 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF84, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF84 BINDING SITE, designated SEQ ID:9480, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89199] Another function of VGAM2651 is therefore inhibition of

Zinc Finger Protein 84 (HPF2) (ZNF84, Accession NM_003428). Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF84. LOC152328 (Accession XM_087420) is another VGAM2651 host target gene. LOC152328 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152328, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152328 BINDING SITE, designated SEQ ID:39244, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89200] Another function of VGAM2651 is therefore inhibition of LOC152328 (Accession XM_087420). Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152328. LOC255533 (Accession XM_173073) is another VGAM2651 host target gene. LOC255533 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255533, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255533 BINDING SITE, designated SEQ ID:46333, to the nucleotide sequence of VGAM2651 RNA, herein designated VGAM RNA, also designated SEQ ID:5362.

[89201] Another function of VGAM2651 is therefore inhibition of LOC255533 (Accession XM_173073). Accordingly, utilities of VGAM2651 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255533. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2652 (VGAM2652) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89202] VGAM2652 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2652 was detected is described hereinabove with reference to Figs. 1-8.

[89203] VGAM2652 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sorghum Mosaic Virus. VGAM2652 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[89204] VGAM2652 gene encodes a VGAM2652 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2652 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2652 precursor RNA is designated SEQ ID:2638, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2638 is located at position 6180 relative to the genome of Sorghum Mosaic Virus.

[89205] VGAM2652 precursor RNA folds onto itself, forming VGAM2652 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89206] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2652 folded precursor RNA into VGAM2652

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2652 RNA is designated SEQ ID:5363, and is provided hereinbelow with reference to the sequence listing part.

[89207] VGAM2652 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2652 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89208] VGAM2652 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2652 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2652 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89209] The complementary binding of VGAM2652 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2652 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2652 host target RNA into VGAM2652 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[89210] It is appreciated that VGAM2652 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2652 host target genes. The mRNA of each one of this plurality of VGAM2652 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2652 RNA, herein designated VGAM RNA, and which when bound by VGAM2652 RNA causes inhibition of translation of respective one or more VGAM2652 host target proteins.

[89211] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2652 gene, herein designated VGAM GENE, on one or more VGAM2652 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89212] It is yet further appreciated that a function of VGAM2652 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of viral infection by Sorghum Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2652 correlate with, and may be deduced from, the identity of the host target genes which VGAM2652 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89213] Nucleotide sequences of the VGAM2652 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2652 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2652 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2652 are further described hereinbelow with reference to Table 1.

[89214] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2652 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2652 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89215] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2652 gene, herein designated VGAM is inhibition of expression of VGAM2652 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2652 correlate with, and may be deduced from, the identity of the target genes which VGAM2652 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89216] Alpha-1-B Glycoprotein (A1BG, Accession NM_130786) is a VGAM2652 host target gene. A1BG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by A1BG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of A1BG BINDING SITE, designated SEQ ID:28278, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA,

also designated SEQ ID:5363.

[89217] A function of VGAM2652 is therefore inhibition of Alpha-1-B Glycoprotein (A1BG, Accession NM_130786), a gene which a plasma protein of unknown function. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A1BG. The function of A1BG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.A Disintegrin-like and Metalloprotease (reprolysin type) with Thrombospondin Type 1 Motif, 4 (ADAMTS4, Accession NM_005099) is another VGAM2652 host target gene. ADAMTS4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAMTS4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAMTS4 BINDING SITE, designated SEQ ID:11570, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89218] Another function of VGAM2652 is therefore inhibition of A Disintegrin-like and Metalloprotease (reprolysin type) with

Thrombospondin Type 1 Motif, 4 (ADAMTS4, Accession NM_005099), a gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS4. The function of ADAMTS4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM809.Aryl Hydrocarbon Receptor (AHR, Accession NM_001621) is another VGAM2652 host target gene. AHR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AHR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AHR BINDING SITE, designated SEQ ID:7334, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89219] Another function of VGAM2652 is therefore inhibition of Aryl Hydrocarbon Receptor (AHR, Accession NM_001621), a gene which plays a role in modulating carcinogenesis through the induction of xenobiotic-metabolizing en-

zymes. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AHR. The function of AHR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM368.ATPase, H+ Transporting, Lysosomal 70kDa, V1 Subunit A, Isoform 1 (ATP6V1A1, Accession NM_001690) is another VGAM2652 host target gene. ATP6V1A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP6V1A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP6V1A1 BINDING SITE, designated SEQ ID:7410, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89220] Another function of VGAM2652 is therefore inhibition of ATPase, H+ Transporting, Lysosomal 70kDa, V1 Subunit A, Isoform 1 (ATP6V1A1, Accession NM_001690), a gene which is responsible for acidifying a variety of intracellular compartments in eukaryotic cells. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ATP6V1A1. The function of ATP6V1A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM827.BRIP1 (Accession NM_032043) is another VGAM2652 host target gene. BRIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRIP1 BINDING SITE, designated SEQ ID:25756, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89221] Another function of VGAM2652 is therefore inhibition of BRIP1 (Accession NM_032043). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRIP1. Cholinergic Receptor, Nicotinic, Beta Polypeptide 4 (CHRNB4, Accession NM_000750) is another VGAM2652 host target gene. CHRNB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHRNB4, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRNB4 BINDING SITE, designated SEQ ID:6404, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89222] Another function of VGAM2652 is therefore inhibition of Cholinergic Receptor, Nicotinic, Beta Polypeptide 4 (CHRNB4, Accession NM_000750), a gene which mediates fast signal transmission at synapses. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRNB4. The function of CHRNB4 has been established by previous studies. Transmitter-gated cation channels are detectors of excitatory chemical signals at synapses in the nervous system. Khakh et al. (2000) showed that structurally distinct alpha-3-beta-4 nicotinic and P2X(2) (OMIM Ref. No. 600844) channels influence each other when coactivated. The activation of one channel type affects distinct kinetic and conductance states of the other, and coactivation results in nonadditive responses owing to inhibition of both channel types. State-dependent inhibition of nicotinic channels was revealed most clearly with mu-

tant P2X(2) channels, and inhibition was decreased at lower densities of channel expression. In synaptically coupled myenteric neurons, nicotinic fast excitatory postsynaptic currents were occluded during activation of endogenously coexpressed P2X channels. Khakh et al. (2000) concluded that their data provide a molecular basis and a synaptic context for cross-inhibition between transmitter-gated channels. Transmitter-gated cation channels are detectors of excitatory chemical signals at synapses in the nervous system. Khakh et al. (2000) showed that structurally distinct alpha-3-beta-4 nicotinic and P2X(2) (OMIM Ref. No. 600844) channels influence each other when coactivated. The activation of one channel type affects distinct kinetic and conductance states of the other, and coactivation results in nonadditive responses owing to inhibition of both channel types. State-dependent inhibition of nicotinic channels was revealed most clearly with mutant P2X(2) channels, and inhibition was decreased at lower densities of channel expression. In synaptically coupled myenteric neurons, nicotinic fast excitatory postsynaptic currents were occluded during activation of endogenously coexpressed P2X channels. Khakh et al. (2000) concluded that their data provide a molecular basis

and a synaptic context for cross-inhibition between transmitter-gated channels

[89223] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[89224] Khakh, B. S.; Zhou, X.; Sydes, J.; Galligan, J. J.; Lester, H. A. : State-dependent cross-inhibition between transmitter-gated cation channels. Nature 406: 405-410, 2000. ; and

[89225] Tarroni, P.; Rubboli, F.; Chini, B.; Zwart, R.; Oortgiesen, M.; Sher, E.; Clementi, F. : Neuronal-type nicotinic receptors in human neuroblastoma and small-cell lung carcinoma cell line.

[89226] Further studies establishing the function and utilities of CHRNB4 are found in John Hopkins OMIM database record ID 118509, and in sited publications numbered 33, 390, 9944, 1268 and 12696 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.COX15 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX15, Accession NM_078470) is another VGAM2652 host target gene. COX15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COX15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COX15 BINDING SITE, designated SEQ ID:27793, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89227] Another function of VGAM2652 is therefore inhibition of COX15 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX15, Accession NM_078470). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COX15. Cytochrome P450, Subfamily IIB (phenobarbital-inducible), Polypeptide 6 (CYP2B6, Accession NM_000767) is another VGAM2652 host target gene. CYP2B6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP2B6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP2B6 BINDING SITE, designated SEQ ID:6415, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89228] Another function of VGAM2652 is therefore inhibition of

Cytochrome P450, Subfamily IIB (phenobarbital-inducible), Polypeptide 6 (CYP2B6, Accession NM_000767), a gene which oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2B6. The function of CYP2B6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Fc Fragment of IgA, Receptor For (FCAR, Accession NM_133269) is another VGAM2652 host target gene. FCAR BINDING SITE1 through FCAR BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FCAR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE5, designated SEQ ID:28424, SEQ ID:7728, SEQ ID:28428, SEQ ID:28426 and SEQ ID:28430 respectively, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89229] Another function of VGAM2652 is therefore inhibition of Fc Fragment of IgA, Receptor For (FCAR, Accession NM_133269), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCAR. The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM923.Glucose-6-phosphatase, Catalytic (glycogen storage disease type I, von Gierke disease) (G6PC, Accession NM_000151) is another VGAM2652 host target gene. G6PC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by G6PC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE, designated SEQ ID:5659, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89230] Another function of VGAM2652 is therefore inhibition of Glucose-6-phosphatase, Catalytic (glycogen storage dis-

ease type I, von Gierke disease) (G6PC, Accession NM_000151). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PC. G Protein-coupled Receptor 56 (GPR56, Accession NM_005682) is another VGAM2652 host target gene. GPR56 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GPR56, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR56 BINDING SITE, designated SEQ ID:12240, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89231] Another function of VGAM2652 is therefore inhibition of G Protein-coupled Receptor 56 (GPR56, Accession NM_005682), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR56. The function of GPR56 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM782.Membrane Component, Chromosome 11, Surface Marker 1 (M11S1, Accession NM_005898) is another VGAM2652 host target gene. M11S1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by M11S1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of M11S1 BINDING SITE, designated SEQ ID:12519, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89232] Another function of VGAM2652 is therefore inhibition of Membrane Component, Chromosome 11, Surface Marker 1 (M11S1, Accession NM_005898), a gene which may play a role in transporting nutrients from the gut lumen across the gutlining epithelial cell layer. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with M11S1. The function of M11S1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM131.Male Germ Cell-associated Kinase (MAK, Ac-

cession NM_005906) is another VGAM2652 host target gene. MAK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAK BINDING SITE, designated SEQ ID:12530, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89233] Another function of VGAM2652 is therefore inhibition of Male Germ Cell-associated Kinase (MAK, Accession NM_005906), a gene which plays an important role in spermatogenesis. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAK. The function of MAK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1322.MADS Box Transcription Enhancer Factor 2, Polypeptide A (myocyte enhancer factor 2A) (MEF2A, Accession NM_005587) is another VGAM2652 host target gene. MEF2A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

MEF2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEF2A BINDING SITE, designated SEQ ID:12117, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89234] Another function of VGAM2652 is therefore inhibition of MADS Box Transcription Enhancer Factor 2, Polypeptide A (myocyte enhancer factor 2A) (MEF2A, Accession NM_005587), a gene which binds a consensus sequence that regulates transcription. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEF2A. The function of MEF2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM46.MHC Class II Transactivator (MHC2TA, Accession NM_000246) is another VGAM2652 host target gene. MHC2TA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MHC2TA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE, designated SEQ ID:5781, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89235] Another function of VGAM2652 is therefore inhibition of MHC Class II Transactivator (MHC2TA, Accession NM_000246). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA. Myeloproliferative Leukemia Virus Oncogene (MPL, Accession NM_005373) is another VGAM2652 host target gene. MPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPL BINDING SITE, designated SEQ ID:11851, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89236] Another function of VGAM2652 is therefore inhibition of Myeloproliferative Leukemia Virus Oncogene (MPL, Accession NM_005373). Accordingly, utilities of VGAM2652 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with MPL. Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071) is another VGAM2652 host target gene. NCOA6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NCOA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE, designated SEQ ID:15292, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89237] Another function of VGAM2652 is therefore inhibition of Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071), a gene which activates gene transcription through ligand-dependent association with coactivators. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6. The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.Phosphodiesterase 6B, CGMP-specific, Rod, Beta

(congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NM_000283) is another VGAM2652 host target gene. PDE6B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE6B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE6B BINDING SITE, designated SEQ ID:5829, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89238] Another function of VGAM2652 is therefore inhibition of Phosphodiesterase 6B, CGMP-specific, Rod, Beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NM_000283). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE6B. Phosphoinositide-3-kinase, Catalytic, Delta Polypeptide (PIK3CD, Accession NM_005026) is another VGAM2652 host target gene. PIK3CD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIK3CD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIK3CD BINDING SITE, designated SEQ ID:11464, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89239] Another function of VGAM2652 is therefore inhibition of Phosphoinositide-3-kinase, Catalytic, Delta Polypeptide (PIK3CD, Accession NM_005026), a gene which regulating cell growth. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3CD. The function of PIK3CD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2434.POU Domain, Class 2, Associating Factor 1 (POU2AF1, Accession NM_006235) is another VGAM2652 host target gene. POU2AF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU2AF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:12893, to the nucleotide sequence of

VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89240] Another function of VGAM2652 is therefore inhibition of POU Domain, Class 2, Associating Factor 1 (POU2AF1, Accession NM_006235), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2AF1. The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM171.Protein Kinase, Interferon-inducible Double Stranded RNA Dependent (PRKR, Accession NM_002759) is another VGAM2652 host target gene. PRKR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKR BINDING SITE, designated SEQ ID:8646, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89241] Another function of VGAM2652 is therefore inhibition of Protein Kinase, Interferon-inducible Double Stranded RNA Dependent (PRKR, Accession NM_002759), a gene which catalyze the phosphorylation of the alpha subunit of eif2. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKR. The function of PRKR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1890.Retinoblastoma Binding Protein 9 (RBBP9, Accession XM_046553) is another VGAM2652 host target gene. RBBP9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBBP9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBBP9 BINDING SITE, designated SEQ ID:34747, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89242] Another function of VGAM2652 is therefore inhibition of Retinoblastoma Binding Protein 9 (RBBP9, Accession XM_046553). Accordingly, utilities of VGAM2652 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP9. Stearoyl-CoA Desaturase (delta-9-desaturase) (SCD, Accession NM_005063) is another VGAM2652 host target gene. SCD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCD BINDING SITE, designated SEQ ID:11498, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89243] Another function of VGAM2652 is therefore inhibition of Stearoyl-CoA Desaturase (delta-9-desaturase) (SCD, Accession NM_005063), a gene which functions in the synthesis of unsaturated fatty acids. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCD. The function of SCD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM314.Thromboxane A2 Receptor (TBXA2R, Accession NM_001060) is another VGAM2652 host target gene.

TBXA2R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBXA2R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBXA2R BINDING SITE, designated SEQ ID:6728, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89244] Another function of VGAM2652 is therefore inhibition of Thromboxane A2 Receptor (TBXA2R, Accession NM_001060), a gene which activates Ca2+-activated chloride channels; stimulates platelet aggregation and smooth muscle constriction. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBXA2R. The function of TBXA2R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Transmembrane, Cochlear Expressed, 1 (TMC1, Accession NM_138691) is another VGAM2652 host target gene. TMC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region

of mRNA encoded by TMC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMC1 BINDING SITE, designated SEQ ID:28934, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89245] Another function of VGAM2652 is therefore inhibition of Transmembrane, Cochlear Expressed, 1 (TMC1, Accession NM_138691), a gene which is required for normal function of cochlear hair cells. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMC1. The function of TMC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM554.Tumor Necrosis Factor Receptor Superfamily, Member 10b (TNFRSF10B, Accession NM_003842) is another VGAM2652 host target gene. TNFRSF10B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF10B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE, designated SEQ ID:9938, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89246] Another function of VGAM2652 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 10b (TNFRSF10B, Accession NM_003842), a gene which forms complex that induces apoptosis. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF10B. The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM400.TNF Receptor-associated Factor 5 (TRAF5, Accession NM_004619) is another VGAM2652 host target gene. TRAF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRAF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:10968, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5363.

[89247] Another function of VGAM2652 is therefore inhibition of TNF Receptor-associated Factor 5 (TRAF5, Accession NM_004619), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5. The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM76.Von Hippel-Lindau Syndrome (VHL, Accession NM_000551) is another VGAM2652 host target gene. VHL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VHL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VHL BINDING SITE, designated SEQ ID:6165, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89248] Another function of VGAM2652 is therefore inhibition of Von Hippel-Lindau Syndrome (VHL, Accession

NM_000551), a gene which may control rna stability through the selective degradation of rna-bound proteins. Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VHL. The function of VHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM197.Rho GTPase Activating Protein 9 (ARHGAP9, Accession NM_032496) is another VGAM2652 host target gene. ARHGAP9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARHGAP9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP9 BINDING SITE, designated SEQ ID:26248, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89249] Another function of VGAM2652 is therefore inhibition of Rho GTPase Activating Protein 9 (ARHGAP9, Accession NM_032496). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP9. Ankyrin Repeat

and SOCS Box-containing 16 (ASB16, Accession NM_080863) is another VGAM2652 host target gene. ASB16 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ASB16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASB16 BINDING SITE, designated SEQ ID:28108, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89250] Another function of VGAM2652 is therefore inhibition of Ankyrin Repeat and SOCS Box-containing 16 (ASB16, Accession NM_080863). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB16. BA108L7.2 (Accession NM_030971) is another VGAM2652 host target gene. BA108L7.2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BA108L7.2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BA108L7.2 BINDING SITE, desig-

nated SEQ ID:25241, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89251] Another function of VGAM2652 is therefore inhibition of BA108L7.2 (Accession NM_030971). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BA108L7.2. C6orf5 (Accession NM_015524) is another VGAM2652 host target gene. C6orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6orf5 BINDING SITE, designated SEQ ID:17782, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89252] Another function of VGAM2652 is therefore inhibition of C6orf5 (Accession NM_015524). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf5. Chromatin Accessibility Complex 1 (CHRAC1, Accession NM_017444) is another VGAM2652 host target gene.

CHRAC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHRAC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRAC1 BINDING SITE, designated SEQ ID:18907, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89253] Another function of VGAM2652 is therefore inhibition of Chromatin Accessibility Complex 1 (CHRAC1, Accession NM_017444). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRAC1. Collectin Subfamily Member 12 (COLEC12, Accession NM_030781) is another VGAM2652 host target gene. COLEC12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COLEC12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COLEC12 BINDING SITE, designated SEQ ID:25071, to the nucleotide sequence of VGAM2652 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5363.

[89254] Another function of VGAM2652 is therefore inhibition of Collectin Sub-family Member 12 (COLEC12, Accession NM_030781). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC12. Cylicin, Basic Protein of Sperm Head Cytoskeleton 2 (CYLC2, Accession NM_001340) is another VGAM2652 host target gene. CYLC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYLC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYLC2 BINDING SITE, designated SEQ ID:7019, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89255] Another function of VGAM2652 is therefore inhibition of Cylicin, Basic Protein of Sperm Head Cytoskeleton 2 (CYLC2, Accession NM_001340). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYLC2. DKFZp434A2417 (Accession XM_038526) is another VGAM2652 host target gene. DKFZp434A2417 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434A2417, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434A2417 BINDING SITE, designated SEQ ID:32865, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89256] Another function of VGAM2652 is therefore inhibition of DKFZp434A2417 (Accession XM_038526). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434A2417. DKFZP434D146 (Accession NM_015595) is another VGAM2652 host target gene. DKFZP434D146 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434D146, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434D146 BINDING SITE, designated SEQ ID:17873, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5363.

[89257] Another function of VGAM2652 is therefore inhibition of DKFZP434D146 (Accession NM_015595). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434D146. DKFZp547H025 (Accession NM_020161) is another VGAM2652 host target gene. DKFZp547H025 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547H025, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547H025 BINDING SITE, designated SEQ ID:21374, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89258] Another function of VGAM2652 is therefore inhibition of DKFZp547H025 (Accession NM_020161). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547H025. DKFZP564G092 (Accession NM_015601) is another VGAM2652 host target gene. DKFZP564G092 BINDING SITE is HOST TARGET binding site

found in the 5` untranslated region of mRNA encoded by DKFZP564G092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564G092 BINDING SITE, designated SEQ ID:17877, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89259] Another function of VGAM2652 is therefore inhibition of DKFZP564G092 (Accession NM_015601). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564G092. Ecotropic Viral Integration Site 5 (EVI5, Accession NM_005665) is another VGAM2652 host target gene. EVI5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EVI5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EVI5 BINDING SITE, designated SEQ ID:12208, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89260] Another function of VGAM2652 is therefore inhibition of Ecotropic Viral Integration Site 5 (EVI5, Accession NM_005665). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVI5. FLJ12687 (Accession NM_024917) is another VGAM2652 host target gene. FLJ12687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12687 BINDING SITE, designated SEQ ID:24446, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89261] Another function of VGAM2652 is therefore inhibition of FLJ12687 (Accession NM_024917). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12687. FLJ13188 (Accession NM_022063) is another VGAM2652 host target gene. FLJ13188 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13188, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13188 BINDING SITE, designated SEQ ID:22608, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89262] Another function of VGAM2652 is therefore inhibition of FLJ13188 (Accession NM_022063). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13188. FLJ14957 (Accession NM_032866) is another VGAM2652 host target gene. FLJ14957 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14957, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14957 BINDING SITE, designated SEQ ID:26683, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89263] Another function of VGAM2652 is therefore inhibition of FLJ14957 (Accession NM_032866). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ14957. FLJ20034 (Accession NM_017630) is another VGAM2652 host target gene. FLJ20034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20034 BINDING SITE, designated SEQ ID:19137, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89264] Another function of VGAM2652 is therefore inhibition of FLJ20034 (Accession NM_017630). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20034. FLJ22002 (Accession NM_024838) is another VGAM2652 host target gene. FLJ22002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22002 BINDING SITE, designated SEQ ID:24248, to the nucleotide

sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89265] Another function of VGAM2652 is therefore inhibition of FLJ22002 (Accession NM_024838). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22002. FLJ22531 (Accession NM_024650) is another VGAM2652 host target gene. FLJ22531 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22531, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22531 BINDING SITE, designated SEQ ID:23947, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89266] Another function of VGAM2652 is therefore inhibition of FLJ22531 (Accession NM_024650). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22531. FLJ22794 (Accession XM_166220) is another VGAM2652 host target gene. FLJ22794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ22794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:44036, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89267] Another function of VGAM2652 is therefore inhibition of FLJ22794 (Accession XM_166220). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22794. FLJ31153 (Accession NM_144600) is another VGAM2652 host target gene. FLJ31153 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ31153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ31153 BINDING SITE, designated SEQ ID:29414, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89268] Another function of VGAM2652 is therefore inhibition of FLJ31153 (Accession NM_144600). Accordingly, utilities of

VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31153. FLJ32865 (Accession NM_144613) is another VGAM2652 host target gene. FLJ32865 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:29431, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89269] Another function of VGAM2652 is therefore inhibition of FLJ32865 (Accession NM_144613). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865. Glycoprotein V (platelet) (GP5, Accession NM_004488) is another VGAM2652 host target gene. GP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

GP5 BINDING SITE, designated SEQ ID:10822, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89270] Another function of VGAM2652 is therefore inhibition of Glycoprotein V (platelet) (GP5, Accession NM_004488). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GP5. GTPBG3 (Accession NM_032620) is another VGAM2652 host target gene. GTPBG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTPBG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTPBG3 BINDING SITE, designated SEQ ID:26334, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89271] Another function of VGAM2652 is therefore inhibition of GTPBG3 (Accession NM_032620). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBG3. Histamine Receptor H4 (HRH4, Accession

NM_021624) is another VGAM2652 host target gene. HRH4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRH4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE, designated SEQ ID:22262, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89272] Another function of VGAM2652 is therefore inhibition of Histamine Receptor H4 (HRH4, Accession NM_021624). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH4. HSMPP8 (Accession XM_167894) is another VGAM2652 host target gene. HSMPP8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSMPP8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSMPP8 BINDING SITE, designated SEQ ID:44904, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ

ID:5363.

[89273] Another function of VGAM2652 is therefore inhibition of HSMPP8 (Accession XM_167894). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSMPP8. KIAA0472 (Accession XM_050147) is another VGAM2652 host target gene. KIAA0472 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0472, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0472 BINDING SITE, designated SEQ ID:35582, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89274] Another function of VGAM2652 is therefore inhibition of KIAA0472 (Accession XM_050147). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0472. KIAA0513 (Accession NM_014732) is another VGAM2652 host target gene. KIAA0513 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0513, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:16360, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89275] Another function of VGAM2652 is therefore inhibition of KIAA0513 (Accession NM_014732). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513. KIAA0555 (Accession NM_014790) is another VGAM2652 host target gene. KIAA0555 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:16686, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89276] Another function of VGAM2652 is therefore inhibition of KIAA0555 (Accession NM_014790). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0555. KIAA0557 (Accession XM_085507) is another VGAM2652 host target gene. KIAA0557 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0557, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0557 BINDING SITE, designated SEQ ID:38210, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89277] Another function of VGAM2652 is therefore inhibition of KIAA0557 (Accession XM_085507). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0557. KIAA0836 (Accession XM_035390) is another VGAM2652 host target gene. KIAA0836 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0836, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0836 BINDING SITE, designated SEQ ID:32248, to the

nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89278] Another function of VGAM2652 is therefore inhibition of KIAA0836 (Accession XM_035390). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0836. KIAA0924 (Accession NM_014897) is another VGAM2652 host target gene. KIAA0924 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0924, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0924 BINDING SITE, designated SEQ ID:17066, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89279] Another function of VGAM2652 is therefore inhibition of KIAA0924 (Accession NM_014897). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0924. KIAA1028 (Accession XM_166324) is another VGAM2652 host target gene. KIAA1028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1028 BINDING SITE, designated SEQ ID:44163, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89280] Another function of VGAM2652 is therefore inhibition of KIAA1028 (Accession XM_166324). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1028. KIAA1373 (Accession XM_048195) is another VGAM2652 host target gene. KIAA1373 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1373, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1373 BINDING SITE, designated SEQ ID:35129, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89281] Another function of VGAM2652 is therefore inhibition of KIAA1373 (Accession XM_048195). Accordingly, utilities

of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1373. KIAA1473 (Accession XM_047550) is another VGAM2652 host target gene. KIAA1473 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1473, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1473 BINDING SITE, designated SEQ ID:34997, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89282] Another function of VGAM2652 is therefore inhibition of KIAA1473 (Accession XM_047550). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1473. KIAA1617 (Accession XM_166140) is another VGAM2652 host target gene. KIAA1617 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1617, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1617 BINDING SITE, designated SEQ ID:43944, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89283] Another function of VGAM2652 is therefore inhibition of KIAA1617 (Accession XM_166140). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1617. KIAA1712 (Accession XM_041497) is another VGAM2652 host target gene. KIAA1712 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE, designated SEQ ID:33539, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89284] Another function of VGAM2652 is therefore inhibition of KIAA1712 (Accession XM_041497). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712. KIAA1737 (Accession XM_041115) is another VGAM2652 host target gene. KIAA1737 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1737, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1737 BINDING SITE, designated SEQ ID:33449, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89285] Another function of VGAM2652 is therefore inhibition of KIAA1737 (Accession XM_041115). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1737. KIAA1826 (Accession XM_040784) is another VGAM2652 host target gene. KIAA1826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1826 BINDING SITE, designated SEQ ID:33376, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89286] Another function of VGAM2652 is therefore inhibition of

KIAA1826 (Accession XM_040784). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1826. MGC4638 (Accession NM_031479) is another VGAM2652 host target gene. MGC4638 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4638, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4638 BINDING SITE, designated SEQ ID:25558, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89287] Another function of VGAM2652 is therefore inhibition of MGC4638 (Accession NM_031479). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4638. Mitochondrial Ribosomal Protein L44 (MRPL44, Accession NM_022915) is another VGAM2652 host target gene. MRPL44 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of MRPL44 BINDING SITE, designated SEQ ID:23228, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89288] Another function of VGAM2652 is therefore inhibition of Mitochondrial Ribosomal Protein L44 (MRPL44, Accession NM_022915). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL44. NDP52 (Accession NM_005831) is another VGAM2652 host target gene. NDP52 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDP52, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDP52 BINDING SITE, designated SEQ ID:12445, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89289] Another function of VGAM2652 is therefore inhibition of NDP52 (Accession NM_005831). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with NDP52. Nucleoredoxin (NXN, Accession NM_022463) is another VGAM2652 host target gene. NXN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:22812, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89290] Another function of VGAM2652 is therefore inhibition of Nucleoredoxin (NXN, Accession NM_022463). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXN. PRO0529 (Accession NM_014074) is another VGAM2652 host target gene. PRO0529 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0529, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0529 BINDING SITE, designated SEQ ID:15300, to the nucleotide

sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89291] Another function of VGAM2652 is therefore inhibition of PRO0529 (Accession NM_014074). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0529. PRO2955 (Accession NM_018545) is another VGAM2652 host target gene. PRO2955 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2955 BINDING SITE, designated SEQ ID:20622, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89292] Another function of VGAM2652 is therefore inhibition of PRO2955 (Accession NM_018545). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2955. Proline-serine-threonine Phosphatase Interacting Protein 2 (PSTPIP2, Accession NM_024430) is another VGAM2652 host target gene. PSTPIP2 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSTPIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSTPIP2 BINDING SITE, designated SEQ ID:23683, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89293] Another function of VGAM2652 is therefore inhibition of Proline-serine-threonine Phosphatase Interacting Protein 2 (PSTPIP2, Accession NM_024430). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSTPIP2. RAB33B, Member RAS Oncogene Family (RAB33B, Accession NM_031296) is another VGAM2652 host target gene. RAB33B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB33B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB33B BINDING SITE, designated SEQ ID:25330, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ

ID:5363.

[89294] Another function of VGAM2652 is therefore inhibition of RAB33B, Member RAS Oncogene Family (RAB33B, Accession NM_031296). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB33B. SCAN Domain Containing 2 (SCAND2, Accession NM_022050) is another VGAM2652 host target gene. SCAND2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAND2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAND2 BINDING SITE, designated SEQ ID:22577, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89295] Another function of VGAM2652 is therefore inhibition of SCAN Domain Containing 2 (SCAND2, Accession NM_022050). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAND2. SCYA22 (Accession XM_165651) is another VGAM2652 host target gene. SCYA22 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by SCYA22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCYA22 BINDING SITE, designated SEQ ID:43716, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89296] Another function of VGAM2652 is therefore inhibition of SCYA22 (Accession XM_165651). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYA22. Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065) is another VGAM2652 host target gene. SIRPB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIRPB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIRPB1 BINDING SITE, designated SEQ ID:12710, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89297] Another function of VGAM2652 is therefore inhibition of Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB1. Solute Carrier Family 6 (neurotransmitter transporter), Member 14 (SLC6A14, Accession NM_007231) is another VGAM2652 host target gene. SLC6A14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC6A14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC6A14 BINDING SITE, designated SEQ ID:14104, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89298] Another function of VGAM2652 is therefore inhibition of Solute Carrier Family 6 (neurotransmitter transporter), Member 14 (SLC6A14, Accession NM_007231). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A14. Synaptosomal-associated Protein, 91kDa Homolog (mouse) (SNAP91, Accession NM_014841)

is another VGAM2652 host target gene. SNAP91 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNAP91, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNAP91 BINDING SITE, designated SEQ ID:16871, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89299] Another function of VGAM2652 is therefore inhibition of Synaptosomal-associated Protein, 91kDa Homolog (mouse) (SNAP91, Accession NM_014841). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP91. T-cell Leukemia/lymphoma 6 (TCL6, Accession NM_014418) is another VGAM2652 host target gene. TCL6 BINDING SITE1 through TCL6 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TCL6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 through TCL6 BINDING SITE4, designated SEQ ID:15769,

SEQ ID:21762, SEQ ID:14845 and SEQ ID:21771 respectively, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89300] Another function of VGAM2652 is therefore inhibition of T-cell Leukemia/lymphoma 6 (TCL6, Accession NM_014418). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6. TU12B1-TY (Accession NM_016575) is another VGAM2652 host target gene. TU12B1-TY BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TU12B1-TY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TU12B1-TY BINDING SITE, designated SEQ ID:18650, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89301] Another function of VGAM2652 is therefore inhibition of TU12B1-TY (Accession NM_016575). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

TU12B1-TY. Ubiquitin Specific Protease 3 (USP3, Accession XM_116973) is another VGAM2652 host target gene. USP3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by USP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP3 BINDING SITE, designated SEQ ID:43172, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89302] Another function of VGAM2652 is therefore inhibition of Ubiquitin Specific Protease 3 (USP3, Accession XM_116973). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP3. Zinc Finger Protein 338 (ZNF338, Accession NM_022088) is another VGAM2652 host target gene. ZNF338 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF338, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF338 BINDING SITE, designated SEQ ID:22634, to the nucleotide

sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89303] Another function of VGAM2652 is therefore inhibition of Zinc Finger Protein 338 (ZNF338, Accession NM_022088). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF338. LOC113675 (Accession NM_138432) is another VGAM2652 host target gene. LOC113675 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC113675, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113675 BINDING SITE, designated SEQ ID:28796, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89304] Another function of VGAM2652 is therefore inhibition of LOC113675 (Accession NM_138432). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113675. LOC126364 (Accession XM_065047) is another VGAM2652 host target gene. LOC126364 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126364, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126364 BINDING SITE, designated SEQ ID:37272, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89305] Another function of VGAM2652 is therefore inhibition of LOC126364 (Accession XM_065047). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126364. LOC135293 (Accession XM_072402) is another VGAM2652 host target gene. LOC135293 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135293, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135293 BINDING SITE, designated SEQ ID:37497, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89306] Another function of VGAM2652 is therefore inhibition of

LOC135293 (Accession XM_072402). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135293. LOC143241 (Accession NM_138812) is another VGAM2652 host target gene. LOC143241 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143241, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143241 BINDING SITE, designated SEQ ID:29036, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89307] Another function of VGAM2652 is therefore inhibition of LOC143241 (Accession NM_138812). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143241. LOC144524 (Accession XM_096624) is another VGAM2652 host target gene. LOC144524 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144524, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC144524 BINDING SITE, designated SEQ ID:40435, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89308] Another function of VGAM2652 is therefore inhibition of LOC144524 (Accession XM_096624). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144524. LOC144776 (Accession XM_084964) is another VGAM2652 host target gene. LOC144776 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144776 BINDING SITE, designated SEQ ID:37788, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89309] Another function of VGAM2652 is therefore inhibition of LOC144776 (Accession XM_084964). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144776. LOC145757 (Accession XM_085227) is an-

other VGAM2652 host target gene. LOC145757 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145757, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE, designated SEQ ID:37974, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89310] Another function of VGAM2652 is therefore inhibition of LOC145757 (Accession XM_085227). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757. LOC146050 (Accession XM_085301) is another VGAM2652 host target gene. LOC146050 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146050, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146050 BINDING SITE, designated SEQ ID:38056, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89311] Another function of VGAM2652 is therefore inhibition of LOC146050 (Accession XM_085301). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146050. LOC146894 (Accession NM_145273) is another VGAM2652 host target gene. LOC146894 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146894, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146894 BINDING SITE, designated SEQ ID:29784, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89312] Another function of VGAM2652 is therefore inhibition of LOC146894 (Accession NM_145273). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146894. LOC147817 (Accession XM_085903) is another VGAM2652 host target gene. LOC147817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147817, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE, designated SEQ ID:38388, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89313] Another function of VGAM2652 is therefore inhibition of LOC147817 (Accession XM_085903). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817. LOC148189 (Accession XM_086087) is another VGAM2652 host target gene. LOC148189 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148189 BINDING SITE, designated SEQ ID:38485, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89314] Another function of VGAM2652 is therefore inhibition of LOC148189 (Accession XM_086087). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC148189. LOC148198 (Accession XM_047554) is another VGAM2652 host target gene. LOC148198 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148198, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148198 BINDING SITE, designated SEQ ID:35000, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89315] Another function of VGAM2652 is therefore inhibition of LOC148198 (Accession XM_047554). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148198. LOC149171 (Accession XM_086450) is another VGAM2652 host target gene. LOC149171 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149171, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149171 BINDING SITE, designated SEQ ID:38668, to the nucleotide sequence of VGAM2652 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5363.

[89316] Another function of VGAM2652 is therefore inhibition of LOC149171 (Accession XM_086450). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149171. LOC149267 (Accession NM_138480) is another VGAM2652 host target gene. LOC149267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149267 BINDING SITE, designated SEQ ID:28833, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89317] Another function of VGAM2652 is therefore inhibition of LOC149267 (Accession NM_138480). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149267. LOC149478 (Accession XM_086536) is another VGAM2652 host target gene. LOC149478 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149478, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149478 BINDING SITE, designated SEQ ID:38755, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89318] Another function of VGAM2652 is therefore inhibition of LOC149478 (Accession XM_086536). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478. LOC149577 (Accession XM_097675) is another VGAM2652 host target gene. LOC149577 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149577 BINDING SITE, designated SEQ ID:41023, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89319] Another function of VGAM2652 is therefore inhibition of LOC149577 (Accession XM_097675). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC149577. LOC149711 (Accession XM_097720) is another VGAM2652 host target gene. LOC149711 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149711, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149711 BINDING SITE, designated SEQ ID:41075, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89320] Another function of VGAM2652 is therefore inhibition of LOC149711 (Accession XM_097720). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149711. LOC150054 (Accession XM_097797) is another VGAM2652 host target gene. LOC150054 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150054 BINDING SITE, designated SEQ ID:41126, to

the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89321] Another function of VGAM2652 is therefore inhibition of LOC150054 (Accession XM_097797). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150054. LOC150696 (Accession NM_144707) is another VGAM2652 host target gene. LOC150696 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150696, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150696 BINDING SITE, designated SEQ ID:29530, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89322] Another function of VGAM2652 is therefore inhibition of LOC150696 (Accession NM_144707). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150696. LOC151057 (Accession XM_097998) is another VGAM2652 host target gene. LOC151057 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC151057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:41295, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89323] Another function of VGAM2652 is therefore inhibition of LOC151057 (Accession XM_097998). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057. LOC152300 (Accession XM_087432) is another VGAM2652 host target gene. LOC152300 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152300, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152300 BINDING SITE, designated SEQ ID:39252, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89324] Another function of VGAM2652 is therefore inhibition of LOC152300 (Accession XM_087432). Accordingly, utilities

of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152300. LOC152925 (Accession XM_087559) is another VGAM2652 host target gene. LOC152925 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152925, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152925 BINDING SITE, designated SEQ ID:39336, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89325] Another function of VGAM2652 is therefore inhibition of LOC152925 (Accession XM_087559). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152925. LOC157858 (Accession XM_098833) is another VGAM2652 host target gene. LOC157858 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157858, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC157858 BINDING SITE, designated SEQ ID:41869, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89326] Another function of VGAM2652 is therefore inhibition of LOC157858 (Accession XM_098833). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157858. LOC169611 (Accession XM_095809) is another VGAM2652 host target gene. LOC169611 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169611, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169611 BINDING SITE, designated SEQ ID:40286, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89327] Another function of VGAM2652 is therefore inhibition of LOC169611 (Accession XM_095809). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169611. LOC196264 (Accession XM_113683) is another VGAM2652 host target gene. LOC196264 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, designated SEQ ID:42337, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89328] Another function of VGAM2652 is therefore inhibition of LOC196264 (Accession XM_113683). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264. LOC196411 (Accession XM_113714) is another VGAM2652 host target gene. LOC196411 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196411 BINDING SITE, designated SEQ ID:42365, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89329] Another function of VGAM2652 is therefore inhibition of

LOC196411 (Accession XM_113714). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196411. LOC199725 (Accession XM_117119) is another VGAM2652 host target gene. LOC199725 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199725, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199725 BINDING SITE, designated SEQ ID:43243, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89330] Another function of VGAM2652 is therefore inhibition of LOC199725 (Accession XM_117119). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199725. LOC199906 (Accession XM_114052) is another VGAM2652 host target gene. LOC199906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC199906 BINDING SITE, designated SEQ ID:42658, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89331] Another function of VGAM2652 is therefore inhibition of LOC199906 (Accession XM_114052). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199906. LOC200169 (Accession XM_117200) is another VGAM2652 host target gene. LOC200169 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200169, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200169 BINDING SITE, designated SEQ ID:43286, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89332] Another function of VGAM2652 is therefore inhibition of LOC200169 (Accession XM_117200). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200169. LOC200860 (Accession XM_117289) is an-

other VGAM2652 host target gene. LOC200860 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200860, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200860 BINDING SITE, designated SEQ ID:43356, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89333] Another function of VGAM2652 is therefore inhibition of LOC200860 (Accession XM_117289). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200860. LOC201411 (Accession XM_031946) is another VGAM2652 host target gene. LOC201411 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201411 BINDING SITE, designated SEQ ID:31529, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89334] Another function of VGAM2652 is therefore inhibition of LOC201411 (Accession XM_031946). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201411. LOC201696 (Accession XM_032269) is another VGAM2652 host target gene. LOC201696 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201696, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201696 BINDING SITE, designated SEQ ID:31626, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89335] Another function of VGAM2652 is therefore inhibition of LOC201696 (Accession XM_032269). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201696. LOC202908 (Accession XM_114602) is another VGAM2652 host target gene. LOC202908 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202908, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202908 BINDING SITE, designated SEQ ID:42998, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89336] Another function of VGAM2652 is therefore inhibition of LOC202908 (Accession XM_114602). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202908. LOC203197 (Accession XM_114645) is another VGAM2652 host target gene. LOC203197 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203197, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203197 BINDING SITE, designated SEQ ID:43014, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89337] Another function of VGAM2652 is therefore inhibition of LOC203197 (Accession XM_114645). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC203197. LOC220064 (Accession XM_167827) is another VGAM2652 host target gene. LOC220064 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220064, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220064 BINDING SITE, designated SEQ ID:44869, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89338] Another function of VGAM2652 is therefore inhibition of LOC220064 (Accession XM_167827). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220064. LOC220963 (Accession XM_166145) is another VGAM2652 host target gene. LOC220963 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220963, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220963 BINDING SITE, designated SEQ ID:43960, to the nucleotide sequence of VGAM2652 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5363.

[89339] Another function of VGAM2652 is therefore inhibition of LOC220963 (Accession XM_166145). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220963. LOC221174 (Accession XM_167915) is another VGAM2652 host target gene. LOC221174 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221174, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221174 BINDING SITE, designated SEQ ID:44912, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89340] Another function of VGAM2652 is therefore inhibition of LOC221174 (Accession XM_167915). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221174. LOC222031 (Accession XM_168371) is another VGAM2652 host target gene. LOC222031 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222031, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222031 BINDING SITE, designated SEQ ID:45136, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89341] Another function of VGAM2652 is therefore inhibition of LOC222031 (Accession XM_168371). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222031. LOC257017 (Accession XM_173227) is another VGAM2652 host target gene. LOC257017 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257017, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257017 BINDING SITE, designated SEQ ID:46498, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89342] Another function of VGAM2652 is therefore inhibition of LOC257017 (Accession XM_173227). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC257017. LOC57107 (Accession NM_020381) is another VGAM2652 host target gene. LOC57107 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57107, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57107 BINDING SITE, designated SEQ ID:21652, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89343] Another function of VGAM2652 is therefore inhibition of LOC57107 (Accession NM_020381). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57107. LOC90591 (Accession XM_032811) is another VGAM2652 host target gene. LOC90591 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90591, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90591 BINDING SITE, designated SEQ ID:31761, to the

nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89344] Another function of VGAM2652 is therefore inhibition of LOC90591 (Accession XM_032811). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90591. LOC91115 (Accession XM_036218) is another VGAM2652 host target gene. LOC91115 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91115, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE, designated SEQ ID:32400, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89345] Another function of VGAM2652 is therefore inhibition of LOC91115 (Accession XM_036218). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91115. LOC91291 (Accession XM_037478) is another VGAM2652 host target gene. LOC91291 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC91291, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91291 BINDING SITE, designated SEQ ID:32630, to the nucleotide sequence of VGAM2652 RNA, herein designated VGAM RNA, also designated SEQ ID:5363.

[89346] Another function of VGAM2652 is therefore inhibition of LOC91291 (Accession XM_037478). Accordingly, utilities of VGAM2652 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91291. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2653 (VGAM2653) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89347] VGAM2653 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2653 was detected is described hereinabove with reference to Figs. 1-8.

[89348] VGAM2653 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Sorghum Mosaic Virus. VGAM2653 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89349] VGAM2653 gene encodes a VGAM2653 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2653 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2653 precursor RNA is designated SEQ ID:2639, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2639 is located at position 9158 relative to the genome of Sorghum Mosaic Virus.

[89350] VGAM2653 precursor RNA folds onto itself, forming VGAM2653 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89351] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2653 folded precursor RNA into VGAM2653 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2653 RNA is designated SEQ ID:5364, and is provided hereinbelow with reference to the sequence listing part.

[89352] VGAM2653 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2653 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89353] VGAM2653 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2653 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2653 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89354] The complementary binding of VGAM2653 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2653 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2653

host target RNA into VGAM2653 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89355] It is appreciated that VGAM2653 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2653 host target genes. The mRNA of each one of this plurality of VGAM2653 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2653 RNA, herein designated VGAM RNA, and which when bound by VGAM2653 RNA causes inhibition of translation of respective one or more VGAM2653 host target proteins.

[89356] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2653 gene, herein designated VGAM GENE, on one or more VGAM2653 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89357] It is yet further appreciated that a function of VGAM2653 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of viral infection by Sorghum Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2653 correlate with, and may be deduced from, the identity of the host target genes which VGAM2653 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89358] Nucleotide sequences of the VGAM2653 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2653 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2653 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2653 are further

described hereinbelow with reference to Table 1.

[89359] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2653 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2653 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89360] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2653 gene, herein designated VGAM is inhibition of expression of VGAM2653 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2653 correlate with, and may be deduced from, the identity of the target genes which VGAM2653 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89361] BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 2 (BACH2, Accession NM_021813) is a VGAM2653 host target gene. BACH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BACH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of BACH2 BINDING SITE, designated SEQ ID:22378, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89362] A function of VGAM2653 is therefore inhibition of BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 2 (BACH2, Accession NM_021813), a gene which acts as repressor or activator, binds to maf recognition elements. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BACH2. The function of BACH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM331.Cyclin-dependent Kinase Inhibitor 2C (p18, inhibits CDK4) (CDKN2C, Accession NM_001262) is another VGAM2653 host target gene. CDKN2C BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CDKN2C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDKN2C BINDING SITE, designated SEQ ID:6928, to the nucleotide

sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89363] Another function of VGAM2653 is therefore inhibition of Cyclin-dependent Kinase Inhibitor 2C (p18, inhibits CDK4) (CDKN2C, Accession NM_001262), a gene which associate with cyclin-CDK complexes or CDKs alone and inhibit their activity. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKN2C. The function of CDKN2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2054.Chemokine (C-X-C motif) Ligand 16 (CXCL16, Accession NM_022059) is another VGAM2653 host target gene. CXCL16 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXCL16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXCL16 BINDING SITE, designated SEQ ID:22599, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89364] Another function of VGAM2653 is therefore inhibition of Chemokine (C-X-C motif) Ligand 16 (CXCL16, Accession NM_022059), a gene which induces calcium mobilization. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL16. The function of CXCL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1845.Eukaryotic Translation Initiation Factor 2, Subunit 3 Gamma, 52kDa (EIF2S3, Accession NM_001415) is another VGAM2653 host target gene. EIF2S3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF2S3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF2S3 BINDING SITE, designated SEQ ID:7111, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89365] Another function of VGAM2653 is therefore inhibition of Eukaryotic Translation Initiation Factor 2, Subunit 3 Gamma, 52kDa (EIF2S3, Accession NM_001415), a gene

which functions in the early steps of protein synthesis. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2S3. The function of EIF2S3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1254.Insulin-like Growth Factor Binding Protein 3 (IGFBP3, Accession NM_000598) is another VGAM2653 host target gene. IGFBP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IGFBP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IGFBP3 BINDING SITE, designated SEQ ID:6198, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89366] Another function of VGAM2653 is therefore inhibition of Insulin-like Growth Factor Binding Protein 3 (IGFBP3, Accession NM_000598). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IGFBP3. Mel Trans-

forming Oncogene (derived from cell line NK14)- RAB8 Homolog (MEL, Accession NM_005370) is another VGAM2653 host target gene. MEL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEL BINDING SITE, designated SEQ ID:11845, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89367] Another function of VGAM2653 is therefore inhibition of Mel Transforming Oncogene (derived from cell line NK14)- RAB8 Homolog (MEL, Accession NM_005370), a gene which may be involved in vesicular trafficking and neurotransmitter release. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEL. The function of MEL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM40.Oxidative-stress Responsive 1 (OSR1, Accession NM_005109) is another VGAM2653 host target gene.

OSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSR1 BINDING SITE, designated SEQ ID:11589, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89368] Another function of VGAM2653 is therefore inhibition of Oxidative-stress Responsive 1 (OSR1, Accession NM_005109), a gene which mediats stress-activated signals. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSR1. The function of OSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM538.Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 6 (SLC7A6, Accession NM_003983) is another VGAM2653 host target gene. SLC7A6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC7A6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC7A6 BINDING SITE, designated SEQ ID:10127, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89369] Another function of VGAM2653 is therefore inhibition of Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 6 (SLC7A6, Accession NM_003983), a gene which is involved in mediating amino acid transport. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A6. The function of SLC7A6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM87.Transcription Factor EB (TFEB, Accession XM_166390) is another VGAM2653 host target gene. TFEB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TFEB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TFEB BINDING SITE, designated SEQ ID:44239, to the nu-

cleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89370] Another function of VGAM2653 is therefore inhibition of Transcription Factor EB (TFEB, Accession XM_166390), a gene which may function as a transcription factor. Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TFEB. The function of TFEB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Chromosome 11 Open Reading Frame 25 (C11orf25, Accession NM_031418) is another VGAM2653 host target gene. C11orf25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf25 BINDING SITE, designated SEQ ID:25400, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89371] Another function of VGAM2653 is therefore inhibition of

Chromosome 11 Open Reading Frame 25 (C11orf25, Accession NM_031418). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf25. C16orf5 (Accession NM_013399) is another VGAM2653 host target gene. C16orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C16orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C16orf5 BINDING SITE, designated SEQ ID:15052, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89372] Another function of VGAM2653 is therefore inhibition of C16orf5 (Accession NM_013399). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C16orf5. DKFZP566K1924 (Accession XM_057469) is another VGAM2653 host target gene. DKFZP566K1924 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP566K1924, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566K1924 BINDING SITE, designated SEQ ID:36520, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89373] Another function of VGAM2653 is therefore inhibition of DKFZP566K1924 (Accession XM_057469). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566K1924. Dihydropyrimidinase-like 4 (DPYSL4, Accession NM_006426) is another VGAM2653 host target gene. DPYSL4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DPYSL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DPYSL4 BINDING SITE, designated SEQ ID:13141, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89374] Another function of VGAM2653 is therefore inhibition of Dihydropyrimidinase-like 4 (DPYSL4, Accession

NM_006426). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPYSL4. FLJ00024 (Accession XM_033361) is another VGAM2653 host target gene. FLJ00024 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00024 BINDING SITE, designated SEQ ID:31889, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89375] Another function of VGAM2653 is therefore inhibition of FLJ00024 (Accession XM_033361). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00024. FLJ11383 (Accession NM_024938) is another VGAM2653 host target gene. FLJ11383 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11383, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ11383 BINDING SITE, designated SEQ ID:24476, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89376] Another function of VGAM2653 is therefore inhibition of FLJ11383 (Accession NM_024938). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11383. FLJ13114 (Accession NM_024541) is another VGAM2653 host target gene. FLJ13114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:23749, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89377] Another function of VGAM2653 is therefore inhibition of FLJ13114 (Accession NM_024541). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114. FLJ32865 (Accession NM_144613) is another

VGAM2653 host target gene. FLJ32865 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:29425, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89378] Another function of VGAM2653 is therefore inhibition of FLJ32865 (Accession NM_144613). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865. HEF1 (Accession NM_006403) is another VGAM2653 host target gene. HEF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEF1 BINDING SITE, designated SEQ ID:13111, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89379] Another function of VGAM2653 is therefore inhibition of HEF1 (Accession NM_006403). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEF1. Immune Associated Nucleotide 4 Like 1 (mouse) (IAN4L1, Accession NM_018384) is another VGAM2653 host target gene. IAN4L1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IAN4L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IAN4L1 BINDING SITE, designated SEQ ID:20416, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89380] Another function of VGAM2653 is therefore inhibition of Immune Associated Nucleotide 4 Like 1 (mouse) (IAN4L1, Accession NM_018384). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IAN4L1. KIAA1260 (Accession XM_010461) is another VGAM2653 host target gene. KIAA1260 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by KIAA1260, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1260 BINDING SITE, designated SEQ ID:30157, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89381] Another function of VGAM2653 is therefore inhibition of KIAA1260 (Accession XM_010461). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1260. MGC12837 (Accession NM_032726) is another VGAM2653 host target gene. MGC12837 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC12837, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12837 BINDING SITE, designated SEQ ID:26452, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89382] Another function of VGAM2653 is therefore inhibition of MGC12837 (Accession NM_032726). Accordingly, utilities

of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12837. N4BP3 (Accession XM_038920) is another VGAM2653 host target gene. N4BP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by N4BP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of N4BP3 BINDING SITE, designated SEQ ID:32933, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89383] Another function of VGAM2653 is therefore inhibition of N4BP3 (Accession XM_038920). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with N4BP3. Nuclear Factor of Activated T-cells 5, Tonicity-responsive (NFAT5, Accession NM_138714) is another VGAM2653 host target gene. NFAT5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NFAT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of NFAT5 BINDING SITE, designated SEQ ID:28955, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89384] Another function of VGAM2653 is therefore inhibition of Nuclear Factor of Activated T-cells 5, Tonicity-responsive (NFAT5, Accession NM_138714). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFAT5. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840) is another VGAM2653 host target gene. PPP1R16B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R16B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R16B BINDING SITE, designated SEQ ID:30772, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89385] Another function of VGAM2653 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840). Accordingly, utilities

of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R16B. Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202) is another VGAM2653 host target gene. SS18L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS18L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS18L1 BINDING SITE, designated SEQ ID:32560, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89386] Another function of VGAM2653 is therefore inhibition of Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SS18L1. Syntaxin 1B2 (STX1B2, Accession NM_052874) is another VGAM2653 host target gene. STX1B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STX1B2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STX1B2 BINDING SITE, designated SEQ ID:27455, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89387] Another function of VGAM2653 is therefore inhibition of Syntaxin 1B2 (STX1B2, Accession NM_052874). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX1B2. Vacuolar Protein Sorting 4B (yeast) (VPS4B, Accession NM_004869) is another VGAM2653 host target gene. VPS4B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by VPS4B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS4B BINDING SITE, designated SEQ ID:11293, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89388] Another function of VGAM2653 is therefore inhibition of Vacuolar Protein Sorting 4B (yeast) (VPS4B, Accession

NM_004869). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS4B. LOC144871 (Accession XM_096698) is another VGAM2653 host target gene. LOC144871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144871 BINDING SITE, designated SEQ ID:40469, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89389] Another function of VGAM2653 is therefore inhibition of LOC144871 (Accession XM_096698). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144871. LOC158987 (Accession XM_099015) is another VGAM2653 host target gene. LOC158987 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC158987 BINDING SITE, designated SEQ ID:42046, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89390] Another function of VGAM2653 is therefore inhibition of LOC158987 (Accession XM_099015). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158987. LOC201164 (Accession XM_113904) is another VGAM2653 host target gene. LOC201164 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201164, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201164 BINDING SITE, designated SEQ ID:42529, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89391] Another function of VGAM2653 is therefore inhibition of LOC201164 (Accession XM_113904). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201164. LOC255308 (Accession XM_170536) is an-

other VGAM2653 host target gene. LOC255308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255308 BINDING SITE, designated SEQ ID:45354, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89392] Another function of VGAM2653 is therefore inhibition of LOC255308 (Accession XM_170536). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255308. LOC256821 (Accession XM_175144) is another VGAM2653 host target gene. LOC256821 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256821, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256821 BINDING SITE, designated SEQ ID:46638, to the nucleotide sequence of VGAM2653 RNA, herein designated VGAM RNA, also designated SEQ ID:5364.

[89393] Another function of VGAM2653 is therefore inhibition of LOC256821 (Accession XM_175144). Accordingly, utilities of VGAM2653 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256821. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2654 (VGAM2654) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89394] VGAM2654 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2654 was detected is described hereinabove with reference to Figs. 1-8.

[89395] VGAM2654 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sorghum Mosaic Virus. VGAM2654 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89396] VGAM2654 gene encodes a VGAM2654 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2654 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2654 precursor RNA is designated SEQ ID:2640, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2640 is located at position 2508 relative to the genome of Sorghum Mosaic Virus.

[89397] VGAM2654 precursor RNA folds onto itself, forming VGAM2654 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89398] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2654 folded precursor RNA into VGAM2654 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2654 RNA is designated SEQ ID:5365, and is provided hereinbelow with reference to the sequence listing part.

[89399] VGAM2654 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2654 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89400] VGAM2654 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2654 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2654 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89401] The complementary binding of VGAM2654 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2654 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2654 host target RNA into VGAM2654 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89402] It is appreciated that VGAM2654 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2654 host target genes. The mRNA of each one of this plurality of VGAM2654 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2654 RNA, herein designated VGAM RNA, and which when bound by VGAM2654 RNA causes inhibition of translation of respective one or more VGAM2654 host target proteins.

[89403] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2654 gene, herein designated VGAM GENE, on one or more VGAM2654 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89404] It is yet further appreciated that a function of VGAM2654 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2654 include diagnosis, prevention and treatment of viral infection by Sorghum Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2654 correlate with, and may be deduced from, the identity of the host target genes which VGAM2654 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89405] Nucleotide sequences of the VGAM2654 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2654 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2654 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2654 are further described hereinbelow with reference to Table 1.

[89406] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2654 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2654 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[89407] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2654 gene, herein designated VGAM is inhibition of expression of VGAM2654 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2654 correlate with, and may be deduced from, the identity of the target genes which VGAM2654 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89408] Zinc Finger Protein 215 (ZNF215, Accession NM_013250) is a VGAM2654 host target gene. ZNF215 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF215, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF215 BINDING SITE, designated SEQ ID:14911, to the nucleotide sequence of VGAM2654 RNA, herein designated VGAM RNA, also designated SEQ ID:5365.

[89409] A function of VGAM2654 is therefore inhibition of Zinc Finger Protein 215 (ZNF215, Accession NM_013250). Accordingly, utilities of VGAM2654 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with ZNF215. FLJ21820 (Accession NM_021925) is another VGAM2654 host target gene. FLJ21820 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21820, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21820 BINDING SITE, designated SEQ ID:22452, to the nucleotide sequence of VGAM2654 RNA, herein designated VGAM RNA, also designated SEQ ID:5365.

[89410] Another function of VGAM2654 is therefore inhibition of FLJ21820 (Accession NM_021925). Accordingly, utilities of VGAM2654 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21820. Spermatid Perinuclear RNA Binding Protein (STRBP, Accession NM_018387) is another VGAM2654 host target gene. STRBP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by STRBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STRBP BINDING SITE, des-

ignated SEQ ID:20418, to the nucleotide sequence of VGAM2654 RNA, herein designated VGAM RNA, also designated SEQ ID:5365.

[89411] Another function of VGAM2654 is therefore inhibition of Spermatid Perinuclear RNA Binding Protein (STRBP, Accession NM_018387). Accordingly, utilities of VGAM2654 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STRBP. LOC149302 (Accession XM_086489) is another VGAM2654 host target gene. LOC149302 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149302, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149302 BINDING SITE, designated SEQ ID:38707, to the nucleotide sequence of VGAM2654 RNA, herein designated VGAM RNA, also designated SEQ ID:5365.

[89412] Another function of VGAM2654 is therefore inhibition of LOC149302 (Accession XM_086489). Accordingly, utilities of VGAM2654 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149302. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2655 (VGAM2655) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89413] VGAM2655 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2655 was detected is described hereinabove with reference to Figs. 1-8.

[89414] VGAM2655 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sorghum Mosaic Virus. VGAM2655 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89415] VGAM2655 gene encodes a VGAM2655 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2655 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2655 precursor RNA is designated SEQ ID:2641, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2641 is located at position 8865 relative to the genome of Sorghum Mosaic Virus.

[89416] VGAM2655 precursor RNA folds onto itself, forming VGAM2655 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89417] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2655 folded precursor RNA into VGAM2655 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM2655 RNA is designated SEQ ID:5366, and is provided hereinbelow with reference to the sequence listing part.

[89418] VGAM2655 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2655 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89419] VGAM2655 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2655 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2655 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2655 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89420] The complementary binding of VGAM2655 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2655 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2655 host target RNA into VGAM2655 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89421] It is appreciated that VGAM2655 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2655 host target genes. The mRNA of each one of this plurality of VGAM2655 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2655 RNA, herein designated VGAM RNA, and which when bound by VGAM2655 RNA causes inhibition of translation of respective one or more

VGAM2655 host target proteins.

[89422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2655 gene, herein designated VGAM GENE, on one or more VGAM2655 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89423] It is yet further appreciated that a function of VGAM2655 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2655 include diagnosis, prevention and treatment of viral infection by Sorghum Mosaic Virus. Spe-

cific functions, and accordingly utilities, of VGAM2655 correlate with, and may be deduced from, the identity of the host target genes which VGAM2655 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89424] Nucleotide sequences of the VGAM2655 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2655 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2655 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2655 are further described hereinbelow with reference to Table 1.

[89425] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2655 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2655 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89426] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2655 gene, herein designated VGAM is inhibition of expression of VGAM2655 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2655 correlate with, and may be deduced from, the identity of the target genes which VGAM2655 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89427] AP1 Gamma Subunit Binding Protein 1 (AP1GBP1, Accession NM_080551) is a VGAM2655 host target gene. AP1GBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP1GBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE, designated SEQ ID:27880, to the nucleotide sequence of VGAM2655 RNA, herein designated VGAM RNA, also designated SEQ ID:5366.

[89428] A function of VGAM2655 is therefore inhibition of AP1 Gamma Subunit Binding Protein 1 (AP1GBP1, Accession NM_080551). Accordingly, utilities of VGAM2655 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1. LOC158055 (Accession XM_088453) is another VGAM2655 host target gene. LOC158055 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by LOC158055, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158055 BINDING SITE, designated SEQ ID:39705, to the nucleotide sequence of VGAM2655 RNA, herein designated VGAM RNA, also designated SEQ ID:5366.

[89429] Another function of VGAM2655 is therefore inhibition of LOC158055 (Accession XM_088453). Accordingly, utilities of VGAM2655 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158055. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2656 (VGAM2656) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89430] VGAM2656 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2656 was detected is described hereinabove with reference to Figs. 1-8.

[89431] VGAM2656 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Potato Virus A. VGAM2656 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89432] VGAM2656 gene encodes a VGAM2656 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2656 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2656 precursor RNA is designated SEQ ID:2642, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2642 is located at position 5538 relative to the genome of Potato Virus A.

[89433] VGAM2656 precursor RNA folds onto itself, forming VGAM2656 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89434] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2656 folded precursor RNA into VGAM2656 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2656 RNA is designated SEQ ID:5367, and is provided hereinbelow with reference to the sequence listing part.

[89435] VGAM2656 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2656 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89436] VGAM2656 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2656 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2656 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89437] The complementary binding of VGAM2656 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2656 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2656

host target RNA into VGAM2656 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89438] It is appreciated that VGAM2656 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2656 host target genes. The mRNA of each one of this plurality of VGAM2656 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2656 RNA, herein designated VGAM RNA, and which when bound by VGAM2656 RNA causes inhibition of translation of respective one or more VGAM2656 host target proteins.

[89439] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2656 gene, herein designated VGAM GENE, on one or more VGAM2656 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89440] It is yet further appreciated that a function of VGAM2656 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGAM2656 correlate with, and may be deduced from, the identity of the host target genes which VGAM2656 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89441] Nucleotide sequences of the VGAM2656 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2656 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2656 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2656 are further

described hereinbelow with reference to Table 1.

[89442] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2656 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2656 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89443] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2656 gene, herein designated VGAM is inhibition of expression of VGAM2656 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2656 correlate with, and may be deduced from, the identity of the target genes which VGAM2656 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89444] ATP-binding Cassette, Sub-family A (ABC1), Member 1 (ABCA1, Accession NM_005502) is a VGAM2656 host target gene. ABCA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of ABCA1 BINDING SITE, designated SEQ ID:12011, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89445] A function of VGAM2656 is therefore inhibition of ATP-binding Cassette, Sub-family A (ABC1), Member 1 (ABCA1, Accession NM_005502), a gene which camp-dependent and sulfonylurea-sensitive anion transporter. Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA1. The function of ABCA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1956.HLA-G Histocompatibility Antigen, Class I, G (HLA-G, Accession NM_002127) is another VGAM2656 host target gene. HLA-G BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HLA-G, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HLA-G BINDING SITE, designated SEQ ID:7906, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA,

also designated SEQ ID:5367.

[89446] Another function of VGAM2656 is therefore inhibition of HLA-G Histocompatibility Antigen, Class I, G (HLA-G, Accession NM_002127), a gene which involved in the presentation of foreign antigens to the immune system. Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLA-G. The function of HLA-G has been established by previous studies. Extravillous trophoblast from normal human placenta and the BeWo adherent human choriocarcinoma cell line express an unusual form of class I HLA molecule. This molecule has an H chain of approximately 40 kD and is apparently nonpolymorphic. Ellis et al. (1990) isolated and sequenced a cDNA clone for this class I HLA antigen. The nucleotide sequence showed a high degree of homology with the published sequence of a genomic clone, HLA 6.0, which is the product of a class I locus other than A, B, or C. The new locus was provisionally designated HLAG. Using PCR, Ellis et al. (1990) demonstrated similar HLA class I sequences in cDNA from normal extravillous trophoblasts. Although there was some nucleotide sequence polymorphism, the amino acid sequence of the molecule was conserved; hence, it is un-

likely to provoke immune responses even though it is found at the fetal-maternal interface. Considering the well established role of nonclassic HLA-G class I molecules in inhibiting natural killer cell function, the consequence of abnormal HLA-G expression in malignant cells should be the escape of tumors from immunosurveillance. To examine this hypothesis, Paul et al. (1998) analyzed HLA-G expression and NK sensitivity in human malignant melanoma cells. Two melanoma cell lines exhibited a high level of HLA-G transcription with differential HLA-G isoform transcription and protein expression patterns. A higher level of HLA-G transcription ex vivo was detected in a skin melanoma metastasis biopsy compared with a healthy skin fragment from the same individual. HLA-G protein isoforms other than membrane-bound HLA-G1 protected 1 melanoma cell line from NK lysis. It thus appeared of critical importance to consider the specific role of HLA-G expression in tumors in the design of cancer immunotherapies.

[89447] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[89448] Ellis, S. A.; Palmer, M. S.; McMichael, A. J. : Human tro-

phoblast and the choriocarcinoma cell line BeWo express a truncated HLA class I molecule. J. Immun. 144: 731-735, 1990. ; and

[89449] Paul, P.; Rouas-Freiss, N.; Khalil-Daher, I.; Moreau, P.; Riteau, B.; Le Gal, F. A.; Avril, M. F.; Dausset, J.; Guillet, J. G.; Carosella, E. D. : HLA-G expression in melanoma: a way fo.

[89450] Further studies establishing the function and utilities of HLA-G are found in John Hopkins OMIM database record ID 142871, and in sited publications numbered 3295, 11451-11460, 3781, 11461-1146 and 11499-11501 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DKFZp761F2014 (Accession NM_020215) is another VGAM2656 host target gene. DKFZp761F2014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761F2014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761F2014 BINDING SITE, designated SEQ ID:21457, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89451] Another function of VGAM2656 is therefore inhibition of DKFZp761F2014 (Accession NM_020215). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761F2014. KIAA1463 (Accession XM_051160) is another VGAM2656 host target gene. KIAA1463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1463 BINDING SITE, designated SEQ ID:35768, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89452] Another function of VGAM2656 is therefore inhibition of KIAA1463 (Accession XM_051160). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1463. MGC2488 (Accession NM_024039) is another VGAM2656 host target gene. MGC2488 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2488, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2488 BINDING SITE, designated SEQ ID:23473, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89453] Another function of VGAM2656 is therefore inhibition of MGC2488 (Accession NM_024039). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2488. MGC2560 (Accession NM_031452) is another VGAM2656 host target gene. MGC2560 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2560, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2560 BINDING SITE, designated SEQ ID:25466, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89454] Another function of VGAM2656 is therefore inhibition of MGC2560 (Accession NM_031452). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC2560. Synaptotagmin XIII (SYT13, Accession XM_167880) is another VGAM2656 host target gene. SYT13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYT13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYT13 BINDING SITE, designated SEQ ID:44886, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89455] Another function of VGAM2656 is therefore inhibition of Synaptotagmin XIII (SYT13, Accession XM_167880). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT13. LOC113523 (Accession XM_054378) is another VGAM2656 host target gene. LOC113523 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC113523, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113523 BINDING SITE, desig-

nated SEQ ID:36150, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89456] Another function of VGAM2656 is therefore inhibition of LOC113523 (Accession XM_054378). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113523. LOC147343 (Accession XM_097225) is another VGAM2656 host target gene. LOC147343 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147343, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147343 BINDING SITE, designated SEQ ID:40830, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89457] Another function of VGAM2656 is therefore inhibition of LOC147343 (Accession XM_097225). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147343. LOC150245 (Accession XM_097843) is another VGAM2656 host target gene. LOC150245 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150245, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150245 BINDING SITE, designated SEQ ID:41161, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89458] Another function of VGAM2656 is therefore inhibition of LOC150245 (Accession XM_097843). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150245. LOC220477 (Accession XM_071675) is another VGAM2656 host target gene. LOC220477 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220477, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220477 BINDING SITE, designated SEQ ID:37407, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89459] Another function of VGAM2656 is therefore inhibition of

LOC220477 (Accession XM_071675). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220477. LOC254700 (Accession XM_171244) is another VGAM2656 host target gene. LOC254700 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254700, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254700 BINDING SITE, designated SEQ ID:46037, to the nucleotide sequence of VGAM2656 RNA, herein designated VGAM RNA, also designated SEQ ID:5367.

[89460] Another function of VGAM2656 is therefore inhibition of LOC254700 (Accession XM_171244). Accordingly, utilities of VGAM2656 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254700. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2657 (VGAM2657) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[89461] VGAM2657 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2657 was detected is described hereinabove with reference to Figs. 1-8.

[89462] VGAM2657 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Virus A. VGAM2657 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89463] VGAM2657 gene encodes a VGAM2657 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2657 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2657 precursor RNA is designated SEQ ID:2643, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2643 is located at position 7993 relative to the genome of Potato Virus A.

[89464] VGAM2657 precursor RNA folds onto itself, forming VGAM2657 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89465] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2657 folded precursor RNA into VGAM2657 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2657 RNA is designated SEQ ID:5368, and is provided hereinbelow with reference to the sequence listing part.

[89466] VGAM2657 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2657 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89467] VGAM2657 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2657 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2657 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[89468] The complementary binding of VGAM2657 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2657 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2657 host target RNA into VGAM2657 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89469] It is appreciated that VGAM2657 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2657 host target genes. The mRNA of each one of this plurality of VGAM2657 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2657 RNA, herein designated VGAM RNA, and which when bound by VGAM2657 RNA causes inhibition of translation of respective one or more VGAM2657 host target proteins.

[89470] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2657 gene, herein designated VGAM GENE, on one

or more VGAM2657 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89471] It is yet further appreciated that a function of VGAM2657 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGAM2657 correlate with, and may be deduced from, the identity of the host target genes which VGAM2657 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89472] Nucleotide sequences of the VGAM2657 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2657 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2657 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2657 are further described hereinbelow with reference to Table 1.

[89473] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2657 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2657 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89474] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2657 gene, herein designated VGAM is inhibition of expression of VGAM2657 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2657 correlate with, and may be deduced from, the identity of the target genes which VGAM2657 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89475] ATP-binding Cassette, Sub-family C (CFTR/MRP), Member

3 (ABCC3, Accession NM_020038) is a VGAM2657 host target gene. ABCC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCC3 BINDING SITE, designated SEQ ID:21292, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89476] A function of VGAM2657 is therefore inhibition of ATP-binding Cassette, Sub-family C (CFTR/MRP), Member 3 (ABCC3, Accession NM_020038), a gene which may act as an inducible transporter in the biliary and intestinal excretion of organic anions. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC3. The function of ABCC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM505.Cadherin, EGF LAG Seven-pass G-type Receptor 2 (flamingo homolog, Drosophila) (CELSR2, Accession NM_001408) is another VGAM2657 host target gene.

CELSR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CELSR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CELSR2 BINDING SITE, designated SEQ ID:7107, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89477] Another function of VGAM2657 is therefore inhibition of Cadherin, EGF LAG Seven-pass G-type Receptor 2 (flamingo homolog, Drosophila) (CELSR2, Accession NM_001408), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CELSR2. The function of CELSR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM432.FXYD Domain Containing Ion Transport Regulator 6 (FXYD6, Accession NM_022003) is another VGAM2657 host target gene. FXYD6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by FXYD6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FXYD6 BINDING SITE, designated SEQ ID:22548, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89478] Another function of VGAM2657 is therefore inhibition of FXYD Domain Containing Ion Transport Regulator 6 (FXYD6, Accession NM_022003). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FXYD6. Hepatocyte Nuclear Factor 4, Alpha (HNF4A, Accession NM_000457) is another VGAM2657 host target gene. HNF4A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HNF4A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNF4A BINDING SITE, designated SEQ ID:6072, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89479] Another function of VGAM2657 is therefore inhibition of Hepatocyte Nuclear Factor 4, Alpha (HNF4A, Accession NM_000457), a gene which may be essential for development of the liver, kidney, pancreas and intestine. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNF4A. The function of HNF4A has been established by previous studies. Stoffel and Duncan (1997) investigated the molecular mechanism by which the Q268X mutation, which deletes 187 C-terminal amino acids of the HNF4-alpha protein, causes diabetes. They showed that the mutant gene product had lost its transcriptional transactivation activity and failed to dimerize and bind DNA, implying that the MODY1 phenotype is due to a loss of HFN4-alpha function. The effect of loss of function on expression of HNF4-alpha target genes was investigated further in embryonic stem cells, which are amenable to genetic manipulation and can be induced to form visceral endoderm. Because the visceral endoderm shares many properties with the liver and pancreatic beta-cells, including expression of genes for glucose transport and metabolism, it offers an ideal system to investigate HNF4-dependent gene regulation in glucose homeostasis.

With this approach, Stoffel and Duncan (1997) identified several genes encoding components of the glucose-dependent insulin secretion pathway whose expression is dependent upon HNF4-alpha. These included glucose transporter 2 (OMIM Ref. No. 138160), and the glycolytic enzymes aldolase B (OMIM Ref. No. 229600) and glyceraldehyde-3-phosphate dehydrogenase (OMIM Ref. No. 138400), and liver pyruvate kinase (OMIM Ref. No. 266200). In addition, they found that expression of the fatty acid binding proteins and cellular retinol binding protein also are downregulated in the absence of HNF4-alpha. These data provided direct evidence that HNF4-alpha is critical for regulating glucose transport and glycolysis and in doing so is critical for maintaining glucose homeostasis. Animal model experiments lend further support to the function of HNF4A. To study the contribution of HNF4A to hepatic development and differentiation, Li et al. (2000) used a technique in which Hnf4a -/- mouse embryos were complemented with wildtype visceral endoderm to counteract early embryonic lethality. By histologic analyses, the authors found that specification and early development of the liver and liver morphology did not require Hnf4a. In addition, the expression of many

liver genes was unaffected in these mice. However, RT-PCR analysis showed that Hnf4a -/- fetal livers failed to express a large array of genes whose expression in differentiated hepatocytes is essential for a functional hepatic parenchyma, including apolipoproteins (e.g., APOA1; 107680), metabolic proteins (e.g., aldolase B; 229600), transferrin (OMIM Ref. No. 190000), retinol-binding protein (e.g., RBP4; 180250), and erythropoietin (OMIM Ref. No. 133170). The lack of Hnf4a did not affect the expression of most transcription factors but did significantly reduce the levels of Hnf1a (TCF1; 142410) and the pregnane X receptor (NR1I2; 603065), suggesting that HNF4A acts upstream of at least these 2 transcription factors, which are also important in hepatocyte gene expression.

[89480] It is appreciated that the abovementioned animal model for HNF4A is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[89481] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[89482] Li, J.; Ning, G.; Duncan, S. A. : Mammalian hepatocyte differentiation requires the transcription factor HNF-4-alpha.

Genes Dev. 14: 464-474, 2000. ; and

[89483] Stoffel, M.; Duncan, S. A. : The maturity-onset diabetes of the young (MODY1) transcription factor HNF4-alpha regulates expression of genes required for glucose transport and metabolism. P.

[89484] Further studies establishing the function and utilities of HNF4A are found in John Hopkins OMIM database record ID 600281, and in sited publications numbered 4979, 9869-9871, 11607, 12032-9875, 12033-12034, 987 and 12035-9878 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Neural Retina Leucine Zipper (NRL, Accession NM_006177) is another VGAM2657 host target gene. NRL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NRL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRL BINDING SITE, designated SEQ ID:12838, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89485] Another function of VGAM2657 is therefore inhibition of Neural Retina Leucine Zipper (NRL, Accession

NM_006177), a gene which has a basic motif and a leucine zipper domain similar to jun and fos. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRL. The function of NRL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.PACE (Accession NM_002569) is another VGAM2657 host target gene. PACE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PACE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PACE BINDING SITE, designated SEQ ID:8422, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89486] Another function of VGAM2657 is therefore inhibition of PACE (Accession NM_002569), a gene which processes pro-parathyroid hormone, pro-transforming growth factor beta. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PACE. The function of PACE

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM151.RAD52 Homolog (S. cerevisiae) (RAD52, Accession NM_134423) is another VGAM2657 host target gene. RAD52 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAD52, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:28658, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89487] Another function of VGAM2657 is therefore inhibition of RAD52 Homolog (S. cerevisiae) (RAD52, Accession NM_134423). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52. Regulating Synaptic Membrane Exocytosis 1 (RIMS1, Accession XM_052206) is another VGAM2657 host target gene. RIMS1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RIMS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RIMS1 BINDING SITE, designated SEQ ID:35957, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89488] Another function of VGAM2657 is therefore inhibition of Regulating Synaptic Membrane Exocytosis 1 (RIMS1, Accession XM_052206), a gene which may have a regulatory role in the membrane interactions during trafficking of synaptic vesicles. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIMS1. The function of RIMS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2454.Ribonuclease/angiogenin Inhibitor (RNH, Accession XM_006139) is another VGAM2657 host target gene. RNH BINDING SITE1 and RNH BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RNH, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNH BINDING SITE1 and

RNH BINDING SITE2, designated SEQ ID:29993 and SEQ ID:8844 respectively, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89489] Another function of VGAM2657 is therefore inhibition of Ribonuclease/angiogenin Inhibitor (RNH, Accession XM_006139), a gene which is an inhibitor of pancreatic rnase and angiogenin. may also function in the modulation of cellular activities. Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNH. The function of RNH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM484.Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 7 (SLC7A7, Accession NM_003982) is another VGAM2657 host target gene. SLC7A7 BINDING SITE1 and SLC7A7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC7A7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC7A7 BINDING

SITE1 and SLC7A7 BINDING SITE2, designated SEQ ID:10122 and SEQ ID:43809 respectively, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89490] Another function of VGAM2657 is therefore inhibition of Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 7 (SLC7A7, Accession NM_003982). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A7. FLJ22814 (Accession NM_024916) is another VGAM2657 host target gene. FLJ22814 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22814, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22814 BINDING SITE, designated SEQ ID:24443, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89491] Another function of VGAM2657 is therefore inhibition of FLJ22814 (Accession NM_024916). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ22814. FLJ23416 (Accession NM_032238) is another VGAM2657 host target gene. FLJ23416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23416 BINDING SITE, designated SEQ ID:25960, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89492] Another function of VGAM2657 is therefore inhibition of FLJ23416 (Accession NM_032238). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23416. FLJ23519 (Accession XM_044932) is another VGAM2657 host target gene. FLJ23519 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23519 BINDING SITE, designated SEQ ID:34307, to the nucleotide

sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89493] Another function of VGAM2657 is therefore inhibition of FLJ23519 (Accession XM_044932). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23519. Potassium Voltage-gated Channel, Subfamily G, Member 3 (KCNG3, Accession NM_133329) is another VGAM2657 host target gene. KCNG3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNG3 BINDING SITE, designated SEQ ID:28437, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89494] Another function of VGAM2657 is therefore inhibition of Potassium Voltage-gated Channel, Subfamily G, Member 3 (KCNG3, Accession NM_133329). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNG3. KIAA1464 (Accession XM_043069) is another VGAM2657

host target gene. KIAA1464 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1464 BINDING SITE, designated SEQ ID:33879, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89495] Another function of VGAM2657 is therefore inhibition of KIAA1464 (Accession XM_043069). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1464. KIAA1674 (Accession XM_044065) is another VGAM2657 host target gene. KIAA1674 BINDING SITE1 through KIAA1674 BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1674, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1674 BINDING SITE1 through KIAA1674 BINDING SITE6, designated SEQ ID:34104, SEQ ID:34105, SEQ ID:34106, SEQ ID:34107, SEQ ID:34108

and SEQ ID:34109 respectively, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89496] Another function of VGAM2657 is therefore inhibition of KIAA1674 (Accession XM_044065). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1674. MGC2474 (Accession NM_023931) is another VGAM2657 host target gene. MGC2474 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE, designated SEQ ID:23415, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89497] Another function of VGAM2657 is therefore inhibition of MGC2474 (Accession NM_023931). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2474. MGC3047 (Accession NM_032348) is another VGAM2657 host target gene. MGC3047 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3047, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3047 BINDING SITE, designated SEQ ID:26138, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89498] Another function of VGAM2657 is therefore inhibition of MGC3047 (Accession NM_032348). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3047. MGC5391 (Accession NM_032740) is another VGAM2657 host target gene. MGC5391 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC5391, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5391 BINDING SITE, designated SEQ ID:26471, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89499] Another function of VGAM2657 is therefore inhibition of

MGC5391 (Accession NM_032740). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5391. NIFU (Accession XM_041081) is another VGAM2657 host target gene. NIFU BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NIFU, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NIFU BINDING SITE, designated SEQ ID:33436, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89500] Another function of VGAM2657 is therefore inhibition of NIFU (Accession XM_041081). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NIFU. Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654) is another VGAM2657 host target gene. SDC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates

the complementarity of the nucleotide sequences of SDC3 BINDING SITE, designated SEQ ID:16091, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89501] Another function of VGAM2657 is therefore inhibition of Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDC3. Transducer of ERBB2, 2 (TOB2, Accession XM_170995) is another VGAM2657 host target gene. TOB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOB2 BINDING SITE, designated SEQ ID:45771, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89502] Another function of VGAM2657 is therefore inhibition of Transducer of ERBB2, 2 (TOB2, Accession XM_170995). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with TOB2. LOC142927 (Accession XM_084380) is another VGAM2657 host target gene. LOC142927 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142927, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142927 BINDING SITE, designated SEQ ID:37569, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89503] Another function of VGAM2657 is therefore inhibition of LOC142927 (Accession XM_084380). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142927. LOC144571 (Accession XM_096630) is another VGAM2657 host target gene. LOC144571 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144571, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144571 BINDING SITE, designated SEQ ID:40444, to

the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89504] Another function of VGAM2657 is therefore inhibition of LOC144571 (Accession XM_096630). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144571. LOC145195 (Accession XM_096731) is another VGAM2657 host target gene. LOC145195 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145195 BINDING SITE, designated SEQ ID:40512, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89505] Another function of VGAM2657 is therefore inhibition of LOC145195 (Accession XM_096731). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145195. LOC146782 (Accession XM_083963) is another VGAM2657 host target gene. LOC146782 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC146782, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146782 BINDING SITE, designated SEQ ID:37524, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89506] Another function of VGAM2657 is therefore inhibition of LOC146782 (Accession XM_083963). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146782. LOC148709 (Accession XM_086281) is another VGAM2657 host target gene. LOC148709 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148709, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE, designated SEQ ID:38579, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89507] Another function of VGAM2657 is therefore inhibition of LOC148709 (Accession XM_086281). Accordingly, utilities

of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709. LOC149478 (Accession XM_086536) is another VGAM2657 host target gene. LOC149478 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149478, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149478 BINDING SITE, designated SEQ ID:38753, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89508] Another function of VGAM2657 is therefore inhibition of LOC149478 (Accession XM_086536). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478. LOC170395 (Accession XM_084325) is another VGAM2657 host target gene. LOC170395 BINDING SITE1 through LOC170395 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC170395, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of LOC170395 BINDING SITE1 through LOC170395 BINDING SITE3, designated SEQ ID:37543, SEQ ID:37541 and SEQ ID:37542 respectively, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89509] Another function of VGAM2657 is therefore inhibition of LOC170395 (Accession XM_084325). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170395. LOC256158 (Accession XM_175125) is another VGAM2657 host target gene. LOC256158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256158 BINDING SITE, designated SEQ ID:46634, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89510] Another function of VGAM2657 is therefore inhibition of LOC256158 (Accession XM_175125). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC256158. LOC257054 (Accession XM_171010) is another VGAM2657 host target gene. LOC257054 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257054 BINDING SITE, designated SEQ ID:45782, to the nucleotide sequence of VGAM2657 RNA, herein designated VGAM RNA, also designated SEQ ID:5368.

[89511] Another function of VGAM2657 is therefore inhibition of LOC257054 (Accession XM_171010). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257054. LOC90019 (Accession NM_138567) is another VGAM2657 host target gene. LOC90019 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90019, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90019 BINDING SITE, designated SEQ ID:28877, to the nucleotide sequence of VGAM2657 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5368.

[89512] Another function of VGAM2657 is therefore inhibition of LOC90019 (Accession NM_138567). Accordingly, utilities of VGAM2657 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90019. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2658 (VGAM2658) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89513] VGAM2658 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2658 was detected is described hereinabove with reference to Figs. 1-8.

[89514] VGAM2658 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Virus A. VGAM2658 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89515] VGAM2658 gene encodes a VGAM2658 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2658 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2658 precursor RNA is designated SEQ ID:2644, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2644 is located at position 8772 relative to the genome of Potato Virus A.

[89516] VGAM2658 precursor RNA folds onto itself, forming VGAM2658 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89517] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2658 folded precursor RNA into VGAM2658 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2658 RNA is designated SEQ ID:5369, and is provided hereinbelow with reference to the sequence listing part.

[89518] VGAM2658 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2658 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89519] VGAM2658 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2658 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2658 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89520] The complementary binding of VGAM2658 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2658 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2658 host target RNA into VGAM2658 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89521] It is appreciated that VGAM2658 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2658 host target genes. The mRNA of

each one of this plurality of VGAM2658 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2658 RNA, herein designated VGAM RNA, and which when bound by VGAM2658 RNA causes inhibition of translation of respective one or more VGAM2658 host target proteins.

[89522] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2658 gene, herein designated VGAM GENE, on one or more VGAM2658 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[89523] It is yet further appreciated that a function of VGAM2658 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGAM2658 correlate with, and may be deduced from, the identity of the host target genes which VGAM2658 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89524] Nucleotide sequences of the VGAM2658 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2658 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2658 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2658 are further described hereinbelow with reference to Table 1.

[89525] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2658 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2658 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89526] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2658 gene, herein designated VGAM is inhibition of expression of VGAM2658 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2658 correlate with, and may be deduced from, the identity of the target genes which VGAM2658 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89527] Heterogeneous Nuclear Ribonucleoprotein K (HNRPK, Accession NM_002140) is a VGAM2658 host target gene. HNRPK BINDING SITE1 and HNRPK BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HNRPK, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPK BINDING SITE1 and HNRPK BINDING SITE2, designated SEQ ID:7918 and SEQ ID:25282 respectively, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89528] A function of VGAM2658 is therefore inhibition of Hetero-

geneous Nuclear Ribonucleoprotein K (HNRPK, Accession NM_002140), a gene which play a role in the nuclear metabolism of hnrnas, particularly for pre-mrnas that contain cytidine-rich sequence. Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPK. The function of HNRPK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.Ribulose-5-phosphate-3-epimerase (RPE, Accession XM_030834) is another VGAM2658 host target gene. RPE BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RPE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPE BINDING SITE, designated SEQ ID:31157, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89529] Another function of VGAM2658 is therefore inhibition of Ribulose-5-phosphate-3-epimerase (RPE, Accession XM_030834). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with RPE. Chromosome 20 Open Reading Frame 140 (C20orf140, Accession NM_144628) is another VGAM2658 host target gene. C20orf140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf140 BINDING SITE, designated SEQ ID:29444, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89530] Another function of VGAM2658 is therefore inhibition of Chromosome 20 Open Reading Frame 140 (C20orf140, Accession NM_144628). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf140. CCR4-NOT Transcription Complex, Subunit 4 (CNOT4, Accession NM_013316) is another VGAM2658 host target gene. CNOT4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNOT4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of CNOT4 BINDING SITE, designated SEQ ID:14965, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89531] Another function of VGAM2658 is therefore inhibition of CCR4-NOT Transcription Complex, Subunit 4 (CNOT4, Accession NM_013316). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNOT4. KIAA1348 (Accession XM_043826) is another VGAM2658 host target gene. KIAA1348 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1348, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1348 BINDING SITE, designated SEQ ID:34031, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89532] Another function of VGAM2658 is therefore inhibition of KIAA1348 (Accession XM_043826). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1348. KIAA1577 (Accession XM_035299) is another VGAM2658 host target gene. KIAA1577 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1577 BINDING SITE, designated SEQ ID:32210, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89533] Another function of VGAM2658 is therefore inhibition of KIAA1577 (Accession XM_035299). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1577. MGC2835 (Accession NM_024072) is another VGAM2658 host target gene. MGC2835 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2835, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2835 BINDING SITE, designated SEQ ID:23504, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM

RNA, also designated SEQ ID:5369.

[89534] Another function of VGAM2658 is therefore inhibition of MGC2835 (Accession NM_024072). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2835. LOC146823 (Accession XM_097105) is another VGAM2658 host target gene. LOC146823 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146823, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146823 BINDING SITE, designated SEQ ID:40751, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89535] Another function of VGAM2658 is therefore inhibition of LOC146823 (Accession XM_097105). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146823. LOC149302 (Accession XM_086489) is another VGAM2658 host target gene. LOC149302 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149302, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149302 BINDING SITE, designated SEQ ID:38704, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89536] Another function of VGAM2658 is therefore inhibition of LOC149302 (Accession XM_086489). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149302. LOC164397 (Accession XM_092780) is another VGAM2658 host target gene. LOC164397 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC164397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164397 BINDING SITE, designated SEQ ID:40154, to the nucleotide sequence of VGAM2658 RNA, herein designated VGAM RNA, also designated SEQ ID:5369.

[89537] Another function of VGAM2658 is therefore inhibition of LOC164397 (Accession XM_092780). Accordingly, utilities of VGAM2658 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC164397. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2659 (VGAM2659) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89538] VGAM2659 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2659 was detected is described hereinabove with reference to Figs. 1-8.

[89539] VGAM2659 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Virus A. VGAM2659 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89540] VGAM2659 gene encodes a VGAM2659 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2659 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2659 precursor RNA is desig-

nated SEQ ID:2645, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2645 is located at position 3436 relative to the genome of Potato Virus A.

[89541] VGAM2659 precursor RNA folds onto itself, forming VGAM2659 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89542] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2659 folded precursor RNA into VGAM2659 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2659 RNA is designated SEQ ID:5370, and is provided hereinbelow with reference to the sequence

listing part.

[89543] VGAM2659 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2659 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89544] VGAM2659 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2659 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2659 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89545] The complementary binding of VGAM2659 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2659 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2659 host target RNA into VGAM2659 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89546] It is appreciated that VGAM2659 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2659 host target genes. The mRNA of each one of this plurality of VGAM2659 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2659 RNA, herein designated VGAM

RNA, and which when bound by VGAM2659 RNA causes inhibition of translation of respective one or more VGAM2659 host target proteins.

[89547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2659 gene, herein designated VGAM GENE, on one or more VGAM2659 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89548] It is yet further appreciated that a function of VGAM2659 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2659 include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGAM2659 correlate with, and may be deduced from, the identity of the host target genes which VGAM2659 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89549] Nucleotide sequences of the VGAM2659 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2659 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2659 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2659 are further described hereinbelow with reference to Table 1.

[89550] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2659 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2659 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89551] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2659 gene, herein designated VGAM is

inhibition of expression of VGAM2659 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2659 correlate with, and may be deduced from, the identity of the target genes which VGAM2659 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89552] Aldehyde Dehydrogenase 3 Family, Member B1 (ALDH3B1, Accession XM_166190) is a VGAM2659 host target gene. ALDH3B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALDH3B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALDH3B1 BINDING SITE, designated SEQ ID:44001, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89553] A function of VGAM2659 is therefore inhibition of Aldehyde Dehydrogenase 3 Family, Member B1 (ALDH3B1, Accession XM_166190), a gene which may play a major role in the detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation. Accordingly, utilities of VGAM2659 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with ALDH3B1. The function of ALDH3B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2007.AT-binding Transcription Factor 1 (ATBF1, Accession NM_006885) is another VGAM2659 host target gene. ATBF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ATBF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATBF1 BINDING SITE, designated SEQ ID:13750, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89554] Another function of VGAM2659 is therefore inhibition of AT-binding Transcription Factor 1 (ATBF1, Accession NM_006885). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATBF1. Axin 1 (AXIN1, Accession XM_027520) is another VGAM2659 host target gene. AXIN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

AXIN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AXIN1 BINDING SITE, designated SEQ ID:30519, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89555] Another function of VGAM2659 is therefore inhibition of Axin 1 (AXIN1, Accession XM_027520). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXIN1. B-cell CLL/lymphoma 9 (BCL9, Accession NM_004326) is another VGAM2659 host target gene. BCL9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL9 BINDING SITE, designated SEQ ID:10526, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89556] Another function of VGAM2659 is therefore inhibition of B-cell CLL/lymphoma 9 (BCL9, Accession NM_004326), a

gene which recruits of PYGO to the nuclear beta-catenin-TCF complex in Wnt/Wingless signaling. Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL9. The function of BCL9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Cleavage and Polyadenylation Specific Factor 6, 68kDa (CPSF6, Accession NM_007007) is another VGAM2659 host target gene. CPSF6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPSF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPSF6 BINDING SITE, designated SEQ ID:13870, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89557] Another function of VGAM2659 is therefore inhibition of Cleavage and Polyadenylation Specific Factor 6, 68kDa (CPSF6, Accession NM_007007). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF6.

POU Domain, Class 4, Transcription Factor 1 (POU4F1, Accession NM_006237) is another VGAM2659 host target gene. POU4F1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU4F1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU4F1 BINDING SITE, designated SEQ ID:12899, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89558] Another function of VGAM2659 is therefore inhibition of POU Domain, Class 4, Transcription Factor 1 (POU4F1, Accession NM_006237), a gene which plays a role in the regulation of specific gene expression within a subset of neuronal lineages. Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU4F1. The function of POU4F1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1026.SRY (sex determining region Y)-box 4 (SOX4, Accession NM_003107) is another VGAM2659 host target

gene. SOX4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX4 BINDING SITE, designated SEQ ID:9078, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89559] Another function of VGAM2659 is therefore inhibition of SRY (sex determining region Y)-box 4 (SOX4, Accession NM_003107), a gene which binds with high affinity to the t-cell enhancer motif 5'-aacaaag-3' motif. Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX4. The function of SOX4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM409.T-cell Leukemia, Homeobox 1 (TLX1, Accession NM_005521) is another VGAM2659 host target gene. TLX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TLX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of TLX1 BINDING SITE, designated SEQ ID:12047, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89560] Another function of VGAM2659 is therefore inhibition of T-cell Leukemia, Homeobox 1 (TLX1, Accession NM_005521), a gene which controls the spleen development. Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLX1. The function of TLX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1505.Chromosome X Open Reading Frame 1 (CXorf1, Accession NM_004709) is another VGAM2659 host target gene. CXorf1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXorf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXorf1 BINDING SITE, designated SEQ ID:11057, to the nucleotide sequence of VGAM2659 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5370.

[89561] Another function of VGAM2659 is therefore inhibition of Chromosome X Open Reading Frame 1 (CXorf1, Accession NM_004709). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXorf1. DC-TM4F2 (Accession NM_030927) is another VGAM2659 host target gene. DC-TM4F2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DC-TM4F2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DC-TM4F2 BINDING SITE, designated SEQ ID:25200, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89562] Another function of VGAM2659 is therefore inhibition of DC-TM4F2 (Accession NM_030927). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DC-TM4F2. DKFZP566N034 (Accession XM_087115) is another VGAM2659 host target gene. DKFZP566N034 BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by DKFZP566N034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566N034 BINDING SITE, designated SEQ ID:39064, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89563] Another function of VGAM2659 is therefore inhibition of DKFZP566N034 (Accession XM_087115). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566N034. FLJ10597 (Accession NM_018150) is another VGAM2659 host target gene. FLJ10597 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10597, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10597 BINDING SITE, designated SEQ ID:19954, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89564] Another function of VGAM2659 is therefore inhibition of

FLJ10597 (Accession NM_018150). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10597. FLJ12687 (Accession NM_024917) is another VGAM2659 host target gene. FLJ12687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12687 BINDING SITE, designated SEQ ID:24449, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89565] Another function of VGAM2659 is therefore inhibition of FLJ12687 (Accession NM_024917). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12687. FLJ23323 (Accession NM_024654) is another VGAM2659 host target gene. FLJ23323 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ23323 BINDING SITE, designated SEQ ID:23956, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89566] Another function of VGAM2659 is therefore inhibition of FLJ23323 (Accession NM_024654). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23323. FLJ23399 (Accession NM_022763) is another VGAM2659 host target gene. FLJ23399 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23399, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23399 BINDING SITE, designated SEQ ID:23009, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89567] Another function of VGAM2659 is therefore inhibition of FLJ23399 (Accession NM_022763). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23399. Golgi Phosphoprotein 3 (coat-protein)

(GOLPH3, Accession NM_022130) is another VGAM2659 host target gene. GOLPH3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GOLPH3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GOLPH3 BINDING SITE, designated SEQ ID:22688, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89568] Another function of VGAM2659 is therefore inhibition of Golgi Phosphoprotein 3 (coat-protein) (GOLPH3, Accession NM_022130). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLPH3. KIAA1130 (Accession XM_031104) is another VGAM2659 host target gene. KIAA1130 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1130, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1130 BINDING SITE, designated SEQ ID:31288, to the nucleotide sequence of VGAM2659

RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89569] Another function of VGAM2659 is therefore inhibition of KIAA1130 (Accession XM_031104). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1130. KIAA1287 (Accession XM_085753) is another VGAM2659 host target gene. KIAA1287 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1287, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1287 BINDING SITE, designated SEQ ID:38326, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89570] Another function of VGAM2659 is therefore inhibition of KIAA1287 (Accession XM_085753). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1287. KIAA1434 (Accession XM_045585) is another VGAM2659 host target gene. KIAA1434 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1434, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1434 BINDING SITE, designated SEQ ID:34492, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89571] Another function of VGAM2659 is therefore inhibition of KIAA1434 (Accession XM_045585). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1434. KIAA1493 (Accession XM_034415) is another VGAM2659 host target gene. KIAA1493 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1493, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1493 BINDING SITE, designated SEQ ID:32088, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89572] Another function of VGAM2659 is therefore inhibition of KIAA1493 (Accession XM_034415). Accordingly, utilities

of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1493. MGC11352 (Accession XM_035941) is another VGAM2659 host target gene. MGC11352 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC11352, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11352 BINDING SITE, designated SEQ ID:32358, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89573] Another function of VGAM2659 is therefore inhibition of MGC11352 (Accession XM_035941). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11352. PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335) is another VGAM2659 host target gene. PRPF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of PRPF8 BINDING SITE, designated SEQ ID:30690, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89574] Another function of VGAM2659 is therefore inhibition of PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPF8. Scavenger Receptor Cysteine Rich Domain Containing, Group B (4 domains) (SRCRB4D, Accession NM_080744) is another VGAM2659 host target gene. SRCRB4D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SRCRB4D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRCRB4D BINDING SITE, designated SEQ ID:28029, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89575] Another function of VGAM2659 is therefore inhibition of Scavenger Receptor Cysteine Rich Domain Containing, Group B (4 domains) (SRCRB4D, Accession NM_080744).

Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRCRB4D. LOC112616 (Accession NM_138410) is another VGAM2659 host target gene. LOC112616 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112616, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112616 BINDING SITE, designated SEQ ID:28774, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89576] Another function of VGAM2659 is therefore inhibition of LOC112616 (Accession NM_138410). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112616. LOC135763 (Accession NM_138572) is another VGAM2659 host target gene. LOC135763 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC135763 BINDING SITE, designated SEQ ID:28885, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89577] Another function of VGAM2659 is therefore inhibition of LOC135763 (Accession NM_138572). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135763. LOC150279 (Accession XM_086820) is another VGAM2659 host target gene. LOC150279 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150279, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150279 BINDING SITE, designated SEQ ID:38900, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89578] Another function of VGAM2659 is therefore inhibition of LOC150279 (Accession XM_086820). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150279. LOC151516 (Accession XM_087229) is an-

other VGAM2659 host target gene. LOC151516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151516 BINDING SITE, designated SEQ ID:39129, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89579] Another function of VGAM2659 is therefore inhibition of LOC151516 (Accession XM_087229). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151516. LOC152215 (Accession XM_087407) is another VGAM2659 host target gene. LOC152215 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152215, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152215 BINDING SITE, designated SEQ ID:39225, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89580] Another function of VGAM2659 is therefore inhibition of LOC152215 (Accession XM_087407). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152215. LOC152313 (Accession XM_098190) is another VGAM2659 host target gene. LOC152313 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152313, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152313 BINDING SITE, designated SEQ ID:41475, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89581] Another function of VGAM2659 is therefore inhibition of LOC152313 (Accession XM_098190). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152313. LOC158434 (Accession XM_098939) is another VGAM2659 host target gene. LOC158434 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158434, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158434 BINDING SITE, designated SEQ ID:41990, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89582] Another function of VGAM2659 is therefore inhibition of LOC158434 (Accession XM_098939). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158434. LOC167147 (Accession XM_094310) is another VGAM2659 host target gene. LOC167147 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC167147, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC167147 BINDING SITE, designated SEQ ID:40227, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89583] Another function of VGAM2659 is therefore inhibition of LOC167147 (Accession XM_094310). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC167147. LOC220776 (Accession XM_043388) is another VGAM2659 host target gene. LOC220776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220776 BINDING SITE, designated SEQ ID:33940, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89584] Another function of VGAM2659 is therefore inhibition of LOC220776 (Accession XM_043388). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220776. LOC221002 (Accession XM_166156) is another VGAM2659 host target gene. LOC221002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221002 BINDING SITE, designated SEQ ID:43973, to the nucleotide sequence of VGAM2659 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5370.

[89585] Another function of VGAM2659 is therefore inhibition of LOC221002 (Accession XM_166156). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221002. LOC221935 (Accession XM_166537) is another VGAM2659 host target gene. LOC221935 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221935, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221935 BINDING SITE, designated SEQ ID:44502, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89586] Another function of VGAM2659 is therefore inhibition of LOC221935 (Accession XM_166537). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221935. LOC254228 (Accession XM_171123) is another VGAM2659 host target gene. LOC254228 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254228, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254228 BINDING SITE, designated SEQ ID:45922, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89587] Another function of VGAM2659 is therefore inhibition of LOC254228 (Accession XM_171123). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254228. LOC255645 (Accession XM_172967) is another VGAM2659 host target gene. LOC255645 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255645, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255645 BINDING SITE, designated SEQ ID:46220, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89588] Another function of VGAM2659 is therefore inhibition of LOC255645 (Accession XM_172967). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC255645. LOC51619 (Accession NM_015983) is another VGAM2659 host target gene. LOC51619 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51619, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51619 BINDING SITE, designated SEQ ID:18079, to the nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89589] Another function of VGAM2659 is therefore inhibition of LOC51619 (Accession NM_015983). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51619. LOC92573 (Accession XM_045884) is another VGAM2659 host target gene. LOC92573 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92573, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92573 BINDING SITE, designated SEQ ID:34597, to the

nucleotide sequence of VGAM2659 RNA, herein designated VGAM RNA, also designated SEQ ID:5370.

[89590] Another function of VGAM2659 is therefore inhibition of LOC92573 (Accession XM_045884). Accordingly, utilities of VGAM2659 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92573. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2660 (VGAM2660) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89591] VGAM2660 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2660 was detected is described hereinabove with reference to Figs. 1-8.

[89592] VGAM2660 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Virus A.
VGAM2660 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89593] VGAM2660 gene encodes a VGAM2660 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2660 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2660 precursor RNA is designated SEQ ID:2646, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2646 is located at position 4281 relative to the genome of Potato Virus A.

[89594] VGAM2660 precursor RNA folds onto itself, forming VGAM2660 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89595] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2660 folded precursor RNA into VGAM2660 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2660 RNA is designated SEQ ID:5371, and is provided hereinbelow with reference to the sequence listing part.

[89596] VGAM2660 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2660 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89597] VGAM2660 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2660 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2660 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89598] The complementary binding of VGAM2660 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2660 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2660 host target RNA into VGAM2660 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89599] It is appreciated that VGAM2660 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2660 host target genes. The mRNA of each one of this plurality of VGAM2660 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2660 RNA, herein designated VGAM RNA, and which when bound by VGAM2660 RNA causes inhibition of translation of respective one or more VGAM2660 host target proteins.

[89600] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2660 gene, herein designated VGAM GENE, on one or more VGAM2660 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89601] It is yet further appreciated that a function of VGAM2660 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGAM2660 correlate with, and may be deduced from, the identity of the host target genes which VGAM2660 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89602] Nucleotide sequences of the VGAM2660 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2660 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2660 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2660 are further described hereinbelow with reference to Table 1.

[89603] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2660 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2660 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89604] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2660 gene, herein designated VGAM is inhibition of expression of VGAM2660 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2660 correlate with, and may be deduced from, the identity of the target genes which VGAM2660 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89605] Aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1, Accession NM_000385) is a VGAM2660 host target gene. AQP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AQP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AQP1 BINDING SITE, designated SEQ ID:5959, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89606] A function of VGAM2660 is therefore inhibition of Aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1,

Accession NM_000385). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP1. Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST, Accession NM_001933) is another VGAM2660 host target gene. DLST BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLST BINDING SITE, designated SEQ ID:7644, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89607] Another function of VGAM2660 is therefore inhibition of Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST, Accession NM_001933), a gene which catalyzes the oxidative decarboxylation of alpha-keto acids. Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLST. The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to VGAM656.Deoxyribonuclease I-like 1 (DNASE1L1, Accession NM_006730) is another VGAM2660 host target gene. DNASE1L1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DNASE1L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNASE1L1 BINDING SITE, designated SEQ ID:13569, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89608] Another function of VGAM2660 is therefore inhibition of Deoxyribonuclease I-like 1 (DNASE1L1, Accession NM_006730), a gene which seems to be involved in cell death. Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNASE1L1. The function of DNASE1L1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM885.Homeo Box D4 (HOXD4, Accession NM_014621) is another VGAM2660 host target gene.

HOXD4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HOXD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXD4 BINDING SITE, designated SEQ ID:15980, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89609] Another function of VGAM2660 is therefore inhibition of Homeo Box D4 (HOXD4, Accession NM_014621), a gene which is part of a developmental regulatory system. Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXD4. The function of HOXD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM330.Loss of Heterozygosity, 11, Chromosomal Region 2, Gene A (LOH11CR2A, Accession NM_014622) is another VGAM2660 host target gene. LOH11CR2A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOH11CR2A, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOH11CR2A BINDING SITE, designated SEQ ID:15984, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89610] Another function of VGAM2660 is therefore inhibition of Loss of Heterozygosity, 11, Chromosomal Region 2, Gene A (LOH11CR2A, Accession NM_014622). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOH11CR2A. Chromosome 14 Open Reading Frame 4 (C14orf4, Accession XM_041104) is another VGAM2660 host target gene. C14orf4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C14orf4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C14orf4 BINDING SITE, designated SEQ ID:33445, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89611] Another function of VGAM2660 is therefore inhibition of

Chromosome 14 Open Reading Frame 4 (C14orf4, Accession XM_041104). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf4. FLJ21791 (Accession XM_028958) is another VGAM2660 host target gene. FLJ21791 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21791, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21791 BINDING SITE, designated SEQ ID:30809, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89612] Another function of VGAM2660 is therefore inhibition of FLJ21791 (Accession XM_028958). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21791. KIAA0449 (Accession NM_017596) is another VGAM2660 host target gene. KIAA0449 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0449, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0449 BINDING SITE, designated SEQ ID:19052, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89613] Another function of VGAM2660 is therefore inhibition of KIAA0449 (Accession NM_017596). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0449. TUBB5 (Accession NM_006087) is another VGAM2660 host target gene. TUBB5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUBB5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUBB5 BINDING SITE, designated SEQ ID:12731, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89614] Another function of VGAM2660 is therefore inhibition of TUBB5 (Accession NM_006087). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUBB5.

LOC163782 (Accession XM_089138) is another VGAM2660 host target gene. LOC163782 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC163782, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163782 BINDING SITE, designated SEQ ID:39965, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89615] Another function of VGAM2660 is therefore inhibition of LOC163782 (Accession XM_089138). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163782. LOC221922 (Accession XM_166555) is another VGAM2660 host target gene. LOC221922 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221922, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221922 BINDING SITE, designated SEQ ID:44535, to the nucleotide sequence of VGAM2660 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5371.

[89616] Another function of VGAM2660 is therefore inhibition of LOC221922 (Accession XM_166555). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221922. LOC254848 (Accession XM_173133) is another VGAM2660 host target gene. LOC254848 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254848, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254848 BINDING SITE, designated SEQ ID:46382, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89617] Another function of VGAM2660 is therefore inhibition of LOC254848 (Accession XM_173133). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254848. LOC255452 (Accession XM_174088) is another VGAM2660 host target gene. LOC255452 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255452, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255452 BINDING SITE, designated SEQ ID:46577, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89618] Another function of VGAM2660 is therefore inhibition of LOC255452 (Accession XM_174088). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255452. LOC93496 (Accession XM_051698) is another VGAM2660 host target gene. LOC93496 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93496, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93496 BINDING SITE, designated SEQ ID:35866, to the nucleotide sequence of VGAM2660 RNA, herein designated VGAM RNA, also designated SEQ ID:5371.

[89619] Another function of VGAM2660 is therefore inhibition of LOC93496 (Accession XM_051698). Accordingly, utilities of VGAM2660 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC93496. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2661 (VGAM2661) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89620] VGAM2661 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2661 was detected is described hereinabove with reference to Figs. 1-8.

[89621] VGAM2661 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Virus A. VGAM2661 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89622] VGAM2661 gene encodes a VGAM2661 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2661 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2661 precursor RNA is desig-

nated SEQ ID:2647, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2647 is located at position 2878 relative to the genome of Potato Virus A.

[89623] VGAM2661 precursor RNA folds onto itself, forming VGAM2661 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89624] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2661 folded precursor RNA into VGAM2661 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2661 RNA is designated SEQ ID:5372, and is provided hereinbelow with reference to the sequence

listing part.

[89625] VGAM2661 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2661 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89626] VGAM2661 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2661 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2661 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89627] The complementary binding of VGAM2661 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2661 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2661 host target RNA into VGAM2661 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89628] It is appreciated that VGAM2661 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2661 host target genes. The mRNA of each one of this plurality of VGAM2661 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2661 RNA, herein designated VGAM

RNA, and which when bound by VGAM2661 RNA causes inhibition of translation of respective one or more VGAM2661 host target proteins.

[89629] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2661 gene, herein designated VGAM GENE, on one or more VGAM2661 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89630] It is yet further appreciated that a function of VGAM2661 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2661 include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGAM2661 correlate with, and may be deduced from, the identity of the host target genes which VGAM2661 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89631] Nucleotide sequences of the VGAM2661 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2661 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2661 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2661 are further described hereinbelow with reference to Table 1.

[89632] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2661 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2661 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89633] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2661 gene, herein designated VGAM is

inhibition of expression of VGAM2661 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2661 correlate with, and may be deduced from, the identity of the target genes which VGAM2661 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89634] Coagulation Factor VIII, Procoagulant Component (hemophilia A) (F8, Accession NM_000132) is a VGAM2661 host target gene. F8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by F8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of F8 BINDING SITE, designated SEQ ID:5618, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89635] A function of VGAM2661 is therefore inhibition of Coagulation Factor VIII, Procoagulant Component (hemophilia A) (F8, Accession NM_000132). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F8. DKFZP434L187 (Accession XM_044070) is another

VGAM2661 host target gene. DKFZP434L187 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434L187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L187 BINDING SITE, designated SEQ ID:34120, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89636] Another function of VGAM2661 is therefore inhibition of DKFZP434L187 (Accession XM_044070). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434L187. FLJ13262 (Accession NM_024914) is another VGAM2661 host target gene. FLJ13262 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13262, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13262 BINDING SITE, designated SEQ ID:24431, to the nucleotide sequence of VGAM2661 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5372.

[89637] Another function of VGAM2661 is therefore inhibition of FLJ13262 (Accession NM_024914). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13262. Heterogeneous Nuclear Ribonucleoprotein A3 (HNRPA3, Accession NM_005758) is another VGAM2661 host target gene. HNRPA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HNRPA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPA3 BINDING SITE, designated SEQ ID:12324, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89638] Another function of VGAM2661 is therefore inhibition of Heterogeneous Nuclear Ribonucleoprotein A3 (HNRPA3, Accession NM_005758). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPA3. KIAA1437 (Accession XM_026998) is another VGAM2661 host target gene. KIAA1437 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1437, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1437 BINDING SITE, designated SEQ ID:30383, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89639] Another function of VGAM2661 is therefore inhibition of KIAA1437 (Accession XM_026998). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1437. Proprotein Convertase Subtilisin/kexin Type 7 (PCSK7, Accession NM_004716) is another VGAM2661 host target gene. PCSK7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCSK7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCSK7 BINDING SITE, designated SEQ ID:11074, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89640] Another function of VGAM2661 is therefore inhibition of Proprotein Convertase Subtilisin/kexin Type 7 (PCSK7, Accession NM_004716). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK7. LOC129676 (Accession XM_065341) is another VGAM2661 host target gene. LOC129676 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC129676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129676 BINDING SITE, designated SEQ ID:37283, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89641] Another function of VGAM2661 is therefore inhibition of LOC129676 (Accession XM_065341). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129676. LOC148918 (Accession XM_086361) is another VGAM2661 host target gene. LOC148918 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148918, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148918 BINDING SITE, designated SEQ ID:38613, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89642] Another function of VGAM2661 is therefore inhibition of LOC148918 (Accession XM_086361). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148918. LOC164832 (Accession XM_092184) is another VGAM2661 host target gene. LOC164832 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC164832, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164832 BINDING SITE, designated SEQ ID:40110, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89643] Another function of VGAM2661 is therefore inhibition of LOC164832 (Accession XM_092184). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC164832. LOC220988 (Accession XM_165561) is another VGAM2661 host target gene. LOC220988 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220988 BINDING SITE, designated SEQ ID:43684, to the nucleotide sequence of VGAM2661 RNA, herein designated VGAM RNA, also designated SEQ ID:5372.

[89644] Another function of VGAM2661 is therefore inhibition of LOC220988 (Accession XM_165561). Accordingly, utilities of VGAM2661 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220988. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2662 (VGAM2662) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89645] VGAM2662 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2662 was detected is described hereinabove with reference to Figs. 1-8.

[89646] VGAM2662 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Virus A. VGAM2662 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89647] VGAM2662 gene encodes a VGAM2662 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2662 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2662 precursor RNA is designated SEQ ID:2648, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2648 is located at position 4423 relative to the genome of Potato Virus A.

[89648] VGAM2662 precursor RNA folds onto itself, forming VGAM2662 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89649] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2662 folded precursor RNA into VGAM2662 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2662 RNA is designated SEQ ID:5373, and is provided hereinbelow with reference to the sequence listing part.

[89650] VGAM2662 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2662 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89651] VGAM2662 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2662 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2662 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89652] The complementary binding of VGAM2662 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2662 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2662 host target RNA into VGAM2662 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89653] It is appreciated that VGAM2662 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2662 host target genes. The mRNA of each one of this plurality of VGAM2662 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2662 RNA, herein designated VGAM RNA, and which when bound by VGAM2662 RNA causes inhibition of translation of respective one or more VGAM2662 host target proteins.

[89654] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2662 gene, herein designated VGAM GENE, on one or more VGAM2662 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89655] It is yet further appreciated that a function of VGAM2662 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGAM2662 correlate with, and may be deduced from, the identity of the host target genes which VGAM2662 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89656] Nucleotide sequences of the VGAM2662 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2662 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2662 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2662 are further described hereinbelow with reference to Table 1.

[89657] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2662 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2662 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89658] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2662 gene, herein designated VGAM is inhibition of expression of VGAM2662 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2662 correlate with, and may be deduced from, the identity of the target genes which VGAM2662 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89659] Dihydropyrimidinase-like 3 (DPYSL3, Accession NM_001387) is a VGAM2662 host target gene. DPYSL3 BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by DPYSL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DPYSL3 BINDING SITE, designated SEQ ID:7073, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89660] A function of VGAM2662 is therefore inhibition of Dihydropyrimidinase-like 3 (DPYSL3, Accession NM_001387), a gene which is a member of the dihydropyrimidinase family. Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPYSL3. The function of DPYSL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM24.Fanconi Anemia, Complementation Group C (FANCC, Accession XM_047190) is another VGAM2662 host target gene. FANCC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FANCC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of FANCC BINDING SITE, designated SEQ ID:34905, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89661] Another function of VGAM2662 is therefore inhibition of Fanconi Anemia, Complementation Group C (FANCC, Accession XM_047190). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCC. FLJ13055 (Accession NM_022737) is another VGAM2662 host target gene. FLJ13055 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13055, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13055 BINDING SITE, designated SEQ ID:22943, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89662] Another function of VGAM2662 is therefore inhibition of FLJ13055 (Accession NM_022737). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13055. KIAA0352 (Accession NM_014830) is another VGAM2662 host target gene. KIAA0352 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0352, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0352 BINDING SITE, designated SEQ ID:16823, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89663] Another function of VGAM2662 is therefore inhibition of KIAA0352 (Accession NM_014830). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0352. KIAA1136 (Accession XM_166110) is another VGAM2662 host target gene. KIAA1136 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1136, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1136 BINDING SITE, designated SEQ ID:43884, to the nucleotide sequence of VGAM2662 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5373.

[89664] Another function of VGAM2662 is therefore inhibition of KIAA1136 (Accession XM_166110). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1136. KR18 (Accession NM_033288) is another VGAM2662 host target gene. KR18 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KR18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KR18 BINDING SITE, designated SEQ ID:27116, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89665] Another function of VGAM2662 is therefore inhibition of KR18 (Accession NM_033288). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KR18. MGC16386 (Accession NM_080668) is another VGAM2662 host target gene. MGC16386 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC16386, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16386 BINDING SITE, designated SEQ ID:27958, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89666] Another function of VGAM2662 is therefore inhibition of MGC16386 (Accession NM_080668). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16386. Phosphatidylserine Decarboxylase (PISD, Accession NM_014338) is another VGAM2662 host target gene. PISD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PISD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PISD BINDING SITE, designated SEQ ID:15654, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89667] Another function of VGAM2662 is therefore inhibition of Phosphatidylserine Decarboxylase (PISD, Accession NM_014338). Accordingly, utilities of VGAM2662 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with PISD. TA-PP2C (Accession NM_139283) is another VGAM2662 host target gene. TA-PP2C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TA-PP2C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TA-PP2C BINDING SITE, designated SEQ ID:29281, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89668] Another function of VGAM2662 is therefore inhibition of TA-PP2C (Accession NM_139283). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TA-PP2C. LOC136288 (Accession XM_059832) is another VGAM2662 host target gene. LOC136288 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC136288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC136288 BINDING SITE, designated SEQ ID:37100, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89669] Another function of VGAM2662 is therefore inhibition of LOC136288 (Accession XM_059832). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC136288. LOC203392 (Accession XM_114696) is another VGAM2662 host target gene. LOC203392 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203392, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203392 BINDING SITE, designated SEQ ID:43042, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89670] Another function of VGAM2662 is therefore inhibition of LOC203392 (Accession XM_114696). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203392. LOC64116 (Accession NM_022154) is another VGAM2662 host target gene. LOC64116 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC64116, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC64116 BINDING SITE, designated SEQ ID:22713, to the nucleotide sequence of VGAM2662 RNA, herein designated VGAM RNA, also designated SEQ ID:5373.

[89671] Another function of VGAM2662 is therefore inhibition of LOC64116 (Accession NM_022154). Accordingly, utilities of VGAM2662 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC64116. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2663 (VGAM2663) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89672] VGAM2663 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2663 was detected is described hereinabove with reference to Figs. 1-8.

[89673] VGAM2663 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Virus A. VGAM2663 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89674] VGAM2663 gene encodes a VGAM2663 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2663 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2663 precursor RNA is designated SEQ ID:2649, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2649 is located at position 3193 relative to the genome of Potato Virus A.

[89675] VGAM2663 precursor RNA folds onto itself, forming VGAM2663 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[89676] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2663 folded precursor RNA into VGAM2663 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2663 RNA is designated SEQ ID:5374, and is provided hereinbelow with reference to the sequence listing part.

[89677] VGAM2663 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2663 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89678] VGAM2663 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2663 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2663 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2663 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89679] The complementary binding of VGAM2663 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2663 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2663 host target RNA into VGAM2663 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89680] It is appreciated that VGAM2663 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2663 host target genes. The mRNA of each one of this plurality of VGAM2663 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2663 RNA, herein designated VGAM RNA, and which when bound by VGAM2663 RNA causes inhibition of translation of respective one or more VGAM2663 host target proteins.

[89681] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2663 gene, herein designated VGAM GENE, on one or more VGAM2663 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89682] It is yet further appreciated that a function of VGAM2663 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2663 include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGAM2663 correlate with, and may be deduced from, the identity of the host target genes which VGAM2663 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89683] Nucleotide sequences of the VGAM2663 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2663 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2663 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2663 are further described hereinbelow with reference to Table 1.

[89684] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2663 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2663 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89685] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2663 gene, herein designated VGAM is inhibition of expression of VGAM2663 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2663 correlate with, and may be deduced from, the identity of the target genes which VGAM2663 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89686] RAP1 (Accession NM_018975) is a VGAM2663 host target gene. RAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of RAP1 BINDING SITE, designated SEQ ID:21045, to the nucleotide sequence of VGAM2663 RNA, herein designated VGAM RNA, also designated SEQ ID:5374.

[89687] A function of VGAM2663 is therefore inhibition of RAP1 (Accession NM_018975), a gene which is an ortholog of the yeast telomeric protein Rap1 and may be a general characteristic of sequence-specific transcriptional factors. Accordingly, utilities of VGAM2663 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP1. The function of RAP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2083.FLJ22029 (Accession NM_024949) is another VGAM2663 host target gene. FLJ22029 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22029, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22029 BINDING SITE, designated SEQ ID:24505, to the nucleotide sequence of VGAM2663 RNA, herein designated VGAM RNA, also designated SEQ ID:5374.

[89688] Another function of VGAM2663 is therefore inhibition of FLJ22029 (Accession NM_024949). Accordingly, utilities of VGAM2663 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22029. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2664 (VGAM2664) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89689] VGAM2664 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2664 was detected is described hereinabove with reference to Figs. 1-8.

[89690] VGAM2664 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria Parasitica Mitovirus 1-NB631. VGAM2664 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89691] VGAM2664 gene encodes a VGAM2664 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2664 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2664 precursor RNA is designated SEQ ID:2650, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2650 is located at position 1630 relative to the genome of Cryphonectria Parasitica Mitovirus 1-NB631.

[89692] VGAM2664 precursor RNA folds onto itself, forming VGAM2664 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89693] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2664 folded precursor RNA into VGAM2664 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2664 RNA is designated SEQ ID:5375, and is provided hereinbelow with reference to the sequence listing part.

[89694] VGAM2664 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2664 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89695] VGAM2664 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2664 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2664 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89696] The complementary binding of VGAM2664 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2664 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2664 host target RNA into VGAM2664 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89697] It is appreciated that VGAM2664 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2664 host target genes. The mRNA of each one of this plurality of VGAM2664 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2664 RNA, herein designated VGAM RNA, and which when bound by VGAM2664 RNA causes inhibition of translation of respective one or more VGAM2664 host target proteins.

[89698] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2664 gene, herein designated VGAM GENE, on one or more VGAM2664 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89699] It is yet further appreciated that a function of VGAM2664 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of viral infection by Cryphonectria Parasitica Mitovirus 1-NB631. Specific functions, and accordingly utilities, of VGAM2664 correlate with, and may be deduced from, the identity of the host target genes which VGAM2664 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89700] Nucleotide sequences of the VGAM2664 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2664 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2664 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2664 are further described hereinbelow with reference to Table 1.

[89701] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2664 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2664 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[89702] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2664 gene, herein designated VGAM is inhibition of expression of VGAM2664 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2664 correlate with, and may be deduced from, the identity of the target genes which VGAM2664 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89703] Heparan Sulfate 2-O-sulfotransferase 1 (HS2ST1, Accession NM_012262) is a VGAM2664 host target gene. HS2ST1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HS2ST1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HS2ST1 BINDING SITE, designated SEQ ID:14580, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89704] A function of VGAM2664 is therefore inhibition of Heparan Sulfate 2-O-sulfotransferase 1 (HS2ST1, Accession NM_012262). Accordingly, utilities of VGAM2664 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with HS2ST1. Myotubularin Related Protein 2 (MTMR2, Accession NM_016156) is another VGAM2664 host target gene. MTMR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTMR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTMR2 BINDING SITE, designated SEQ ID:18245, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89705] Another function of VGAM2664 is therefore inhibition of Myotubularin Related Protein 2 (MTMR2, Accession NM_016156). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTMR2. Stress 70 Protein Chaperone, Microsome-associated, 60kDa (STCH, Accession NM_006948) is another VGAM2664 host target gene. STCH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STCH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of STCH BINDING SITE, designated SEQ ID:13833, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89706] Another function of VGAM2664 is therefore inhibition of Stress 70 Protein Chaperone, Microsome-associated, 60kDa (STCH, Accession NM_006948), a gene which has peptide-independent atpase activity. Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STCH. The function of STCH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM550.DKFZP761E2110 (Accession NM_030953) is another VGAM2664 host target gene. DKFZP761E2110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761E2110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761E2110 BINDING SITE, designated SEQ ID:25225, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5375.

[89707] Another function of VGAM2664 is therefore inhibition of DKFZP761E2110 (Accession NM_030953). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761E2110. KIAA0009 (Accession NM_014637) is another VGAM2664 host target gene. KIAA0009 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0009 BINDING SITE, designated SEQ ID:16021, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89708] Another function of VGAM2664 is therefore inhibition of KIAA0009 (Accession NM_014637). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0009. KIAA0795 (Accession NM_025010) is another VGAM2664 host target gene. KIAA0795 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0795, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0795 BINDING SITE, designated SEQ ID:24584, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89709] Another function of VGAM2664 is therefore inhibition of KIAA0795 (Accession NM_025010). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0795. KIAA1348 (Accession XM_043826) is another VGAM2664 host target gene. KIAA1348 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1348, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1348 BINDING SITE, designated SEQ ID:34032, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89710] Another function of VGAM2664 is therefore inhibition of KIAA1348 (Accession XM_043826). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1348. Solute Carrier Family 1 (glutamate transporter), Member 7 (SLC1A7, Accession NM_006671) is another VGAM2664 host target gene. SLC1A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC1A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC1A7 BINDING SITE, designated SEQ ID:13491, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89711] Another function of VGAM2664 is therefore inhibition of Solute Carrier Family 1 (glutamate transporter), Member 7 (SLC1A7, Accession NM_006671). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A7. LOC203197 (Accession XM_114645) is another VGAM2664 host target gene. LOC203197 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203197, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC203197 BINDING SITE, designated SEQ ID:43012, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89712] Another function of VGAM2664 is therefore inhibition of LOC203197 (Accession XM_114645). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203197. LOC221692 (Accession XM_166420) is another VGAM2664 host target gene. LOC221692 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221692, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221692 BINDING SITE, designated SEQ ID:44300, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89713] Another function of VGAM2664 is therefore inhibition of LOC221692 (Accession XM_166420). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221692. LOC257464 (Accession XM_116972) is an-

other VGAM2664 host target gene. LOC257464 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257464 BINDING SITE, designated SEQ ID:43170, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89714] Another function of VGAM2664 is therefore inhibition of LOC257464 (Accession XM_116972). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257464. LOC92719 (Accession XM_046853) is another VGAM2664 host target gene. LOC92719 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92719 BINDING SITE, designated SEQ ID:34846, to the nucleotide sequence of VGAM2664 RNA, herein designated VGAM RNA, also designated SEQ ID:5375.

[89715] Another function of VGAM2664 is therefore inhibition of LOC92719 (Accession XM_046853). Accordingly, utilities of VGAM2664 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92719. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2665 (VGAM2665) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89716] VGAM2665 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2665 was detected is described hereinabove with reference to Figs. 1-8.

[89717] VGAM2665 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria Parasitica Mitovirus 1-NB631. VGAM2665 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89718] VGAM2665 gene encodes a VGAM2665 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2665 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2665 precursor RNA is designated SEQ ID:2651, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2651 is located at position 1362 relative to the genome of Cryphonectria Parasitica Mitovirus 1-NB631.

[89719] VGAM2665 precursor RNA folds onto itself, forming VGAM2665 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89720] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2665 folded precursor RNA into VGAM2665 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2665 RNA is designated SEQ ID:5376, and is provided hereinbelow with reference to the sequence listing part.

[89721] VGAM2665 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2665 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89722] VGAM2665 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2665 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2665 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89723] The complementary binding of VGAM2665 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2665 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2665 host target RNA into VGAM2665 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89724] It is appreciated that VGAM2665 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2665 host target genes. The mRNA of each one of this plurality of VGAM2665 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2665 RNA, herein designated VGAM RNA, and which when bound by VGAM2665 RNA causes inhibition of translation of respective one or more VGAM2665 host target proteins.

[89725] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2665 gene, herein designated VGAM GENE, on one or more VGAM2665 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89726] It is yet further appreciated that a function of VGAM2665 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of viral infection by Cryphonectria Parasitica Mitovirus 1-NB631. Specific functions, and accordingly utilities, of VGAM2665 correlate with, and may be deduced from, the identity of the host target genes which VGAM2665 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89727] Nucleotide sequences of the VGAM2665 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2665 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2665 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2665 are further described hereinbelow with reference to Table 1.

[89728] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2665 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2665 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[89729] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2665 gene, herein designated VGAM is inhibition of expression of VGAM2665 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2665 correlate with, and may be deduced from, the identity of the target genes which VGAM2665 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89730] Agouti Related Protein Homolog (mouse) (AGRP, Accession NM_001138) is a VGAM2665 host target gene. AGRP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AGRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AGRP BINDING SITE, designated SEQ ID:6806, to the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, also designated SEQ ID:5376.

[89731] A function of VGAM2665 is therefore inhibition of Agouti Related Protein Homolog (mouse) (AGRP, Accession NM_001138), a gene which plays a role in weight homeostasis. Accordingly, utilities of VGAM2665 include diag-

nosis, prevention and treatment of diseases and clinical conditions associated with AGRP. The function of AGRP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.Cell Adhesion Molecule with Homology to L1CAM (close homolog of L1) (CHL1, Accession NM_006614) is another VGAM2665 host target gene. CHL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHL1 BINDING SITE, designated SEQ ID:13399, to the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, also designated SEQ ID:5376.

[89732] Another function of VGAM2665 is therefore inhibition of Cell Adhesion Molecule with Homology to L1CAM (close homolog of L1) (CHL1, Accession NM_006614). Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHL1. DKFZp761A132 (Accession NM_032296) is another VGAM2665 host target gene. DKFZp761A132

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761A132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761A132 BINDING SITE, designated SEQ ID:26077, to the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, also designated SEQ ID:5376.

[89733] Another function of VGAM2665 is therefore inhibition of DKFZp761A132 (Accession NM_032296). Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761A132. FLJ10375 (Accession NM_018075) is another VGAM2665 host target gene. FLJ10375 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10375, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10375 BINDING SITE, designated SEQ ID:19838, to the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, also designated SEQ ID:5376.

[89734] Another function of VGAM2665 is therefore inhibition of FLJ10375 (Accession NM_018075). Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10375. FLJ11726 (Accession NM_024971) is another VGAM2665 host target gene. FLJ11726 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11726, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11726 BINDING SITE, designated SEQ ID:24529, to the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, also designated SEQ ID:5376.

[89735] Another function of VGAM2665 is therefore inhibition of FLJ11726 (Accession NM_024971). Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11726. KIAA1956 (Accession XM_085836) is another VGAM2665 host target gene. KIAA1956 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1956, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1956 BINDING SITE, designated SEQ ID:38364, to the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, also designated SEQ ID:5376.

[89736] Another function of VGAM2665 is therefore inhibition of KIAA1956 (Accession XM_085836). Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1956. MGC12217 (Accession NM_032771) is another VGAM2665 host target gene. MGC12217 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC12217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12217 BINDING SITE, designated SEQ ID:26517, to the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, also designated SEQ ID:5376.

[89737] Another function of VGAM2665 is therefore inhibition of MGC12217 (Accession NM_032771). Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC12217. LOC51622 (Accession NM_015622) is another VGAM2665 host target gene. LOC51622 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51622, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51622 BINDING SITE, designated SEQ ID:17885, to the nucleotide sequence of VGAM2665 RNA, herein designated VGAM RNA, also designated SEQ ID:5376.

[89738] Another function of VGAM2665 is therefore inhibition of LOC51622 (Accession NM_015622). Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51622. LOC93082 (Accession NM_138397) is another VGAM2665 host target gene. LOC93082 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93082 BINDING SITE, designated SEQ ID:28767, to the nucleotide sequence of VGAM2665 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5376.

[89739] Another function of VGAM2665 is therefore inhibition of LOC93082 (Accession NM_138397). Accordingly, utilities of VGAM2665 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93082. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2666 (VGAM2666) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89740] VGAM2666 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2666 was detected is described hereinabove with reference to Figs. 1-8.

[89741] VGAM2666 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cryphonectria Parasitica Mitovirus 1-NB631. VGAM2666 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89742] VGAM2666 gene encodes a VGAM2666 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2666 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2666 precursor RNA is designated SEQ ID:2652, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2652 is located at position 680 relative to the genome of Cryphonectria Parasitica Mitovirus 1-NB631.

[89743] VGAM2666 precursor RNA folds onto itself, forming VGAM2666 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89744] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2666 folded precursor RNA into VGAM2666 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2666 RNA is designated SEQ ID:5377, and is provided hereinbelow with reference to the sequence listing part.

[89745] VGAM2666 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2666 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89746] VGAM2666 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2666 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2666 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89747] The complementary binding of VGAM2666 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2666 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2666 host target RNA into VGAM2666 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89748] It is appreciated that VGAM2666 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2666 host target genes. The mRNA of

each one of this plurality of VGAM2666 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2666 RNA, herein designated VGAM RNA, and which when bound by VGAM2666 RNA causes inhibition of translation of respective one or more VGAM2666 host target proteins.

[89749] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2666 gene, herein designated VGAM GENE, on one or more VGAM2666 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[89750] It is yet further appreciated that a function of VGAM2666 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of viral infection by Cryphonectria Parasitica Mitovirus 1-NB631. Specific functions, and accordingly utilities, of VGAM2666 correlate with, and may be deduced from, the identity of the host target genes which VGAM2666 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89751] Nucleotide sequences of the VGAM2666 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2666 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2666 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2666 are further described hereinbelow with reference to Table 1.

[89752] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2666 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2666 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89753] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2666 gene, herein designated VGAM is inhibition of expression of VGAM2666 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2666 correlate with, and may be deduced from, the identity of the target genes which VGAM2666 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89754] APG5 Autophagy 5-like (S. cerevisiae) (APG5L, Accession NM_004849) is a VGAM2666 host target gene. APG5L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APG5L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APG5L BINDING SITE, designated SEQ ID:11262, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89755] A function of VGAM2666 is therefore inhibition of APG5 Autophagy 5-like (S. cerevisiae) (APG5L, Accession NM_004849), a gene which conjugates to apg12 and as-

sociates with isolation membrane to form cup-shaped isolation membrane and autophagosome. Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APG5L. The function of APG5L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM492.Complement Component (3b/4b) Receptor 1, Including Knops Blood Group System (CR1, Accession NM_000573) is another VGAM2666 host target gene. CR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:6174, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89756] Another function of VGAM2666 is therefore inhibition of Complement Component (3b/4b) Receptor 1, Including Knops Blood Group System (CR1, Accession NM_000573). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with CR1. Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071) is another VGAM2666 host target gene. NCOA6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NCOA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE, designated SEQ ID:15290, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89757] Another function of VGAM2666 is therefore inhibition of Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071), a gene which activates gene transcription through ligand-dependent association with coactivators. Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6. The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.Peroxiredoxin 3 (PRDX3, Accession XM_055573) is another VGAM2666 host target gene. PRDX3 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRDX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDX3 BINDING SITE, designated SEQ ID:36303, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89758] Another function of VGAM2666 is therefore inhibition of Peroxiredoxin 3 (PRDX3, Accession XM_055573), a gene which functions as an antioxidant protein and is required to maintain normal mitochondrial function. Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDX3. The function of PRDX3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.Recombination Activating Gene 1 (RAG1, Accession NM_000448) is another VGAM2666 host target gene. RAG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAG1 BINDING SITE, designated SEQ ID:6036, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89759] Another function of VGAM2666 is therefore inhibition of Recombination Activating Gene 1 (RAG1, Accession NM_000448). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAG1. Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695) is another VGAM2666 host target gene. VANGL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VANGL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VANGL2 BINDING SITE, designated SEQ ID:35482, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89760] Another function of VGAM2666 is therefore inhibition of Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695), a gene which may take part in defining the

lateral boundary of floorplate differentiation. Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VANGL2. The function of VANGL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.CAP350 (Accession NM_014810) is another VGAM2666 host target gene. CAP350 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAP350, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAP350 BINDING SITE, designated SEQ ID:16769, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89761] Another function of VGAM2666 is therefore inhibition of CAP350 (Accession NM_014810). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAP350. DKFZP434I092 (Accession XM_042042) is another VGAM2666 host target gene. DKFZP434I092 BIND-

ING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434I092 BINDING SITE, designated SEQ ID:33671, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89762] Another function of VGAM2666 is therefore inhibition of DKFZP434I092 (Accession XM_042042). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I092. FLJ10874 (Accession NM_018252) is another VGAM2666 host target gene. FLJ10874 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10874, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10874 BINDING SITE, designated SEQ ID:20219, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89763] Another function of VGAM2666 is therefore inhibition of FLJ10874 (Accession NM_018252). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10874. FLJ11383 (Accession NM_024938) is another VGAM2666 host target gene. FLJ11383 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11383, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11383 BINDING SITE, designated SEQ ID:24477, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89764] Another function of VGAM2666 is therefore inhibition of FLJ11383 (Accession NM_024938). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11383. KIAA0459 (Accession XM_027862) is another VGAM2666 host target gene. KIAA0459 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:30576, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89765] Another function of VGAM2666 is therefore inhibition of KIAA0459 (Accession XM_027862). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459. KIAA0599 (Accession XM_085127) is another VGAM2666 host target gene. KIAA0599 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0599, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0599 BINDING SITE, designated SEQ ID:37851, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89766] Another function of VGAM2666 is therefore inhibition of KIAA0599 (Accession XM_085127). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0599. KIAA0669 (Accession NM_014779) is another VGAM2666 host target gene. KIAA0669 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0669, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0669 BINDING SITE, designated SEQ ID:16627, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89767] Another function of VGAM2666 is therefore inhibition of KIAA0669 (Accession NM_014779). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0669. KIAA1317 (Accession XM_098368) is another VGAM2666 host target gene. KIAA1317 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1317 BINDING SITE, designated SEQ ID:41621, to the nucleotide sequence of VGAM2666 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5377.

[89768] Another function of VGAM2666 is therefore inhibition of KIAA1317 (Accession XM_098368). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1317. LOC158722 (Accession XM_088653) is another VGAM2666 host target gene. LOC158722 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158722, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158722 BINDING SITE, designated SEQ ID:39888, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89769] Another function of VGAM2666 is therefore inhibition of LOC158722 (Accession XM_088653). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158722. LOC169026 (Accession XM_095471) is another VGAM2666 host target gene. LOC169026 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169026, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169026 BINDING SITE, designated SEQ ID:40263, to the nucleotide sequence of VGAM2666 RNA, herein designated VGAM RNA, also designated SEQ ID:5377.

[89770] Another function of VGAM2666 is therefore inhibition of LOC169026 (Accession XM_095471). Accordingly, utilities of VGAM2666 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169026. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2667 (VGAM2667) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89771] VGAM2667 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2667 was detected is described hereinabove with reference to Figs. 1-8.

[89772] VGAM2667 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean Common Mosaic

Necrosis Virus. VGAM2667 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89773] VGAM2667 gene encodes a VGAM2667 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2667 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2667 precursor RNA is designated SEQ ID:2653, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2653 is located at position 9077 relative to the genome of Bean Common Mosaic Necrosis Virus.

[89774] VGAM2667 precursor RNA folds onto itself, forming VGAM2667 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89775] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2667 folded precursor RNA into VGAM2667 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2667 RNA is designated SEQ ID:5378, and is provided hereinbelow with reference to the sequence listing part.

[89776] VGAM2667 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2667 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89777] VGAM2667 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2667 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2667 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89778] The complementary binding of VGAM2667 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2667 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2667 host target RNA into VGAM2667 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89779] It is appreciated that VGAM2667 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2667 host target genes. The mRNA of each one of this plurality of VGAM2667 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2667 RNA, herein designated VGAM RNA, and which when bound by VGAM2667 RNA causes inhibition of translation of respective one or more VGAM2667 host target proteins.

[89780] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2667 gene, herein designated VGAM GENE, on one or more VGAM2667 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89781] It is yet further appreciated that a function of VGAM2667 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of viral infection by Bean Common Mosaic Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2667 correlate with, and may be deduced from, the identity of the host target genes which VGAM2667 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89782] Nucleotide sequences of the VGAM2667 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2667 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2667 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2667 are further described hereinbelow with reference to Table 1.

[89783] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2667 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2667 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89784] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2667 gene, herein designated VGAM is inhibition of expression of VGAM2667 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2667 correlate with, and may be deduced from, the identity of the target genes which VGAM2667 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89785] CASP8 Associated Protein 2 (CASP8AP2, Accession NM_012115) is a VGAM2667 host target gene. CASP8AP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CASP8AP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASP8AP2 BINDING SITE, designated SEQ

ID:14430, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89786] A function of VGAM2667 is therefore inhibition of CASP8 Associated Protein 2 (CASP8AP2, Accession NM_012115), a gene which interacts with and activates caspase-8 in Fas-mediated apoptosis. Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP8AP2. The function of CASP8AP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM581.Leukemia Inhibitory Factor Receptor (LIFR, Accession NM_002310) is another VGAM2667 host target gene. LIFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIFR BINDING SITE, designated SEQ ID:8105, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89787] Another function of VGAM2667 is therefore inhibition of Leukemia Inhibitory Factor Receptor (LIFR, Accession NM_002310). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIFR. NDRG Family Member 3 (NDRG3, Accession NM_032013) is another VGAM2667 host target gene. NDRG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDRG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDRG3 BINDING SITE, designated SEQ ID:25721, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89788] Another function of VGAM2667 is therefore inhibition of NDRG Family Member 3 (NDRG3, Accession NM_032013). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG3. Polycystic Kidney Disease 2 (autosomal dominant) (PKD2, Accession XM_011124) is another VGAM2667 host target gene. PKD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by PKD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PKD2 BINDING SITE, designated SEQ ID:30176, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89789] Another function of VGAM2667 is therefore inhibition of Polycystic Kidney Disease 2 (autosomal dominant) (PKD2, Accession XM_011124). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKD2. C16orf5 (Accession NM_013399) is another VGAM2667 host target gene. C16orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C16orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C16orf5 BINDING SITE, designated SEQ ID:15055, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89790] Another function of VGAM2667 is therefore inhibition of

C16orf5 (Accession NM_013399). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C16orf5. FLJ22635 (Accession NM_025092) is another VGAM2667 host target gene. FLJ22635 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22635, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22635 BINDING SITE, designated SEQ ID:24718, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89791] Another function of VGAM2667 is therefore inhibition of FLJ22635 (Accession NM_025092). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22635. KIAA0391 (Accession NM_014672) is another VGAM2667 host target gene. KIAA0391 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0391, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0391 BINDING SITE, designated SEQ ID:16135, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89792] Another function of VGAM2667 is therefore inhibition of KIAA0391 (Accession NM_014672). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0391. KIAA1340 (Accession XM_044836) is another VGAM2667 host target gene. KIAA1340 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1340, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1340 BINDING SITE, designated SEQ ID:34297, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89793] Another function of VGAM2667 is therefore inhibition of KIAA1340 (Accession XM_044836). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1340. KIAA1576 (Accession XM_038186) is another

VGAM2667 host target gene. KIAA1576 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1576 BINDING SITE, designated SEQ ID:32777, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89794] Another function of VGAM2667 is therefore inhibition of KIAA1576 (Accession XM_038186). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1576. MGC13033 (Accession NM_031447) is another VGAM2667 host target gene. MGC13033 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC13033, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13033 BINDING SITE, designated SEQ ID:25461, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89795] Another function of VGAM2667 is therefore inhibition of MGC13033 (Accession NM_031447). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13033. Protein Kinase C and Casein Kinase Substrate In Neurons 2 (PACSIN2, Accession NM_007229) is another VGAM2667 host target gene. PACSIN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PACSIN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PACSIN2 BINDING SITE, designated SEQ ID:14099, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89796] Another function of VGAM2667 is therefore inhibition of Protein Kinase C and Casein Kinase Substrate In Neurons 2 (PACSIN2, Accession NM_007229). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PACSIN2. PRO2015 (Accession NM_018512) is another VGAM2667 host target gene. PRO2015 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by PRO2015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2015 BINDING SITE, designated SEQ ID:20583, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89797] Another function of VGAM2667 is therefore inhibition of PRO2015 (Accession NM_018512). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2015. Rpo1-2 (Accession NM_019014) is another VGAM2667 host target gene. Rpo1-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Rpo1-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rpo1-2 BINDING SITE, designated SEQ ID:21107, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89798] Another function of VGAM2667 is therefore inhibition of Rpo1-2 (Accession NM_019014). Accordingly, utilities of

VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rpo1-2. STI2 (Accession XM_114335) is another VGAM2667 host target gene. STI2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STI2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STI2 BINDING SITE, designated SEQ ID:42878, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89799] Another function of VGAM2667 is therefore inhibition of STI2 (Accession XM_114335). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STI2. LOC140214 (Accession XM_071283) is another VGAM2667 host target gene. LOC140214 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC140214, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC140214 BINDING SITE, designated SEQ ID:37399, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89800] Another function of VGAM2667 is therefore inhibition of LOC140214 (Accession XM_071283). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC140214. LOC142927 (Accession XM_084380) is another VGAM2667 host target gene. LOC142927 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142927, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142927 BINDING SITE, designated SEQ ID:37566, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89801] Another function of VGAM2667 is therefore inhibition of LOC142927 (Accession XM_084380). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142927. LOC150311 (Accession XM_086858) is another VGAM2667 host target gene. LOC150311 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150311, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150311 BINDING SITE, designated SEQ ID:38928, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89802] Another function of VGAM2667 is therefore inhibition of LOC150311 (Accession XM_086858). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150311. LOC158267 (Accession XM_088528) is another VGAM2667 host target gene. LOC158267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158267 BINDING SITE, designated SEQ ID:39791, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89803] Another function of VGAM2667 is therefore inhibition of

LOC158267 (Accession XM_088528). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158267. LOC219445 (Accession XM_166212) is another VGAM2667 host target gene. LOC219445 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219445 BINDING SITE, designated SEQ ID:44010, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89804] Another function of VGAM2667 is therefore inhibition of LOC219445 (Accession XM_166212). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219445. LOC220514 (Accession XM_017498) is another VGAM2667 host target gene. LOC220514 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC220514 BINDING SITE, designated SEQ ID:30323, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89805] Another function of VGAM2667 is therefore inhibition of LOC220514 (Accession XM_017498). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220514. LOC90841 (Accession XM_034427) is another VGAM2667 host target gene. LOC90841 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90841 BINDING SITE, designated SEQ ID:32110, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89806] Another function of VGAM2667 is therefore inhibition of LOC90841 (Accession XM_034427). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90841. LOC93259 (Accession XM_050105) is another

VGAM2667 host target gene. LOC93259 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93259 BINDING SITE, designated SEQ ID:35555, to the nucleotide sequence of VGAM2667 RNA, herein designated VGAM RNA, also designated SEQ ID:5378.

[89807] Another function of VGAM2667 is therefore inhibition of LOC93259 (Accession XM_050105). Accordingly, utilities of VGAM2667 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93259. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2668 (VGAM2668) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89808] VGAM2668 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2668 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[89809] VGAM2668 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean Common Mosaic Necrosis Virus. VGAM2668 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89810] VGAM2668 gene encodes a VGAM2668 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2668 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2668 precursor RNA is designated SEQ ID:2654, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2654 is located at position 5617 relative to the genome of Bean Common Mosaic Necrosis Virus.

[89811] VGAM2668 precursor RNA folds onto itself, forming VGAM2668 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89812] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2668 folded precursor RNA into VGAM2668 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2668 RNA is designated SEQ ID:5379, and is provided hereinbelow with reference to the sequence listing part.

[89813] VGAM2668 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2668 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89814] VGAM2668 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2668 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2668 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2668 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89815] The complementary binding of VGAM2668 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2668 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2668 host target RNA into VGAM2668 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89816] It is appreciated that VGAM2668 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2668 host target genes. The mRNA of each one of this plurality of VGAM2668 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2668 RNA, herein designated VGAM RNA, and which when bound by VGAM2668 RNA causes inhibition of translation of respective one or more VGAM2668 host target proteins.

[89817] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2668 gene, herein designated VGAM GENE, on one or more VGAM2668 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89818] It is yet further appreciated that a function of VGAM2668 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2668 include diagnosis, prevention and treatment of viral infection by Bean Common Mosaic Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2668 correlate with, and may be deduced from, the identity of the host target genes which VGAM2668 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89819] Nucleotide sequences of the VGAM2668 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2668 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2668 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2668 are further described hereinbelow with reference to Table 1.

[89820] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2668 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2668 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89821] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2668 gene, herein designated VGAM is inhibition of expression of VGAM2668 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2668 correlate with, and may be deduced from, the identity of the target genes which VGAM2668 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89822] ZF (Accession NM_021212) is a VGAM2668 host target gene. ZF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of ZF BINDING SITE, designated SEQ ID:22192, to the nucleotide sequence of VGAM2668 RNA, herein designated VGAM RNA, also designated SEQ ID:5379.

[89823] A function of VGAM2668 is therefore inhibition of ZF (Accession NM_021212). Accordingly, utilities of VGAM2668 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZF. LOC114984 (Accession XM_054962) is another VGAM2668 host target gene. LOC114984 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC114984, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC114984 BINDING SITE, designated SEQ ID:36219, to the nucleotide sequence of VGAM2668 RNA, herein designated VGAM RNA, also designated SEQ ID:5379.

[89824] Another function of VGAM2668 is therefore inhibition of LOC114984 (Accession XM_054962). Accordingly, utilities of VGAM2668 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC114984. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2669 (VGAM2669) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89825] VGAM2669 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2669 was detected is described hereinabove with reference to Figs. 1-8.

[89826] VGAM2669 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean Common Mosaic Necrosis Virus. VGAM2669 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89827] VGAM2669 gene encodes a VGAM2669 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2669 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2669 precursor RNA is designated SEQ ID:2655, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2655 is located at position 1919 relative to the genome of Bean Common Mosaic Necrosis Virus.

[89828] VGAM2669 precursor RNA folds onto itself, forming VGAM2669 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89829] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2669 folded precursor RNA into VGAM2669 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2669 RNA is designated SEQ ID:5380, and is provided hereinbelow with reference to the sequence listing part.

[89830] VGAM2669 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2669 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2669 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89831] VGAM2669 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2669 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2669 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2669 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2669 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89832] The complementary binding of VGAM2669 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2669 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2669 host target RNA into VGAM2669 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89833] It is appreciated that VGAM2669 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2669 host target genes. The mRNA of each one of this plurality of VGAM2669 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2669 RNA, herein designated VGAM RNA, and which when bound by VGAM2669 RNA causes inhibition of translation of respective one or more

VGAM2669 host target proteins.

[89834] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2669 gene, herein designated VGAM GENE, on one or more VGAM2669 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89835] It is yet further appreciated that a function of VGAM2669 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of viral infection by Bean Common Mosaic

Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2669 correlate with, and may be deduced from, the identity of the host target genes which VGAM2669 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89836] Nucleotide sequences of the VGAM2669 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2669 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2669 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2669 are further described hereinbelow with reference to Table 1.

[89837] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2669 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2669 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89838] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2669 gene, herein designated VGAM is inhibition of expression of VGAM2669 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2669 correlate with, and may be deduced from, the identity of the target genes which VGAM2669 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89839] BRCA1 Associated Protein-1 (ubiquitin carboxy-terminal hydrolase) (BAP1, Accession NM_004656) is a VGAM2669 host target gene. BAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAP1 BINDING SITE, designated SEQ ID:11022, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89840] A function of VGAM2669 is therefore inhibition of BRCA1 Associated Protein-1 (ubiquitin carboxy-terminal hydrolase) (BAP1, Accession NM_004656). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAP1. D12S2489E (Accession NM_007360) is another VGAM2669 host target gene. D12S2489E BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by D12S2489E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of D12S2489E BINDING SITE, designated SEQ ID:14290, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89841] Another function of VGAM2669 is therefore inhibition of D12S2489E (Accession NM_007360), a gene which interacts in the inhibition and activation of NK cells. Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D12S2489E. The function of D12S2489E and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM156.Dystrobrevin, Alpha (DTNA, Accession NM_032978) is another VGAM2669 host target gene. DTNA BINDING SITE1 through DTNA BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DTNA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

DTNA BINDING SITE1 through DTNA BINDING SITE4, designated SEQ ID:26837, SEQ ID:26842, SEQ ID:26847 and SEQ ID:7079 respectively, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89842] Another function of VGAM2669 is therefore inhibition of Dystrobrevin, Alpha (DTNA, Accession NM_032978), a gene which may be involved in the formation and stability of synapses. Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DTNA. The function of DTNA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1021.Forkhead Box F1 (FOXF1, Accession NM_001451) is another VGAM2669 host target gene. FOXF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FOXF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXF1 BINDING SITE, designated SEQ ID:7185, to the nucleotide sequence of VGAM2669 RNA, herein

designated VGAM RNA, also designated SEQ ID:5380.

[89843] Another function of VGAM2669 is therefore inhibition of Forkhead Box F1 (FOXF1, Accession NM_001451), a gene which is a probable transcription activator for a number of lung- specific genes. Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXF1. The function of FOXF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM292.Hermansky-Pudlak Syndrome 1 (HPS1, Accession NM_000195) is another VGAM2669 host target gene. HPS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HPS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HPS1 BINDING SITE, designated SEQ ID:5692, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89844] Another function of VGAM2669 is therefore inhibition of Hermansky-Pudlak Syndrome 1 (HPS1, Accession NM_000195). Accordingly, utilities of VGAM2669 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with HPS1. Protein Kinase, CGMP-dependent, Type II (PRKG2, Accession NM_006259) is another VGAM2669 host target gene. PRKG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKG2 BINDING SITE, designated SEQ ID:12939, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89845] Another function of VGAM2669 is therefore inhibition of Protein Kinase, CGMP-dependent, Type II (PRKG2, Accession NM_006259), a gene which regulate a great variety of functions, including smooth muscle relaxation, neuronal excitability, and epithelial electrolyte transport. Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKG2. The function of PRKG2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM16.Zinc Finger Protein 216

(ZNF216, Accession NM_006007) is another VGAM2669 host target gene. ZNF216 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF216, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF216 BINDING SITE, designated SEQ ID:12620, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89846] Another function of VGAM2669 is therefore inhibition of Zinc Finger Protein 216 (ZNF216, Accession NM_006007). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF216. ATP-binding Cassette, Subfamily A (ABC1), Member 10 (ABCA10, Accession NM_080282) is another VGAM2669 host target gene. ABCA10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ABCA10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCA10 BINDING SITE, designated SEQ

ID:27823, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89847] Another function of VGAM2669 is therefore inhibition of ATP-binding Cassette, Sub-family A (ABC1), Member 10 (ABCA10, Accession NM_080282). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA10. FLJ12425 (Accession XM_098290) is another VGAM2669 host target gene. FLJ12425 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12425, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12425 BINDING SITE, designated SEQ ID:41561, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89848] Another function of VGAM2669 is therefore inhibition of FLJ12425 (Accession XM_098290). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12425. FLJ12484 (Accession NM_022767) is another

VGAM2669 host target gene. FLJ12484 BINDING SITE1 and FLJ12484 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ12484, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12484 BINDING SITE1 and FLJ12484 BINDING SITE2, designated SEQ ID:23015 and SEQ ID:34513 respectively, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89849] Another function of VGAM2669 is therefore inhibition of FLJ12484 (Accession NM_022767). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12484. FLJ22195 (Accession NM_022758) is another VGAM2669 host target gene. FLJ22195 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22195 BINDING SITE, designated SEQ ID:22996, to the nucleotide

sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89850] Another function of VGAM2669 is therefore inhibition of FLJ22195 (Accession NM_022758). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22195. KIAA0472 (Accession XM_050147) is another VGAM2669 host target gene. KIAA0472 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0472, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0472 BINDING SITE, designated SEQ ID:35573, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89851] Another function of VGAM2669 is therefore inhibition of KIAA0472 (Accession XM_050147). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0472. KIAA0794 (Accession XM_087353) is another VGAM2669 host target gene. KIAA0794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0794 BINDING SITE, designated SEQ ID:39176, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89852] Another function of VGAM2669 is therefore inhibition of KIAA0794 (Accession XM_087353). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0794. p21(CDKN1A)-activated Kinase 6 (PAK6, Accession NM_020168) is another VGAM2669 host target gene. PAK6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PAK6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAK6 BINDING SITE, designated SEQ ID:21387, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89853] Another function of VGAM2669 is therefore inhibition of p21(CDKN1A)-activated Kinase 6 (PAK6, Accession

NM_020168). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAK6. Retinoic Acid Induced 17 (RAI17, Accession XM_166091) is another VGAM2669 host target gene. RAI17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAI17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:43856, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89854] Another function of VGAM2669 is therefore inhibition of Retinoic Acid Induced 17 (RAI17, Accession XM_166091). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17. RHO6 (Accession NM_014470) is another VGAM2669 host target gene. RHO6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RHO6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of RHO6 BINDING SITE, designated SEQ ID:15819, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89855] Another function of VGAM2669 is therefore inhibition of RHO6 (Accession NM_014470). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHO6. LOC155006 (Accession XM_088117) is another VGAM2669 host target gene. LOC155006 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155006, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155006 BINDING SITE, designated SEQ ID:39522, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89856] Another function of VGAM2669 is therefore inhibition of LOC155006 (Accession XM_088117). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155006. LOC199926 (Accession XM_117157) is an-

other VGAM2669 host target gene. LOC199926 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199926, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199926 BINDING SITE, designated SEQ ID:43258, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89857] Another function of VGAM2669 is therefore inhibition of LOC199926 (Accession XM_117157). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199926. LOC202316 (Accession XM_117380) is another VGAM2669 host target gene. LOC202316 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202316, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202316 BINDING SITE, designated SEQ ID:43422, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89858] Another function of VGAM2669 is therefore inhibition of LOC202316 (Accession XM_117380). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202316. LOC219899 (Accession XM_166173) is another VGAM2669 host target gene. LOC219899 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219899, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219899 BINDING SITE, designated SEQ ID:43992, to the nucleotide sequence of VGAM2669 RNA, herein designated VGAM RNA, also designated SEQ ID:5380.

[89859] Another function of VGAM2669 is therefore inhibition of LOC219899 (Accession XM_166173). Accordingly, utilities of VGAM2669 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219899. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2670 (VGAM2670) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[89860] VGAM2670 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2670 was detected is described hereinabove with reference to Figs. 1-8.

[89861] VGAM2670 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bean Common Mosaic Necrosis Virus. VGAM2670 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89862] VGAM2670 gene encodes a VGAM2670 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2670 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2670 precursor RNA is designated SEQ ID:2656, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2656 is located at position 5302 relative to the genome of Bean Common Mosaic Necrosis Virus.

[89863] VGAM2670 precursor RNA folds onto itself, forming VGAM2670 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89864] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2670 folded precursor RNA into VGAM2670 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2670 RNA is designated SEQ ID:5381, and is provided hereinbelow with reference to the sequence listing part.

[89865] VGAM2670 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2670 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89866] VGAM2670 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2670 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2670 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89867] The complementary binding of VGAM2670 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2670 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2670 host target RNA into VGAM2670 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89868] It is appreciated that VGAM2670 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2670 host target genes. The mRNA of each one of this plurality of VGAM2670 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2670 RNA, herein designated VGAM RNA, and which when bound by VGAM2670 RNA causes inhibition of translation of respective one or more VGAM2670 host target proteins.

[89869] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2670 gene, herein designated VGAM GENE, on one or more VGAM2670 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89870] It is yet further appreciated that a function of VGAM2670 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2670 include diagnosis, prevention and treatment of viral infection by Bean Common Mosaic Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2670 correlate with, and may be deduced from, the identity of the host target genes which VGAM2670 binds and inhibits, and the function of these

host target genes, as elaborated hereinbelow.

[89871] Nucleotide sequences of the VGAM2670 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2670 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2670 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2670 are further described hereinbelow with reference to Table 1.

[89872] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2670 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2670 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89873] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2670 gene, herein designated VGAM is inhibition of expression of VGAM2670 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2670 correlate with, and may be deduced from, the identity of the target genes which VGAM2670 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89874] ATP Synthase, H+ Transporting, Mitochondrial F1 Complex, Beta Polypeptide (ATP5B, Accession XM_006710) is a VGAM2670 host target gene. ATP5B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ATP5B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP5B BINDING SITE, designated SEQ ID:30005, to the nucleotide sequence of VGAM2670 RNA, herein designated VGAM RNA, also designated SEQ ID:5381.

[89875] A function of VGAM2670 is therefore inhibition of ATP Synthase, H+ Transporting, Mitochondrial F1 Complex, Beta Polypeptide (ATP5B, Accession XM_006710). Accordingly, utilities of VGAM2670 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP5B. ISL1 Transcription Factor, LIM/homeodomain, (islet-1) (ISL1, Accession NM_002202) is another VGAM2670 host target gene. ISL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ISL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ISL1 BINDING SITE, designated SEQ ID:7959, to the nucleotide sequence of VGAM2670 RNA, herein designated VGAM RNA, also designated SEQ ID:5381.

[89876] Another function of VGAM2670 is therefore inhibition of ISL1 Transcription Factor, LIM/homeodomain, (islet-1) (ISL1, Accession NM_002202), a gene which binds to one of the cis-acting domain of the insulin gene enhancer. Accordingly, utilities of VGAM2670 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ISL1. The function of ISL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM464.TRIM (Accession NM_016388) is another VGAM2670 host target gene. TRIM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM BINDING SITE, designated SEQ ID:18529, to the nucleotide sequence of VGAM2670 RNA, herein designated VGAM RNA, also designated SEQ ID:5381.

[89877] Another function of VGAM2670 is therefore inhibition of TRIM (Accession NM_016388), a gene which plays a role in recruiting signaling proteins to the plasma membrane upon T-cell receptor (TCR) complex activation in T cells. Accordingly, utilities of VGAM2670 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM. The function of TRIM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM227.Rho Guanine Nucleotide Exchange Factor (GEF) 15 (ARHGEF15, Accession NM_014958) is another VGAM2670 host target gene. ARHGEF15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGEF15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF15 BINDING SITE, designated SEQ ID:17317, to the nucleotide sequence of VGAM2670 RNA, herein designated VGAM RNA, also designated SEQ ID:5381.

[89878] Another function of VGAM2670 is therefore inhibition of Rho Guanine Nucleotide Exchange Factor (GEF) 15

(ARHGEF15, Accession NM_014958). Accordingly, utilities of VGAM2670 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF15. KIAA0326 (Accession XM_034819) is another VGAM2670 host target gene. KIAA0326 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0326, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0326 BINDING SITE, designated SEQ ID:32158, to the nucleotide sequence of VGAM2670 RNA, herein designated VGAM RNA, also designated SEQ ID:5381.

[89879] Another function of VGAM2670 is therefore inhibition of KIAA0326 (Accession XM_034819). Accordingly, utilities of VGAM2670 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0326. KIAA0416 (Accession NM_015564) is another VGAM2670 host target gene. KIAA0416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0416 BINDING SITE, designated SEQ ID:17833, to the nucleotide sequence of VGAM2670 RNA, herein designated VGAM RNA, also designated SEQ ID:5381.

[89880] Another function of VGAM2670 is therefore inhibition of KIAA0416 (Accession NM_015564). Accordingly, utilities of VGAM2670 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0416. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2671 (VGAM2671) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89881] VGAM2671 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2671 was detected is described hereinabove with reference to Figs. 1-8.

[89882] VGAM2671 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Mitovirus 3a. VGAM2671 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[89883] VGAM2671 gene encodes a VGAM2671 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2671 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2671 precursor RNA is designated SEQ ID:2657, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2657 is located at position 673 relative to the genome of Ophiostoma Mitovirus 3a.

[89884] VGAM2671 precursor RNA folds onto itself, forming VGAM2671 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89885] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2671 folded precursor RNA into VGAM2671 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2671 RNA is designated SEQ ID:5382, and is provided hereinbelow with reference to the sequence listing part.

[89886] VGAM2671 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2671 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89887] VGAM2671 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2671 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2671 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89888] The complementary binding of VGAM2671 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2671 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2671 host target RNA into VGAM2671 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89889] It is appreciated that VGAM2671 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2671 host target genes. The mRNA of each one of this plurality of VGAM2671 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2671 RNA, herein designated VGAM RNA, and which when bound by VGAM2671 RNA causes inhibition of translation of respective one or more VGAM2671 host target proteins.

[89890] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2671 gene, herein designated VGAM GENE, on one or more VGAM2671 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89891] It is yet further appreciated that a function of VGAM2671 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2671 include diagnosis, prevention and treatment of viral infection by Ophiostoma Mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2671 correlate with, and may be deduced from, the identity of the host target genes which VGAM2671 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89892] Nucleotide sequences of the VGAM2671 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2671 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2671 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2671 are further described hereinbelow with reference to Table 1.

[89893] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2671 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2671 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89894] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2671 gene, herein designated VGAM is inhibition of expression of VGAM2671 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2671 correlate with, and may be deduced from, the identity of the target genes which VGAM2671 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89895] MGC15705 (Accession NM_032757) is a VGAM2671 host target gene. MGC15705 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC15705, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15705 BINDING SITE, designated SEQ ID:26499, to the nucleotide sequence of VGAM2671 RNA, herein designated VGAM RNA, also designated SEQ ID:5382.

[89896] A function of VGAM2671 is therefore inhibition of MGC15705 (Accession NM_032757). Accordingly, utilities of VGAM2671 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15705. LOC153561 (Accession XM_087708) is another VGAM2671 host target gene. LOC153561 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153561, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153561 BINDING SITE, designated SEQ ID:39401, to the nucleotide sequence of VGAM2671 RNA, herein designated VGAM RNA, also designated SEQ ID:5382.

[89897] Another function of VGAM2671 is therefore inhibition of LOC153561 (Accession XM_087708). Accordingly, utilities of VGAM2671 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153561. LOC223073 (Accession XM_170293) is another VGAM2671 host target gene. LOC223073 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC223073, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC223073 BINDING SITE, designated SEQ ID:45315, to the nucleotide sequence of VGAM2671 RNA, herein designated VGAM RNA, also designated SEQ ID:5382.

[89898] Another function of VGAM2671 is therefore inhibition of LOC223073 (Accession XM_170293). Accordingly, utilities of VGAM2671 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC223073. LOC255231 (Accession XM_170908) is another VGAM2671 host target gene. LOC255231 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255231 BINDING SITE, designated SEQ ID:45672, to the nucleotide sequence of VGAM2671 RNA, herein designated VGAM RNA, also designated SEQ ID:5382.

[89899] Another function of VGAM2671 is therefore inhibition of LOC255231 (Accession XM_170908). Accordingly, utilities of VGAM2671 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC255231. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2672 (VGAM2672) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89900] VGAM2672 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2672 was detected is described hereinabove with reference to Figs. 1-8.

[89901] VGAM2672 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Mitovirus 3a. VGAM2672 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89902] VGAM2672 gene encodes a VGAM2672 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2672 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2672 precursor RNA is designated SEQ ID:2658, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2658 is located at position 1136 relative to the genome of Ophiostoma Mitovirus 3a.

[89903] VGAM2672 precursor RNA folds onto itself, forming VGAM2672 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89904] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2672 folded precursor RNA into VGAM2672 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2672 RNA is designated SEQ ID:5383, and is provided hereinbelow with reference to the sequence listing part.

[89905] VGAM2672 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2672 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89906] VGAM2672 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2672 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2672 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89907] The complementary binding of VGAM2672 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2672 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2672 host target RNA into VGAM2672 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89908] It is appreciated that VGAM2672 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2672 host target genes. The mRNA of each one of this plurality of VGAM2672 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2672 RNA, herein designated VGAM RNA, and which when bound by VGAM2672 RNA causes

inhibition of translation of respective one or more VGAM2672 host target proteins.

[89909] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2672 gene, herein designated VGAM GENE, on one or more VGAM2672 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89910] It is yet further appreciated that a function of VGAM2672 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2672 include diagnosis, prevention and

treatment of viral infection by Ophiostoma Mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2672 correlate with, and may be deduced from, the identity of the host target genes which VGAM2672 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89911] Nucleotide sequences of the VGAM2672 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2672 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2672 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2672 are further described hereinbelow with reference to Table 1.

[89912] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2672 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2672 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89913] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2672 gene, herein designated VGAM is inhibition of expression of VGAM2672 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2672 correlate with, and may be deduced from, the identity of the target genes which VGAM2672 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89914] DXYS155E (Accession NM_005088) is a VGAM2672 host target gene. DXYS155E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DXYS155E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DXYS155E BINDING SITE, designated SEQ ID:11542, to the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89915] A function of VGAM2672 is therefore inhibition of DXYS155E (Accession NM_005088), a gene which may be involved in b-cell activation. may also be involved in signal transduction and gene regulation. Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DXYS155E. The function of DXYS155E and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM766.Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 2 (MLLT2, Accession NM_005935) is another VGAM2672 host target gene. MLLT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MLLT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLLT2 BINDING SITE, designated SEQ ID:12572, to the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89916] Another function of VGAM2672 is therefore inhibition of Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 2 (MLLT2, Accession NM_005935), a gene which is a Putative transcription factor. Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLLT2. The function of MLLT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM57.DKFZP761E2110 (Accession NM_030953) is another VGAM2672 host target gene. DKFZP761E2110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761E2110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761E2110 BINDING SITE, designated SEQ ID:25227, to the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89917] Another function of VGAM2672 is therefore inhibition of DKFZP761E2110 (Accession NM_030953). Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761E2110. Phosphoinositide-3-kinase, Regulatory Subunit 4, P150 (PIK3R4, Accession XM_030812) is another VGAM2672 host target gene. PIK3R4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PIK3R4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

PIK3R4 BINDING SITE, designated SEQ ID:31149, to the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89918] Another function of VGAM2672 is therefore inhibition of Phosphoinositide-3-kinase, Regulatory Subunit 4, P150 (PIK3R4, Accession XM_030812). Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3R4. Transmembrane Protease, Serine 5 (spinesin) (TMPRSS5, Accession NM_030770) is another VGAM2672 host target gene. TMPRSS5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMPRSS5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMPRSS5 BINDING SITE, designated SEQ ID:25055, to the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89919] Another function of VGAM2672 is therefore inhibition of Transmembrane Protease, Serine 5 (spinesin) (TMPRSS5, Accession NM_030770). Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with TMPRSS5. LOC129011 (Accession XM_059326) is another VGAM2672 host target gene. LOC129011 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC129011, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129011 BINDING SITE, designated SEQ ID:36966, to the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89920] Another function of VGAM2672 is therefore inhibition of LOC129011 (Accession XM_059326). Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129011. LOC132235 (Accession XM_072302) is another VGAM2672 host target gene. LOC132235 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132235, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132235 BINDING SITE, designated SEQ ID:37481, to

the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89921] Another function of VGAM2672 is therefore inhibition of LOC132235 (Accession XM_072302). Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132235. LOC144363 (Accession XM_084843) is another VGAM2672 host target gene. LOC144363 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144363, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144363 BINDING SITE, designated SEQ ID:37731, to the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89922] Another function of VGAM2672 is therefore inhibition of LOC144363 (Accession XM_084843). Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144363. LOC144571 (Accession XM_096630) is another VGAM2672 host target gene. LOC144571 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC144571, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144571 BINDING SITE, designated SEQ ID:40443, to the nucleotide sequence of VGAM2672 RNA, herein designated VGAM RNA, also designated SEQ ID:5383.

[89923] Another function of VGAM2672 is therefore inhibition of LOC144571 (Accession XM_096630). Accordingly, utilities of VGAM2672 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144571. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2673 (VGAM2673) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89924] VGAM2673 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2673 was detected is described hereinabove with reference to Figs. 1-8.

[89925] VGAM2673 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Ophiostoma Mitovirus 3a. VGAM2673 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89926] VGAM2673 gene encodes a VGAM2673 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2673 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2673 precursor RNA is designated SEQ ID:2659, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2659 is located at position 308 relative to the genome of Ophiostoma Mitovirus 3a.

[89927] VGAM2673 precursor RNA folds onto itself, forming VGAM2673 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89928] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2673 folded precursor RNA into VGAM2673 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2673 RNA is designated SEQ ID:5384, and is provided hereinbelow with reference to the sequence listing part.

[89929] VGAM2673 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2673 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89930] VGAM2673 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2673 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2673 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89931] The complementary binding of VGAM2673 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2673 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2673

host target RNA into VGAM2673 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89932] It is appreciated that VGAM2673 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2673 host target genes. The mRNA of each one of this plurality of VGAM2673 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2673 RNA, herein designated VGAM RNA, and which when bound by VGAM2673 RNA causes inhibition of translation of respective one or more VGAM2673 host target proteins.

[89933] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2673 gene, herein designated VGAM GENE, on one or more VGAM2673 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89934] It is yet further appreciated that a function of VGAM2673 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2673 include diagnosis, prevention and treatment of viral infection by Ophiostoma Mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2673 correlate with, and may be deduced from, the identity of the host target genes which VGAM2673 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89935] Nucleotide sequences of the VGAM2673 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2673 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2673 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2673 are further

described hereinbelow with reference to Table 1.

[89936] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2673 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2673 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89937] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2673 gene, herein designated VGAM is inhibition of expression of VGAM2673 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2673 correlate with, and may be deduced from, the identity of the target genes which VGAM2673 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89938] Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615) is a VGAM2673 host target gene. SLC4A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC4A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of SLC4A7 BINDING SITE, designated SEQ ID:9669, to the nucleotide sequence of VGAM2673 RNA, herein designated VGAM RNA, also designated SEQ ID:5384.

[89939] A function of VGAM2673 is therefore inhibition of Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615), a gene which mediates the coupled movement of sodium and bicarbonate ions across the plasma membrane. Accordingly, utilities of VGAM2673 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A7. The function of SLC4A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM66.LEC3 (Accession NM_015236) is another VGAM2673 host target gene. LEC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LEC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LEC3 BINDING SITE, designated SEQ ID:17570, to the nucleotide sequence of VGAM2673 RNA, herein designated VGAM

RNA, also designated SEQ ID:5384.

[89940] Another function of VGAM2673 is therefore inhibition of LEC3 (Accession NM_015236). Accordingly, utilities of VGAM2673 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEC3. MGC2835 (Accession NM_024072) is another VGAM2673 host target gene. MGC2835 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2835, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2835 BINDING SITE, designated SEQ ID:23502, to the nucleotide sequence of VGAM2673 RNA, herein designated VGAM RNA, also designated SEQ ID:5384.

[89941] Another function of VGAM2673 is therefore inhibition of MGC2835 (Accession NM_024072). Accordingly, utilities of VGAM2673 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2835. LOC196264 (Accession XM_113683) is another VGAM2673 host target gene. LOC196264 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, designated SEQ ID:42332, to the nucleotide sequence of VGAM2673 RNA, herein designated VGAM RNA, also designated SEQ ID:5384.

[89942] Another function of VGAM2673 is therefore inhibition of LOC196264 (Accession XM_113683). Accordingly, utilities of VGAM2673 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264. LOC202460 (Accession XM_114493) is another VGAM2673 host target gene. LOC202460 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202460, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202460 BINDING SITE, designated SEQ ID:42980, to the nucleotide sequence of VGAM2673 RNA, herein designated VGAM RNA, also designated SEQ ID:5384.

[89943] Another function of VGAM2673 is therefore inhibition of LOC202460 (Accession XM_114493). Accordingly, utilities of VGAM2673 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC202460. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2674 (VGAM2674) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89944] VGAM2674 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2674 was detected is described hereinabove with reference to Figs. 1-8.

[89945] VGAM2674 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Mitovirus 3a. VGAM2674 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89946] VGAM2674 gene encodes a VGAM2674 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2674 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2674 precursor RNA is desig-

nated SEQ ID:2660, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2660 is located at position 2100 relative to the genome of Ophiostoma Mitovirus 3a.

[89947] VGAM2674 precursor RNA folds onto itself, forming VGAM2674 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89948] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2674 folded precursor RNA into VGAM2674 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2674 RNA is designated SEQ ID:5385, and is provided hereinbelow with reference to the sequence

listing part.

[89949] VGAM2674 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2674 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89950] VGAM2674 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2674 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2674 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89951] The complementary binding of VGAM2674 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2674 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2674 host target RNA into VGAM2674 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89952] It is appreciated that VGAM2674 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2674 host target genes. The mRNA of each one of this plurality of VGAM2674 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2674 RNA, herein designated VGAM

RNA, and which when bound by VGAM2674 RNA causes inhibition of translation of respective one or more VGAM2674 host target proteins.

[89953] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2674 gene, herein designated VGAM GENE, on one or more VGAM2674 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89954] It is yet further appreciated that a function of VGAM2674 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2674 include diagnosis, prevention and treatment of viral infection by Ophiostoma Mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2674 correlate with, and may be deduced from, the identity of the host target genes which VGAM2674 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[89955] Nucleotide sequences of the VGAM2674 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2674 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2674 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2674 are further described hereinbelow with reference to Table 1.

[89956] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2674 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2674 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[89957] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2674 gene, herein designated VGAM is

inhibition of expression of VGAM2674 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2674 correlate with, and may be deduced from, the identity of the target genes which VGAM2674 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[89958] B-cell CLL/lymphoma 10 (BCL10, Accession NM_003921) is a VGAM2674 host target gene. BCL10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BCL10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL10 BINDING SITE, designated SEQ ID:10008, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89959] A function of VGAM2674 is therefore inhibition of B-cell CLL/lymphoma 10 (BCL10, Accession NM_003921), a gene which is a positive regulator of lymphocyte proliferation, NF-kappaB activator. Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL10. The function of BCL10 and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Claudin 14 (CLDN14, Accession NM_144492) is another VGAM2674 host target gene. CLDN14 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CLDN14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLDN14 BINDING SITE, designated SEQ ID:29310, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89960] Another function of VGAM2674 is therefore inhibition of Claudin 14 (CLDN14, Accession NM_144492), a gene which provides structural support for the auditory neuroepithelium. Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN14. The function of CLDN14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1316.Glucosamine-6-phosphate Isomerase (GNPI, Accession NM_005471) is another VGAM2674 host target

gene. GNPI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNPI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNPI BINDING SITE, designated SEQ ID:11967, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89961] Another function of VGAM2674 is therefore inhibition of Glucosamine-6-phosphate Isomerase (GNPI, Accession NM_005471), a gene which converts glucosamine-6-phosphate to fructose-6-phosphate. Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPI. The function of GNPI and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM124.Ornithine Carbamoyltransferase (OTC, Accession NM_000531) is another VGAM2674 host target gene. OTC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by OTC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of OTC BINDING SITE, designated SEQ ID:6133, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89962] Another function of VGAM2674 is therefore inhibition of Ornithine Carbamoyltransferase (OTC, Accession NM_000531). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTC. Arginine-glutamic Acid Dipeptide (RE) Repeats (RERE, Accession NM_012102) is another VGAM2674 host target gene. RERE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RERE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RERE BINDING SITE, designated SEQ ID:14406, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89963] Another function of VGAM2674 is therefore inhibition of Arginine-glutamic Acid Dipeptide (RE) Repeats (RERE, Accession NM_012102), a gene which binds DRPLA and locates in the nucleus. Accordingly, utilities of VGAM2674

include diagnosis, prevention and treatment of diseases and clinical conditions associated with RERE. The function of RERE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM51.Asporin (LRR class 1) (ASPN, Accession NM_017680) is another VGAM2674 host target gene. ASPN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ASPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASPN BINDING SITE, designated SEQ ID:19224, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89964] Another function of VGAM2674 is therefore inhibition of Asporin (LRR class 1) (ASPN, Accession NM_017680). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASPN. Chromosome 12 Open Reading Frame 22 (C12orf22, Accession NM_030809) is another VGAM2674 host target gene. C12orf22 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by C12orf22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C12orf22 BINDING SITE, designated SEQ ID:25127, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89965] Another function of VGAM2674 is therefore inhibition of Chromosome 12 Open Reading Frame 22 (C12orf22, Accession NM_030809). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C12orf22. Caspase 9, Apoptosis-related Cysteine Protease (CASP9, Accession NM_001229) is another VGAM2674 host target gene. CASP9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CASP9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASP9 BINDING SITE, designated SEQ ID:6900, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89966] Another function of VGAM2674 is therefore inhibition of

Caspase 9, Apoptosis-related Cysteine Protease (CASP9, Accession NM_001229). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP9. DKFZP434J193 (Accession XM_048452) is another VGAM2674 host target gene. DKFZP434J193 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434J193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434J193 BINDING SITE, designated SEQ ID:35165, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89967] Another function of VGAM2674 is therefore inhibition of DKFZP434J193 (Accession XM_048452). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434J193. DKFZP564B1162 (Accession NM_031305) is another VGAM2674 host target gene. DKFZP564B1162 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP564B1162, corresponding to a HOST TARGET bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564B1162 BINDING SITE, designated SEQ ID:25338, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89968] Another function of VGAM2674 is therefore inhibition of DKFZP564B1162 (Accession NM_031305). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564B1162. FLJ10997 (Accession NM_018293) is another VGAM2674 host target gene. FLJ10997 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10997, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10997 BINDING SITE, designated SEQ ID:20283, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89969] Another function of VGAM2674 is therefore inhibition of FLJ10997 (Accession NM_018293). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ10997. FLJ12903 (Accession NM_022753) is another VGAM2674 host target gene. FLJ12903 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12903, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12903 BINDING SITE, designated SEQ ID:22979, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89970] Another function of VGAM2674 is therefore inhibition of FLJ12903 (Accession NM_022753). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903. FLJ13189 (Accession NM_024882) is another VGAM2674 host target gene. FLJ13189 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13189 BINDING SITE, designated SEQ ID:24331, to the nucleotide

sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89971] Another function of VGAM2674 is therefore inhibition of FLJ13189 (Accession NM_024882). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13189. FLJ13615 (Accession NM_025114) is another VGAM2674 host target gene. FLJ13615 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13615, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13615 BINDING SITE, designated SEQ ID:24764, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89972] Another function of VGAM2674 is therefore inhibition of FLJ13615 (Accession NM_025114). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13615. FLJ22169 (Accession NM_024085) is another VGAM2674 host target gene. FLJ22169 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ22169, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22169 BINDING SITE, designated SEQ ID:23525, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89973] Another function of VGAM2674 is therefore inhibition of FLJ22169 (Accession NM_024085). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22169. G Protein-coupled Receptor Kinase-interactor 2 (GIT2, Accession NM_057169) is another VGAM2674 host target gene. GIT2 BINDING SITE1 through GIT2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GIT2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GIT2 BINDING SITE1 through GIT2 BINDING SITE3, designated SEQ ID:27685, SEQ ID:27698 and SEQ ID:16603 respectively, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89974] Another function of VGAM2674 is therefore inhibition of G Protein-coupled Receptor Kinase-interactor 2 (GIT2, Accession NM_057169). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GIT2. KIAA1789 (Accession XM_040486) is another VGAM2674 host target gene. KIAA1789 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1789 BINDING SITE, designated SEQ ID:33310, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89975] Another function of VGAM2674 is therefore inhibition of KIAA1789 (Accession XM_040486). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1789. KIAA1805 (Accession XM_086976) is another VGAM2674 host target gene. KIAA1805 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1805, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1805 BINDING SITE, designated SEQ ID:39001, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89976] Another function of VGAM2674 is therefore inhibition of KIAA1805 (Accession XM_086976). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1805. MGC15631 (Accession NM_032753) is another VGAM2674 host target gene. MGC15631 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC15631, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15631 BINDING SITE, designated SEQ ID:26495, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89977] Another function of VGAM2674 is therefore inhibition of MGC15631 (Accession NM_032753). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC15631. MGC5139 (Accession XM_058587) is another VGAM2674 host target gene. MGC5139 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC5139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5139 BINDING SITE, designated SEQ ID:36676, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89978] Another function of VGAM2674 is therefore inhibition of MGC5139 (Accession XM_058587). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5139. Protein Phosphatase 1, Regulatory Subunit 10 (PPP1R10, Accession NM_002714) is another VGAM2674 host target gene. PPP1R10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PPP1R10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R10 BINDING SITE,

designated SEQ ID:8580, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89979] Another function of VGAM2674 is therefore inhibition of Protein Phosphatase 1, Regulatory Subunit 10 (PPP1R10, Accession NM_002714). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R10. RAB35, Member RAS Oncogene Family (RAB35, Accession NM_006861) is another VGAM2674 host target gene. RAB35 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB35, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB35 BINDING SITE, designated SEQ ID:13735, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89980] Another function of VGAM2674 is therefore inhibition of RAB35, Member RAS Oncogene Family (RAB35, Accession NM_006861). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with RAB35. Tripartite Motif-containing 26 (TRIM26, Accession NM_003449) is another VGAM2674 host target gene. TRIM26 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM26 BINDING SITE, designated SEQ ID:9499, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89981] Another function of VGAM2674 is therefore inhibition of Tripartite Motif-containing 26 (TRIM26, Accession NM_003449). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM26. LOC137964 (Accession XM_059933) is another VGAM2674 host target gene. LOC137964 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC137964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC137964 BINDING SITE, desig-

nated SEQ ID:37111, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89982] Another function of VGAM2674 is therefore inhibition of LOC137964 (Accession XM_059933). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137964. LOC144110 (Accession XM_084735) is another VGAM2674 host target gene. LOC144110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144110 BINDING SITE, designated SEQ ID:37680, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89983] Another function of VGAM2674 is therefore inhibition of LOC144110 (Accession XM_084735). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144110. LOC146226 (Accession XM_096946) is another VGAM2674 host target gene. LOC146226 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146226, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146226 BINDING SITE, designated SEQ ID:40663, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89984] Another function of VGAM2674 is therefore inhibition of LOC146226 (Accession XM_096946). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146226. LOC157922 (Accession XM_098841) is another VGAM2674 host target gene. LOC157922 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157922, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157922 BINDING SITE, designated SEQ ID:41889, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89985] Another function of VGAM2674 is therefore inhibition of

LOC157922 (Accession XM_098841). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157922. LOC158125 (Accession XM_088492) is another VGAM2674 host target gene. LOC158125 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158125, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158125 BINDING SITE, designated SEQ ID:39730, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89986] Another function of VGAM2674 is therefore inhibition of LOC158125 (Accession XM_088492). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158125. LOC221773 (Accession XM_165802) is another VGAM2674 host target gene. LOC221773 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC221773 BINDING SITE, designated SEQ ID:43764, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89987] Another function of VGAM2674 is therefore inhibition of LOC221773 (Accession XM_165802). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221773. LOC257494 (Accession XM_175212) is another VGAM2674 host target gene. LOC257494 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257494, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257494 BINDING SITE, designated SEQ ID:46686, to the nucleotide sequence of VGAM2674 RNA, herein designated VGAM RNA, also designated SEQ ID:5385.

[89988] Another function of VGAM2674 is therefore inhibition of LOC257494 (Accession XM_175212). Accordingly, utilities of VGAM2674 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257494. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2675 (VGAM2675) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[89989] VGAM2675 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2675 was detected is described hereinabove with reference to Figs. 1-8.

[89990] VGAM2675 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Mitovirus 3a. VGAM2675 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[89991] VGAM2675 gene encodes a VGAM2675 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2675 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2675 precursor RNA is designated SEQ ID:2661, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2661 is located at position 567 relative to the genome of Ophiostoma Mitovirus 3a.

[89992] VGAM2675 precursor RNA folds onto itself, forming VGAM2675 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[89993] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2675 folded precursor RNA into VGAM2675 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2675 RNA is designated SEQ ID:5386, and is provided hereinbelow with reference to the sequence listing part.

[89994] VGAM2675 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2675 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[89995] VGAM2675 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2675 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2675 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2675 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[89996] The complementary binding of VGAM2675 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2675 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2675 host target RNA into VGAM2675 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[89997] It is appreciated that VGAM2675 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2675 host target genes. The mRNA of each one of this plurality of VGAM2675 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2675 RNA, herein designated VGAM RNA, and which when bound by VGAM2675 RNA causes inhibition of translation of respective one or more

VGAM2675 host target proteins.

[89998] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2675 gene, herein designated VGAM GENE, on one or more VGAM2675 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[89999] It is yet further appreciated that a function of VGAM2675 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of viral infection by Ophiostoma Mitovirus 3a.

Specific functions, and accordingly utilities, of VGAM2675 correlate with, and may be deduced from, the identity of the host target genes which VGAM2675 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90000] Nucleotide sequences of the VGAM2675 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2675 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2675 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2675 are further described hereinbelow with reference to Table 1.

[90001] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2675 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2675 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90002] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2675 gene, herein designated VGAM is inhibition of expression of VGAM2675 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2675 correlate with, and may be deduced from, the identity of the target genes which VGAM2675 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90003] Protocadherin Alpha 9 (PCDHA9, Accession NM_014005) is a VGAM2675 host target gene. PCDHA9 BINDING SITE1 and PCDHA9 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDHA9, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE1 and PCDHA9 BINDING SITE2, designated SEQ ID:15210 and SEQ ID:25602 respectively, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90004] A function of VGAM2675 is therefore inhibition of Protocadherin Alpha 9 (PCDHA9, Accession NM_014005), a gene which is a calcium-dependent cell-adhesion protein. Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9. The function of PCDHA9 and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM71.ARPP-19 (Accession NM_006628) is another VGAM2675 host target gene. ARPP-19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARPP-19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARPP-19 BINDING SITE, designated SEQ ID:13420, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90005] Another function of VGAM2675 is therefore inhibition of ARPP-19 (Accession NM_006628). Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARPP-19. ATPase, H+ Transporting, Lysosomal 56/58kDa, V1 Subunit B, Isoform 2 (ATP6V1B2, Accession NM_001693) is another VGAM2675 host target gene. ATP6V1B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP6V1B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of ATP6V1B2 BINDING SITE, designated SEQ ID:7414, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90006] Another function of VGAM2675 is therefore inhibition of ATPase, H+ Transporting, Lysosomal 56/58kDa, V1 Subunit B, Isoform 2 (ATP6V1B2, Accession NM_001693). Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V1B2. Chromosome 1 Open Reading Frame 34 (C1orf34, Accession XM_027172) is another VGAM2675 host target gene. C1orf34 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf34, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf34 BINDING SITE, designated SEQ ID:30436, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90007] Another function of VGAM2675 is therefore inhibition of Chromosome 1 Open Reading Frame 34 (C1orf34, Accession XM_027172). Accordingly, utilities of VGAM2675 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf34. FLJ13912 (Accession NM_022770) is another VGAM2675 host target gene. FLJ13912 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13912 BINDING SITE, designated SEQ ID:23029, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90008] Another function of VGAM2675 is therefore inhibition of FLJ13912 (Accession NM_022770). Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13912. FLJ20511 (Accession NM_017853) is another VGAM2675 host target gene. FLJ20511 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20511, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20511

BINDING SITE, designated SEQ ID:19527, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90009] Another function of VGAM2675 is therefore inhibition of FLJ20511 (Accession NM_017853). Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20511. HCA127 (Accession NM_018684) is another VGAM2675 host target gene. HCA127 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCA127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCA127 BINDING SITE, designated SEQ ID:20756, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90010] Another function of VGAM2675 is therefore inhibition of HCA127 (Accession NM_018684). Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCA127. LOC254057 (Accession XM_173085) is another VGAM2675 host target gene. LOC254057 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254057 BINDING SITE, designated SEQ ID:46345, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90011] Another function of VGAM2675 is therefore inhibition of LOC254057 (Accession XM_173085). Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254057. LOC92935 (Accession XM_048197) is another VGAM2675 host target gene. LOC92935 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92935, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92935 BINDING SITE, designated SEQ ID:35132, to the nucleotide sequence of VGAM2675 RNA, herein designated VGAM RNA, also designated SEQ ID:5386.

[90012] Another function of VGAM2675 is therefore inhibition of

LOC92935 (Accession XM_048197). Accordingly, utilities of VGAM2675 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92935. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2676 (VGAM2676) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90013] VGAM2676 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2676 was detected is described hereinabove with reference to Figs. 1-8.

[90014] VGAM2676 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Mitovirus 3a. VGAM2676 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90015] VGAM2676 gene encodes a VGAM2676 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2676 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2676 precursor RNA is designated SEQ ID:2662, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2662 is located at position 905 relative to the genome of Ophiostoma Mitovirus 3a.

[90016] VGAM2676 precursor RNA folds onto itself, forming VGAM2676 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90017] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2676 folded precursor RNA into VGAM2676 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide se-

quence of VGAM2676 RNA is designated SEQ ID:5387, and is provided hereinbelow with reference to the sequence listing part.

[90018] VGAM2676 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2676 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90019] VGAM2676 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2676 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2676 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90020] The complementary binding of VGAM2676 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2676 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2676 host target RNA into VGAM2676 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90021] It is appreciated that VGAM2676 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2676 host target genes. The mRNA of each one of this plurality of VGAM2676 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2676 RNA, herein designated VGAM RNA, and which when bound by VGAM2676 RNA causes inhibition of translation of respective one or more VGAM2676 host target proteins.

[90022] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2676 gene, herein designated VGAM GENE, on one or more VGAM2676 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90023] It is yet further appreciated that a function of VGAM2676

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2676 include diagnosis, prevention and treatment of viral infection by Ophiostoma Mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2676 correlate with, and may be deduced from, the identity of the host target genes which VGAM2676 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90024] Nucleotide sequences of the VGAM2676 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2676 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2676 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2676 are further described hereinbelow with reference to Table 1.

[90025] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2676 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2676 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90026] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2676 gene, herein designated VGAM is inhibition of expression of VGAM2676 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2676 correlate with, and may be deduced from, the identity of the target genes which VGAM2676 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90027] Kinesin-like 1 (KNSL1, Accession NM_004523) is a VGAM2676 host target gene. KNSL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KNSL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KNSL1 BINDING SITE, designated SEQ ID:10862, to the nucleotide sequence of VGAM2676 RNA, herein designated VGAM RNA, also designated SEQ ID:5387.

[90028] A function of VGAM2676 is therefore inhibition of Kinesin-like 1 (KNSL1, Accession NM_004523), a gene which is a motor protein required for establishing a bipolar spindle. Accordingly, utilities of VGAM2676 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with KNSL1. The function of KNSL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM252.KIAA0254 (Accession NM_014758) is another VGAM2676 host target gene. KIAA0254 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0254, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0254 BINDING SITE, designated SEQ ID:16505, to the nucleotide sequence of VGAM2676 RNA, herein designated VGAM RNA, also designated SEQ ID:5387.

[90029] Another function of VGAM2676 is therefore inhibition of KIAA0254 (Accession NM_014758). Accordingly, utilities of VGAM2676 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0254. Sulfotransferase Family, Cytosolic, 1C, Member 2 (SULT1C2, Accession NM_006588) is another VGAM2676 host target gene. SULT1C2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SULT1C2, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SULT1C2 BINDING SITE, designated SEQ ID:13351, to the nucleotide sequence of VGAM2676 RNA, herein designated VGAM RNA, also designated SEQ ID:5387.

[90030] Another function of VGAM2676 is therefore inhibition of Sulfotransferase Family, Cytosolic, 1C, Member 2 (SULT1C2, Accession NM_006588). Accordingly, utilities of VGAM2676 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SULT1C2. LOC144519 (Accession XM_084890) is another VGAM2676 host target gene. LOC144519 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144519 BINDING SITE, designated SEQ ID:37755, to the nucleotide sequence of VGAM2676 RNA, herein designated VGAM RNA, also designated SEQ ID:5387.

[90031] Another function of VGAM2676 is therefore inhibition of LOC144519 (Accession XM_084890). Accordingly, utilities

of VGAM2676 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144519. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2677 (VGAM2677) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90032] VGAM2677 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2677 was detected is described hereinabove with reference to Figs. 1-8.

[90033] VGAM2677 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Mitovirus 3a. VGAM2677 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90034] VGAM2677 gene encodes a VGAM2677 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2677 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2677 precursor RNA is designated SEQ ID:2663, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2663 is located at position 1465 relative to the genome of Ophiostoma Mitovirus 3a.

[90035] VGAM2677 precursor RNA folds onto itself, forming VGAM2677 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90036] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2677 folded precursor RNA into VGAM2677 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2677 RNA is designated SEQ ID:5388, and

is provided hereinbelow with reference to the sequence listing part.

[90037] VGAM2677 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2677 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90038] VGAM2677 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2677 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2677 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90039] The complementary binding of VGAM2677 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2677 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2677 host target RNA into VGAM2677 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90040] It is appreciated that VGAM2677 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2677 host target genes. The mRNA of each one of this plurality of VGAM2677 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2677 RNA, herein designated VGAM RNA, and which when bound by VGAM2677 RNA causes inhibition of translation of respective one or more VGAM2677 host target proteins.

[90041] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2677 gene, herein designated VGAM GENE, on one or more VGAM2677 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90042] It is yet further appreciated that a function of VGAM2677 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2677 include diagnosis, prevention and treatment of viral infection by Ophiostoma Mitovirus 3a. Specific functions, and accordingly utilities, of VGAM2677 correlate with, and may be deduced from, the identity of the host target genes which VGAM2677 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90043] Nucleotide sequences of the VGAM2677 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2677 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2677 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2677 are further described hereinbelow with reference to Table 1.

[90044] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2677 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2677 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90045] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2677 gene, herein designated VGAM is inhibition of expression of VGAM2677 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2677 correlate with, and may be deduced from, the identity of the target genes which VGAM2677 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90046] Phosphoribosylaminoimidazole Carboxylase, Phosphoribosylaminoimidazole Succinocarboxamide Synthetase (PAICS, Accession NM_006452) is a VGAM2677 host target gene. PAICS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAICS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAICS BINDING SITE, designated SEQ ID:13162, to the nucleotide sequence of VGAM2677 RNA, herein designated VGAM RNA, also designated SEQ ID:5388.

[90047] A function of VGAM2677 is therefore inhibition of Phosphoribosylaminoimidazole Carboxylase, Phosphoribosylaminoimidazole Succinocarboxamide Synthetase (PAICS, Accession NM_006452), a gene which is required for purine biosynthesis. Accordingly, utilities of VGAM2677

include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAICS. The function of PAICS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM894.KIAA0844 (Accession NM_014951) is another VGAM2677 host target gene. KIAA0844 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0844, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0844 BINDING SITE, designated SEQ ID:17284, to the nucleotide sequence of VGAM2677 RNA, herein designated VGAM RNA, also designated SEQ ID:5388.

[90048] Another function of VGAM2677 is therefore inhibition of KIAA0844 (Accession NM_014951). Accordingly, utilities of VGAM2677 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0844. LOC126669 (Accession XM_060121) is another VGAM2677 host target gene. LOC126669 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126669, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE, designated SEQ ID:37153, to the nucleotide sequence of VGAM2677 RNA, herein designated VGAM RNA, also designated SEQ ID:5388.

[90049] Another function of VGAM2677 is therefore inhibition of LOC126669 (Accession XM_060121). Accordingly, utilities of VGAM2677 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669. LOC145644 (Accession XM_035608) is another VGAM2677 host target gene. LOC145644 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145644, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145644 BINDING SITE, designated SEQ ID:32289, to the nucleotide sequence of VGAM2677 RNA, herein designated VGAM RNA, also designated SEQ ID:5388.

[90050] Another function of VGAM2677 is therefore inhibition of LOC145644 (Accession XM_035608). Accordingly, utilities of VGAM2677 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145644. LOC90829 (Accession XM_034325) is another VGAM2677 host target gene. LOC90829 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90829 BINDING SITE, designated SEQ ID:32055, to the nucleotide sequence of VGAM2677 RNA, herein designated VGAM RNA, also designated SEQ ID:5388.

[90051] Another function of VGAM2677 is therefore inhibition of LOC90829 (Accession XM_034325). Accordingly, utilities of VGAM2677 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90829. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2678 (VGAM2678) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90052] VGAM2678 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2678 was detected is described hereinabove with reference to Figs. 1-8.

[90053] VGAM2678 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld. VGAM2678 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90054] VGAM2678 gene encodes a VGAM2678 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2678 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2678 precursor RNA is designated SEQ ID:2664, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2664 is located at position 1520 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld.

[90055] VGAM2678 precursor RNA folds onto itself, forming VGAM2678 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90056] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2678 folded precursor RNA into VGAM2678 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2678 RNA is designated SEQ ID:5389, and is provided hereinbelow with reference to the sequence listing part.

[90057] VGAM2678 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2678 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90058] VGAM2678 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2678 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2678 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90059] The complementary binding of VGAM2678 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2678 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2678 host target RNA into VGAM2678 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90060] It is appreciated that VGAM2678 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2678 host target genes. The mRNA of each one of this plurality of VGAM2678 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2678 RNA, herein designated VGAM RNA, and which when bound by VGAM2678 RNA causes inhibition of translation of respective one or more VGAM2678 host target proteins.

[90061] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2678 gene, herein designated VGAM GENE, on one or more VGAM2678 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90062] It is yet further appreciated that a function of VGAM2678 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2678 correlate with, and may be deduced from, the identity of the host target genes which VGAM2678 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90063] Nucleotide sequences of the VGAM2678 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2678 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2678 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2678 are further described hereinbelow with reference to Table 1.

[90064] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2678 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2678 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90065] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2678 gene, herein designated VGAM is inhibition of expression of VGAM2678 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2678 correlate with, and may be deduced from, the identity of the target genes which VGAM2678 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90066] Jagged 2 (JAG2, Accession NM_002226) is a VGAM2678 host target gene. JAG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by JAG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAG2 BINDING SITE, designated SEQ ID:8008, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90067] A function of VGAM2678 is therefore inhibition of Jagged 2 (JAG2, Accession NM_002226), a gene which is a putative notch ligand involved in the mediation of notch signaling. Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAG2. The function of JAG2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM136.Mab-21-like 1 (C. elegans) (MAB21L1, Accession NM_005584) is another VGAM2678 host target gene. MAB21L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAB21L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of MAB21L1 BINDING SITE, designated SEQ ID:12114, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90068] Another function of VGAM2678 is therefore inhibition of Mab-21-like 1 (C. elegans) (MAB21L1, Accession NM_005584), a gene which may control cerebellum and eye development; very strongly similar to murine Mm.10798. Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAB21L1. The function of MAB21L1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM39.Myotubular Myopathy 1 (MTM1, Accession NM_000252) is another VGAM2678 host target gene. MTM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTM1 BINDING SITE, designated SEQ ID:5793, to the nucleotide sequence of VGAM2678 RNA, herein

designated VGAM RNA, also designated SEQ ID:5389.

[90069] Another function of VGAM2678 is therefore inhibition of Myotubular Myopathy 1 (MTM1, Accession NM_000252). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTM1. Von Hippel-Lindau Syndrome (VHL, Accession NM_000551) is another VGAM2678 host target gene. VHL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VHL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VHL BINDING SITE, designated SEQ ID:6166, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90070] Another function of VGAM2678 is therefore inhibition of Von Hippel-Lindau Syndrome (VHL, Accession NM_000551), a gene which may control rna stability through the selective degradation of rna-bound proteins. Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VHL. The function of VHL and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM197.ANKT (Accession NM_016359) is another VGAM2678 host target gene. ANKT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANKT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANKT BINDING SITE, designated SEQ ID:18500, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90071] Another function of VGAM2678 is therefore inhibition of ANKT (Accession NM_016359). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKT. DKFZP761L0424 (Accession XM_166112) is another VGAM2678 host target gene. DKFZP761L0424 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761L0424, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761L0424 BINDING SITE, designated

SEQ ID:43892, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90072] Another function of VGAM2678 is therefore inhibition of DKFZP761L0424 (Accession XM_166112). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761L0424. FLJ10852 (Accession NM_019028) is another VGAM2678 host target gene. FLJ10852 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10852, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10852 BINDING SITE, designated SEQ ID:21118, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90073] Another function of VGAM2678 is therefore inhibition of FLJ10852 (Accession NM_019028). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10852. FLJ22054 (Accession XM_170478) is another VGAM2678 host target gene. FLJ22054 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22054 BINDING SITE, designated SEQ ID:45320, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90074] Another function of VGAM2678 is therefore inhibition of FLJ22054 (Accession XM_170478). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22054. FLJ23259 (Accession NM_024727) is another VGAM2678 host target gene. FLJ23259 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23259 BINDING SITE, designated SEQ ID:24064, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90075] Another function of VGAM2678 is therefore inhibition of

FLJ23259 (Accession NM_024727). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23259. HSMPP8 (Accession XM_167894) is another VGAM2678 host target gene. HSMPP8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSMPP8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSMPP8 BINDING SITE, designated SEQ ID:44906, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90076] Another function of VGAM2678 is therefore inhibition of HSMPP8 (Accession XM_167894). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSMPP8. KIAA1014 (Accession XM_037205) is another VGAM2678 host target gene. KIAA1014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1014 BINDING SITE, designated SEQ ID:32572, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90077] Another function of VGAM2678 is therefore inhibition of KIAA1014 (Accession XM_037205). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1014. MGC35558 (Accession NM_145013) is another VGAM2678 host target gene. MGC35558 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC35558, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC35558 BINDING SITE, designated SEQ ID:29618, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90078] Another function of VGAM2678 is therefore inhibition of MGC35558 (Accession NM_145013). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35558. Spir-1 (Accession XM_035640) is another

VGAM2678 host target gene. Spir-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Spir-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Spir-1 BINDING SITE, designated SEQ ID:32309, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90079] Another function of VGAM2678 is therefore inhibition of Spir-1 (Accession XM_035640). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Spir-1. ZFD25 (Accession NM_016220) is another VGAM2678 host target gene. ZFD25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZFD25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFD25 BINDING SITE, designated SEQ ID:18326, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90080] Another function of VGAM2678 is therefore inhibition of ZFD25 (Accession NM_016220). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFD25. LOC157503 (Accession XM_098767) is another VGAM2678 host target gene. LOC157503 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157503, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157503 BINDING SITE, designated SEQ ID:41816, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90081] Another function of VGAM2678 is therefore inhibition of LOC157503 (Accession XM_098767). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157503. LOC201475 (Accession XM_113967) is another VGAM2678 host target gene. LOC201475 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201475, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201475 BINDING SITE, designated SEQ ID:42579, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90082] Another function of VGAM2678 is therefore inhibition of LOC201475 (Accession XM_113967). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201475. LOC221814 (Accession XM_168226) is another VGAM2678 host target gene. LOC221814 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221814, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221814 BINDING SITE, designated SEQ ID:45098, to the nucleotide sequence of VGAM2678 RNA, herein designated VGAM RNA, also designated SEQ ID:5389.

[90083] Another function of VGAM2678 is therefore inhibition of LOC221814 (Accession XM_168226). Accordingly, utilities of VGAM2678 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221814. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2679 (VGAM2679) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90084] VGAM2679 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2679 was detected is described hereinabove with reference to Figs. 1-8.

[90085] VGAM2679 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld. VGAM2679 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90086] VGAM2679 gene encodes a VGAM2679 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2679 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2679 precursor RNA is designated SEQ ID:2665, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2665 is located at position 676 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld.

[90087] VGAM2679 precursor RNA folds onto itself, forming VGAM2679 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90088] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2679 folded precursor RNA into VGAM2679 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2679 RNA is designated SEQ ID:5390, and is provided hereinbelow with reference to the sequence listing part.

[90089] VGAM2679 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2679 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90090] VGAM2679 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2679 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2679 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90091] The complementary binding of VGAM2679 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2679 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2679 host target RNA into VGAM2679 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90092] It is appreciated that VGAM2679 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2679 host target genes. The mRNA of each one of this plurality of VGAM2679 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2679 RNA, herein designated VGAM RNA, and which when bound by VGAM2679 RNA causes

inhibition of translation of respective one or more VGAM2679 host target proteins.

[90093] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2679 gene, herein designated VGAM GENE, on one or more VGAM2679 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90094] It is yet further appreciated that a function of VGAM2679 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2679 include diagnosis, prevention and

treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2679 correlate with, and may be deduced from, the identity of the host target genes which VGAM2679 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90095] Nucleotide sequences of the VGAM2679 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2679 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2679 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2679 are further described hereinbelow with reference to Table 1.

[90096] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2679 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2679 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90097] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2679 gene, herein designated VGAM is inhibition of expression of VGAM2679 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2679 correlate with, and may be deduced from, the identity of the target genes which VGAM2679 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90098] Basic Transcription Element Binding Protein 1 (BTEB1, Accession NM_001206) is a VGAM2679 host target gene. BTEB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTEB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTEB1 BINDING SITE, designated SEQ ID:6871, to the nucleotide sequence of VGAM2679 RNA, herein designated VGAM RNA, also designated SEQ ID:5390.

[90099] A function of VGAM2679 is therefore inhibition of Basic Transcription Element Binding Protein 1 (BTEB1, Accession NM_001206). Accordingly, utilities of VGAM2679 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTEB1. Nuclear Protein, Ataxia-telangiectasia Locus (NPAT, Accession XM_040846) is another VGAM2679 host target gene. NPAT BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by NPAT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPAT BINDING SITE, designated SEQ ID:33387, to the nucleotide sequence of VGAM2679 RNA, herein designated VGAM RNA, also designated SEQ ID:5390.

[90100] Another function of VGAM2679 is therefore inhibition of Nuclear Protein, Ataxia-telangiectasia Locus (NPAT, Accession XM_040846), a gene which is expressed in all tissues. Accordingly, utilities of VGAM2679 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPAT. The function of NPAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM376.PRO0641 (Accession NM_014135) is another VGAM2679 host target gene. PRO0641 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0641, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0641 BINDING SITE, designated

SEQ ID:15401, to the nucleotide sequence of VGAM2679 RNA, herein designated VGAM RNA, also designated SEQ ID:5390.

[90101] Another function of VGAM2679 is therefore inhibition of PRO0641 (Accession NM_014135). Accordingly, utilities of VGAM2679 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0641. RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322) is another VGAM2679 host target gene. RAB14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB14 BINDING SITE, designated SEQ ID:18450, to the nucleotide sequence of VGAM2679 RNA, herein designated VGAM RNA, also designated SEQ ID:5390.

[90102] Another function of VGAM2679 is therefore inhibition of RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322). Accordingly, utilities of VGAM2679 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB14. Wingless-type

MMTV Integration Site Family, Member 2B (WNT2B, Accession NM_004185) is another VGAM2679 host target gene. WNT2B BINDING SITE1 and WNT2B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WNT2B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT2B BINDING SITE1 and WNT2B BINDING SITE2, designated SEQ ID:10392 and SEQ ID:23693 respectively, to the nucleotide sequence of VGAM2679 RNA, herein designated VGAM RNA, also designated SEQ ID:5390.

[90103] Another function of VGAM2679 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 2B (WNT2B, Accession NM_004185). Accordingly, utilities of VGAM2679 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT2B. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2680 (VGAM2680) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90104] VGAM2680 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2680 was detected is described hereinabove with reference to Figs. 1-8.

[90105] VGAM2680 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld. VGAM2680 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90106] VGAM2680 gene encodes a VGAM2680 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2680 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2680 precursor RNA is designated SEQ ID:2666, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2666 is located at position 316 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld.

[90107] VGAM2680 precursor RNA folds onto itself, forming VGAM2680 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90108] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2680 folded precursor RNA into VGAM2680 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2680 RNA is designated SEQ ID:5391, and is provided hereinbelow with reference to the sequence listing part.

[90109] VGAM2680 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2680 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[90110] VGAM2680 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2680 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2680 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90111] The complementary binding of VGAM2680 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2680 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2680 host target RNA into VGAM2680 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90112] It is appreciated that VGAM2680 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2680 host target genes. The mRNA of each one of this plurality of VGAM2680 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2680 RNA, herein designated VGAM RNA, and which when bound by VGAM2680 RNA causes inhibition of translation of respective one or more VGAM2680 host target proteins.

[90113] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2680 gene, herein designated VGAM GENE, on one or more VGAM2680 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90114] It is yet further appreciated that a function of VGAM2680 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2680 correlate with, and may be deduced from, the identity of the host target genes which VGAM2680 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90115] Nucleotide sequences of the VGAM2680 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2680 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2680 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2680 are further described hereinbelow with reference to Table 1.

[90116] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2680 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2680 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90117] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2680 gene, herein designated VGAM is inhibition of expression of VGAM2680 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2680 correlate with, and may be deduced from, the identity of the target genes which VGAM2680 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90118] A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110) is a VGAM2680 host target gene.

ADAM10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM10 BINDING SITE, designated SEQ ID:6767, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90119] A function of VGAM2680 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110), a gene which Member of ADAM family of zinc metalloproteases. Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM10. The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM706.Calcium Channel, Voltage-dependent, Gamma Subunit 2 (CACNG2, Accession NM_006078) is another VGAM2680 host target gene. CACNG2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

CACNG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CACNG2 BINDING SITE, designated SEQ ID:12724, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90120] Another function of VGAM2680 is therefore inhibition of Calcium Channel, Voltage-dependent, Gamma Subunit 2 (CACNG2, Accession NM_006078), a gene which is thought to stabilize the calcium channel in an inactivated (closed) state. Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNG2. The function of CACNG2 has been established by previous studies. Chen et al. (2000) found that stargazer, an ataxic and epileptic mutant mouse, lacks functional AMPA receptors on cerebellar granule cells. Stargazin, the mutant protein, interacts with both AMPA receptor subunits and synaptic PDZ proteins, such as PSD95 (OMIM Ref. No. 602887). Chen et al. (2000) found that the interaction of stargazin with AMPA receptor subunits is essential for delivering functional receptors to the surface membrane of granule cells,

whereas its binding with PSD95 and related PDZ proteins through a carboxy-terminal PDZ-binding domain is required for targeting the AMPA receptor to synapses. Expression of a mutant stargazin lacking the PDZ-binding domain in hippocampal pyramidal cells disrupts synaptic AMPA receptors, indicating that stargazin-like mechanisms for targeting AMPA receptors may be widespread in the central nervous syste. By searching an EST database for sequences homologous to mouse Cacng2, followed by PCR of a cerebellum cDNA library, Black and Lennon (1999) identified a cDNA encoding human CACNG2. The deduced 315-amino acid CACNG2 transmembrane protein is 98% identical to CACGN3 (OMIM Ref. No. 606403) and mouse Cacng2, but only 18% identical to CACNG1 (OMIM Ref. No. 114209).

[90121] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[90122] Chen, L.; Chetkovich, D. M.; Petralla, R. S.; Sweeney, N. T.; Kawasaki, Y.; Wenthold, R. J.; Bredt, D. S.; Nicoli, R. A. : Stargazin regulates synaptic targeting of AMPA receptors by two distinct mechanisms. Nature 408: 936-943, 2000. ; and

[90123] Black, J. L., III; Lennon, V. A. : Identification and cloning of putative human neuronal voltage-gated calcium channel gamma-2 and gamma-3 subunits: neurologic implications. Mayo Clin.

[90124] Further studies establishing the function and utilities of CACNG2 are found in John Hopkins OMIM database record ID 602911, and in sited publications numbered 6188-6190 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.F-box and Leucine-rich Repeat Protein 3A (FBXL3A, Accession NM_012158) is another VGAM2680 host target gene. FBXL3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXL3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXL3A BINDING SITE, designated SEQ ID:14458, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90125] Another function of VGAM2680 is therefore inhibition of F-box and Leucine-rich Repeat Protein 3A (FBXL3A, Accession NM_012158), a gene which is a putative SCF ubiq-

uitin ligase subunit involved in protein degradation. Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXL3A. The function of FBXL3A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1172.Hepatocyte Growth Factor (hepapoietin A; scatter factor) (HGF, Accession XM_168542) is another VGAM2680 host target gene. HGF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HGF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HGF BINDING SITE, designated SEQ ID:45227, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90126] Another function of VGAM2680 is therefore inhibition of Hepatocyte Growth Factor (hepapoietin A; scatter factor) (HGF, Accession XM_168542), a gene which may be required for normal embryonic development; strongly similar to murine Hgf, has kringle domains. Accordingly, utilities of VGAM2680 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with HGF. The function of HGF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM174.Phosphorylase, Glycogen; Brain (PYGB, Accession NM_002862) is another VGAM2680 host target gene. PYGB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PYGB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PYGB BINDING SITE, designated SEQ ID:8765, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90127] Another function of VGAM2680 is therefore inhibition of Phosphorylase, Glycogen; Brain (PYGB, Accession NM_002862). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PYGB. DKFZp564K142 (Accession NM_032121) is another VGAM2680 host target gene. DKFZp564K142 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by DKFZp564K142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp564K142 BINDING SITE, designated SEQ ID:25806, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90128] Another function of VGAM2680 is therefore inhibition of DKFZp564K142 (Accession NM_032121). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp564K142. KIAA0429 (Accession NM_014751) is another VGAM2680 host target gene. KIAA0429 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0429, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0429 BINDING SITE, designated SEQ ID:16470, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90129] Another function of VGAM2680 is therefore inhibition of KIAA0429 (Accession NM_014751). Accordingly, utilities

of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0429. KIAA1691 (Accession XM_166523) is another VGAM2680 host target gene. KIAA1691 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1691, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1691 BINDING SITE, designated SEQ ID:44465, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90130] Another function of VGAM2680 is therefore inhibition of KIAA1691 (Accession XM_166523). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1691. MGC3248 (Accession NM_032486) is another VGAM2680 host target gene. MGC3248 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3248, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3248

BINDING SITE, designated SEQ ID:26233, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90131] Another function of VGAM2680 is therefore inhibition of MGC3248 (Accession NM_032486). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3248. Monocyte to Macrophage Differentiation-associated (MMD, Accession XM_008269) is another VGAM2680 host target gene. MMD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MMD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMD BINDING SITE, designated SEQ ID:30077, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90132] Another function of VGAM2680 is therefore inhibition of Monocyte to Macrophage Differentiation-associated (MMD, Accession XM_008269). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMD.

Phorbol-12-myristate-13-acetate-induced Protein 1 (PMAIP1, Accession NM_021127) is another VGAM2680 host target gene. PMAIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PMAIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMAIP1 BINDING SITE, designated SEQ ID:22103, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90133] Another function of VGAM2680 is therefore inhibition of Phorbol-12-myristate-13-acetate-induced Protein 1 (PMAIP1, Accession NM_021127). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMAIP1. PRO0611 (Accession NM_014076) is another VGAM2680 host target gene. PRO0611 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0611, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0611

BINDING SITE, designated SEQ ID:15303, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90134] Another function of VGAM2680 is therefore inhibition of PRO0611 (Accession NM_014076). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0611. SE57-1 (Accession NM_025214) is another VGAM2680 host target gene. SE57-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SE57-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SE57-1 BINDING SITE, designated SEQ ID:24891, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90135] Another function of VGAM2680 is therefore inhibition of SE57-1 (Accession NM_025214). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SE57-1. LOC127255 (Accession NM_145258) is another VGAM2680 host target gene. LOC127255 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127255 BINDING SITE, designated SEQ ID:29775, to the nucleotide sequence of VGAM2680 RNA, herein designated VGAM RNA, also designated SEQ ID:5391.

[90136] Another function of VGAM2680 is therefore inhibition of LOC127255 (Accession NM_145258). Accordingly, utilities of VGAM2680 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127255. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2681 (VGAM2681) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90137] VGAM2681 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2681 was detected is described hereinabove with reference to Figs. 1-8.

[90138] VGAM2681 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld. VGAM2681 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90139] VGAM2681 gene encodes a VGAM2681 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2681 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2681 precursor RNA is designated SEQ ID:2667, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2667 is located at position 2192 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld.

[90140] VGAM2681 precursor RNA folds onto itself, forming VGAM2681 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[90141] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2681 folded precursor RNA into VGAM2681 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2681 RNA is designated SEQ ID:5392, and is provided hereinbelow with reference to the sequence listing part.

[90142] VGAM2681 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2681 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90143] VGAM2681 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2681 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2681 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2681 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90144] The complementary binding of VGAM2681 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2681 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2681 host target RNA into VGAM2681 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90145] It is appreciated that VGAM2681 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2681 host target genes. The mRNA of each one of this plurality of VGAM2681 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2681 RNA, herein designated VGAM RNA, and which when bound by VGAM2681 RNA causes inhibition of translation of respective one or more VGAM2681 host target proteins.

[90146] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2681 gene, herein designated VGAM GENE, on one or more VGAM2681 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90147] It is yet further appreciated that a function of VGAM2681 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2681 include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2681 correlate with, and may be deduced from, the identity of the host target genes which VGAM2681 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90148] Nucleotide sequences of the VGAM2681 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2681 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2681 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2681 are further described hereinbelow with reference to Table 1.

[90149] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2681 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2681 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90150] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2681 gene, herein designated VGAM is inhibition of expression of VGAM2681 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2681 correlate with, and may be deduced from, the identity of the target genes which VGAM2681 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90151] FLJ13456 (Accession XM_038291) is a VGAM2681 host target gene. FLJ13456 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13456, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of FLJ13456 BINDING SITE, designated SEQ ID:32797, to the nucleotide sequence of VGAM2681 RNA, herein designated VGAM RNA, also designated SEQ ID:5392.

[90152] A function of VGAM2681 is therefore inhibition of FLJ13456 (Accession XM_038291). Accordingly, utilities of VGAM2681 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13456. KIAA1979 (Accession XM_113984) is another VGAM2681 host target gene. KIAA1979 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1979, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1979 BINDING SITE, designated SEQ ID:42590, to the nucleotide sequence of VGAM2681 RNA, herein designated VGAM RNA, also designated SEQ ID:5392.

[90153] Another function of VGAM2681 is therefore inhibition of KIAA1979 (Accession XM_113984). Accordingly, utilities of VGAM2681 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1979. MGC32104 (Accession NM_144684) is another

VGAM2681 host target gene. MGC32104 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC32104, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC32104 BINDING SITE, designated SEQ ID:29501, to the nucleotide sequence of VGAM2681 RNA, herein designated VGAM RNA, also designated SEQ ID:5392.

[90154] Another function of VGAM2681 is therefore inhibition of MGC32104 (Accession NM_144684). Accordingly, utilities of VGAM2681 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC32104. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2682 (VGAM2682) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90155] VGAM2682 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2682 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[90156] VGAM2682 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld. VGAM2682 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90157] VGAM2682 gene encodes a VGAM2682 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2682 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2682 precursor RNA is designated SEQ ID:2668, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2668 is located at position 1099 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld.

[90158] VGAM2682 precursor RNA folds onto itself, forming VGAM2682 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90159] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2682 folded precursor RNA into VGAM2682 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2682 RNA is designated SEQ ID:5393, and is provided hereinbelow with reference to the sequence listing part.

[90160] VGAM2682 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2682 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90161] VGAM2682 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2682 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2682 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2682 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90162] The complementary binding of VGAM2682 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2682 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2682 host target RNA into VGAM2682 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90163] It is appreciated that VGAM2682 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2682 host target genes. The mRNA of each one of this plurality of VGAM2682 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2682 RNA, herein designated VGAM RNA, and which when bound by VGAM2682 RNA causes inhibition of translation of respective one or more VGAM2682 host target proteins.

[90164] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2682 gene, herein designated VGAM GENE, on one or more VGAM2682 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90165] It is yet further appreciated that a function of VGAM2682 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2682 correlate with, and may be deduced from, the identity of the host target genes which VGAM2682 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90166] Nucleotide sequences of the VGAM2682 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2682 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2682 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2682 are further described hereinbelow with reference to Table 1.

[90167] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2682 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2682 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90168] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2682 gene, herein designated VGAM is inhibition of expression of VGAM2682 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2682 correlate with, and may be deduced from, the identity of the target genes which VGAM2682 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90169] Fc Fragment of IgA, Receptor For (FCAR, Accession NM_002000) is a VGAM2682 host target gene. FCAR BINDING SITE1 through FCAR BINDING SITE7 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FCAR, corresponding to HOST TARGET

binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE7, designated SEQ ID:7729, SEQ ID:28429, SEQ ID:28431, SEQ ID:28434, SEQ ID:28435, SEQ ID:28425 and SEQ ID:28427 respectively, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90170] A function of VGAM2682 is therefore inhibition of Fc Fragment of IgA, Receptor For (FCAR, Accession NM_002000), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCAR. The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM923.Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Eta Polypeptide (YWHAH, Accession NM_003405) is another VGAM2682 host target gene. YWHAH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by YWHAH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YWHAH BINDING SITE, designated SEQ ID:9440, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90171] Another function of VGAM2682 is therefore inhibition of Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Eta Polypeptide (YWHAH, Accession NM_003405), a gene which activates tyrosine and tryptophan hydroxylases in the presence of and strongly activates protein kinase c. Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YWHAH. The function of YWHAH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1923.Zinc Finger Protein 10 (KOX 1) (ZNF10, Accession NM_015394) is another VGAM2682 host target gene. ZNF10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF10, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF10 BINDING SITE, designated SEQ ID:17697, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90172] Another function of VGAM2682 is therefore inhibition of Zinc Finger Protein 10 (KOX 1) (ZNF10, Accession NM_015394), a gene which may function as a transcriptional regulator. Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF10. The function of ZNF10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM36.DC8 (Accession NM_015471) is another VGAM2682 host target gene. DC8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DC8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DC8 BINDING SITE, designated SEQ ID:17752, to the nucleotide sequence of VGAM2682 RNA, herein

designated VGAM RNA, also designated SEQ ID:5393.

[90173] Another function of VGAM2682 is therefore inhibition of DC8 (Accession NM_015471). Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DC8. DNA Cross-link Repair 1A (PSO2 homolog, S. cerevisiae) (DCLRE1A, Accession XM_044815) is another VGAM2682 host target gene. DCLRE1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCLRE1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCLRE1A BINDING SITE, designated SEQ ID:34283, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90174] Another function of VGAM2682 is therefore inhibition of DNA Cross-link Repair 1A (PSO2 homolog, S. cerevisiae) (DCLRE1A, Accession XM_044815). Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCLRE1A. FLJ10704 (Accession NM_018185) is another VGAM2682 host target gene. FLJ10704 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10704 BINDING SITE, designated SEQ ID:20035, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90175] Another function of VGAM2682 is therefore inhibition of FLJ10704 (Accession NM_018185). Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10704. FLJ23151 (Accession NM_024772) is another VGAM2682 host target gene. FLJ23151 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23151, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23151 BINDING SITE, designated SEQ ID:24136, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90176] Another function of VGAM2682 is therefore inhibition of

FLJ23151 (Accession NM_024772). Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23151. Nucleoporin 160kDa (NUP160, Accession XM_113678) is another VGAM2682 host target gene. NUP160 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUP160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUP160 BINDING SITE, designated SEQ ID:42328, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90177] Another function of VGAM2682 is therefore inhibition of Nucleoporin 160kDa (NUP160, Accession XM_113678). Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP160. LOC151996 (Accession XM_098151) is another VGAM2682 host target gene. LOC151996 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151996, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151996 BINDING SITE, designated SEQ ID:41417, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90178] Another function of VGAM2682 is therefore inhibition of LOC151996 (Accession XM_098151). Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151996. LOC221596 (Accession XM_166331) is another VGAM2682 host target gene. LOC221596 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221596, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221596 BINDING SITE, designated SEQ ID:44173, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90179] Another function of VGAM2682 is therefore inhibition of LOC221596 (Accession XM_166331). Accordingly, utilities of VGAM2682 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC221596. LOC256073 (Accession XM_172972) is another VGAM2682 host target gene. LOC256073 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256073 BINDING SITE, designated SEQ ID:46231, to the nucleotide sequence of VGAM2682 RNA, herein designated VGAM RNA, also designated SEQ ID:5393.

[90180] Another function of VGAM2682 is therefore inhibition of LOC256073 (Accession XM_172972). Accordingly, utilities of VGAM2682 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256073. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2683 (VGAM2683) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90181] VGAM2683 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2683 was detected is described hereinabove with reference to Figs. 1-8.

[90182] VGAM2683 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld. VGAM2683 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90183] VGAM2683 gene encodes a VGAM2683 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2683 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2683 precursor RNA is designated SEQ ID:2669, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2669 is located at position 2286 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 4-Ld.

[90184] VGAM2683 precursor RNA folds onto itself, forming VGAM2683 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90185] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2683 folded precursor RNA into VGAM2683 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2683 RNA is designated SEQ ID:5394, and is provided hereinbelow with reference to the sequence listing part.

[90186] VGAM2683 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2683 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90187] VGAM2683 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2683 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2683 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90188] The complementary binding of VGAM2683 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2683 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2683 host target RNA into VGAM2683 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90189] It is appreciated that VGAM2683 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2683 host target genes. The mRNA of each one of this plurality of VGAM2683 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2683 RNA, herein designated VGAM RNA, and which when bound by VGAM2683 RNA causes inhibition of translation of respective one or more VGAM2683 host target proteins.

[90190] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2683 gene, herein designated VGAM GENE, on one or more VGAM2683 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90191] It is yet further appreciated that a function of VGAM2683 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2683 include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGAM2683 correlate with, and may be deduced from, the identity of the host target genes which VGAM2683 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90192] Nucleotide sequences of the VGAM2683 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2683 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2683 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2683 are further described hereinbelow with reference to Table 1.

[90193] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2683 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2683 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90194] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2683 gene, herein designated VGAM is inhibition of expression of VGAM2683 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2683 correlate with, and may be deduced from, the identity of the target genes which VGAM2683 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90195] Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS, Accession NM_002076) is a VGAM2683 host target gene. GNS BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by GNS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNS BINDING SITE, designated SEQ ID:7855, to the nucleotide sequence of VGAM2683 RNA, herein designated VGAM RNA, also designated SEQ ID:5394.

[90196] A function of VGAM2683 is therefore inhibition of Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS, Accession NM_002076), a gene which hydrolyzes sulfate groups from glycosaminoglycans. Accordingly, utilities of VGAM2683 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNS. The function of GNS has been established by previous studies. Kresse et al. (1980) found that cultured skin fibroblasts from 2 patients with clinical features of the Sanfilippo syndrome accumulated excessive amounts of heparan sulfate and were unable to release sulfate from N-acetylglucosamine-6-sulfate linkages in heparan sulfate-derived oligosaccharides. Keratan sulfate-derived oligosaccharides bearing the same residue at the nonreducing end were normally degraded. Kinetic differences between the sulfatase activities of normal fibroblasts were

found. Thus, the N-acetylglucosamine-6-sulfate sulfatases degrading heparan sulfate and keratan sulfate are distinct. The activity directed against heparan sulfate is deficient in the new form of Sanfilippo syndrome, designated type D by Kresse et al. (1980). The fibroblasts were from a 7-year-old East Indian boy living in England and a 4-year-old girl from Sardinia. Both patients excreted excessive heparan sulfate in the urine. The boy was mentally retarded and had 'characteristic behavioral disturbances.' The girl showed coarse facies and hirsutism but was not mentally retarded. Gatti et al. (1982) concluded that MPS IIID cannot be distinguished clinically from the other forms of Sanfilippo syndrome. Autosomal recessive inheritance was considered confirmed. Stating that only 2 cases of MPS IIID had been reported in detail, Coppa et al. (1983) added 2 more. Both patients had a high percentage of heparan sulfate in the urinary glycosaminoglycans and severe deficiency of N-acetylglucosamine-6-sulfate sulfatase in cultured skin fibroblasts. One of the patients, who presented at age 9 years 8 months with a history of chronic diarrhea, was only mildly retarded. Kaplan and Wolfe (1987) reported the first cases of type D from North America--2 relatively mildly affected brothers. Neufeld

(1987) suggested that for the sake of simplicity the enzyme deficient in this disorder be termed N-acetylglucosamine 6-sulfatase. Freeman et al. (1987) reported purification and characterization of the enzyme deficient in MPS IIID. They identified 4 forms of the enzyme in liver, which were postulated to be due to differences in the state of processing of a large subunit. The catalytic properties were studied by Freeman and Hopwood (1987). Robertson et al. (1988) pointed out homology in nucleotide sequence to steroid sulfatase (OMIM Ref. No. 308100), a microsomal enzyme.

[90197] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[90198] Freeman, C.; Clements, P. R.; Hopwood, J. J. : Human liver N-acetylglucosamine-6-sulphate sulphatase: purification and characterization. Biochem. J. 246: 347-354, 1987. ; and

[90199] Kresse, H.; Paschke, E.; von Figura, K.; Gilberg, W.; Fuchs, W. : Sanfilippo disease type D: deficiency of N-acetylglucosamine-6-sulfate sulfatase required for heparan sulfate degradati.

[90200] Further studies establishing the function and utilities of

GNS are found in John Hopkins OMIM database record ID 252940, and in sited publications numbered 9242-9248, 656 and 9249-9252 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Myotubular Myopathy 1 (MTM1, Accession NM_000252) is another VGAM2683 host target gene. MTM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTM1 BINDING SITE, designated SEQ ID:5789, to the nucleotide sequence of VGAM2683 RNA, herein designated VGAM RNA, also designated SEQ ID:5394.

[90201] Another function of VGAM2683 is therefore inhibition of Myotubular Myopathy 1 (MTM1, Accession NM_000252). Accordingly, utilities of VGAM2683 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTM1. Chromosome 11 Open Reading Frame 21 (C11orf21, Accession NM_014144) is another VGAM2683 host target gene. C11orf21 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf21, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf21 BINDING SITE, designated SEQ ID:15425, to the nucleotide sequence of VGAM2683 RNA, herein designated VGAM RNA, also designated SEQ ID:5394.

[90202] Another function of VGAM2683 is therefore inhibition of Chromosome 11 Open Reading Frame 21 (C11orf21, Accession NM_014144). Accordingly, utilities of VGAM2683 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf21. Chromosome 20 Open Reading Frame 38 (C20orf38, Accession NM_018327) is another VGAM2683 host target gene. C20orf38 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf38, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf38 BINDING SITE, designated SEQ ID:20322, to the nucleotide sequence of VGAM2683 RNA, herein designated VGAM RNA, also designated SEQ ID:5394.

[90203] Another function of VGAM2683 is therefore inhibition of

Chromosome 20 Open Reading Frame 38 (C20orf38, Accession NM_018327). Accordingly, utilities of VGAM2683 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf38. DREV1 (Accession NM_016025) is another VGAM2683 host target gene. DREV1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DREV1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DREV1 BINDING SITE, designated SEQ ID:18107, to the nucleotide sequence of VGAM2683 RNA, herein designated VGAM RNA, also designated SEQ ID:5394.

[90204] Another function of VGAM2683 is therefore inhibition of DREV1 (Accession NM_016025). Accordingly, utilities of VGAM2683 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DREV1. FLJ10493 (Accession NM_018112) is another VGAM2683 host target gene. FLJ10493 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10493, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10493 BINDING SITE, designated SEQ ID:19884, to the nucleotide sequence of VGAM2683 RNA, herein designated VGAM RNA, also designated SEQ ID:5394.

[90205] Another function of VGAM2683 is therefore inhibition of FLJ10493 (Accession NM_018112). Accordingly, utilities of VGAM2683 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10493. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2684 (VGAM2684) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90206] VGAM2684 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2684 was detected is described hereinabove with reference to Figs. 1-8.

[90207] VGAM2684 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 5-Ld. VGAM2684 host target gene, herein des-

ignated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90208] VGAM2684 gene encodes a VGAM2684 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2684 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2684 precursor RNA is designated SEQ ID:2670, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2670 is located at position 706 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 5-Ld.

[90209] VGAM2684 precursor RNA folds onto itself, forming VGAM2684 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90210] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2684 folded precursor RNA into VGAM2684

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2684 RNA is designated SEQ ID:5395, and is provided hereinbelow with reference to the sequence listing part.

[90211] VGAM2684 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2684 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90212] VGAM2684 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2684 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2684 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90213] The complementary binding of VGAM2684 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2684 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2684 host target RNA into VGAM2684 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[90214] It is appreciated that VGAM2684 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2684 host target genes. The mRNA of each one of this plurality of VGAM2684 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2684 RNA, herein designated VGAM RNA, and which when bound by VGAM2684 RNA causes inhibition of translation of respective one or more VGAM2684 host target proteins.

[90215] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2684 gene, herein designated VGAM GENE, on one or more VGAM2684 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90216] It is yet further appreciated that a function of VGAM2684 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 5-Ld. Specific functions, and accordingly utilities, of VGAM2684 correlate with, and may be deduced from, the identity of the host target genes which VGAM2684 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90217] Nucleotide sequences of the VGAM2684 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2684 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2684 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2684 are further described hereinbelow with reference to Table 1.

[90218] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2684 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2684 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90219] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2684 gene, herein designated VGAM is inhibition of expression of VGAM2684 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2684 correlate with, and may be deduced from, the identity of the target genes which VGAM2684 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90220] Chediak-Higashi Syndrome 1 (CHS1, Accession NM_000081) is a VGAM2684 host target gene. CHS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHS1 BINDING SITE, designated SEQ ID:5526, to the nucleotide sequence of VGAM2684 RNA, herein designated

VGAM RNA, also designated SEQ ID:5395.

[90221] A function of VGAM2684 is therefore inhibition of Chediak-Higashi Syndrome 1 (CHS1, Accession NM_000081), a gene which may sort endosomal resident proteins into late multivesicular endosome. Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHS1. The function of CHS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.Homeo Box C11 (HOXC11, Accession XM_012215) is another VGAM2684 host target gene. HOXC11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HOXC11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXC11 BINDING SITE, designated SEQ ID:30209, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, also designated SEQ ID:5395.

[90222] Another function of VGAM2684 is therefore inhibition of Homeo Box C11 (HOXC11, Accession XM_012215), a gene

which interacts with the lactase-phlorizin hydrolase promoter. Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXC11. The function of HOXC11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2047.Mitogen-activated Protein Kinase 14 (MAPK14, Accession NM_001315) is another VGAM2684 host target gene. MAPK14 BINDING SITE1 through MAPK14 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MAPK14, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK14 BINDING SITE1 through MAPK14 BINDING SITE3, designated SEQ ID:7001, SEQ ID:29105 and SEQ ID:29112 respectively, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, also designated SEQ ID:5395.

[90223] Another function of VGAM2684 is therefore inhibition of Mitogen-activated Protein Kinase 14 (MAPK14, Accession NM_001315), a gene which is important for cytokine pro-

duction; responds to changes in extracellular osmolarity. Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK14. The function of MAPK14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM107.MGC14289 (Accession NM_080660) is another VGAM2684 host target gene. MGC14289 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC14289, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14289 BINDING SITE, designated SEQ ID:27946, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, also designated SEQ ID:5395.

[90224] Another function of VGAM2684 is therefore inhibition of MGC14289 (Accession NM_080660). Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14289. Myosin, Heavy Polypeptide 10, Non-muscle (MYH10, Accession XM_044702) is another VGAM2684

host target gene. MYH10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYH10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYH10 BINDING SITE, designated SEQ ID:34261, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, also designated SEQ ID:5395.

[90225] Another function of VGAM2684 is therefore inhibition of Myosin, Heavy Polypeptide 10, Non-muscle (MYH10, Accession XM_044702). Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYH10. Ubiquitin Specific Protease 10 (USP10, Accession XM_033922) is another VGAM2684 host target gene. USP10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP10 BINDING SITE, designated SEQ ID:31983, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA,

also designated SEQ ID:5395.

[90226] Another function of VGAM2684 is therefore inhibition of Ubiquitin Specific Protease 10 (USP10, Accession XM_033922). Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP10. LOC145368 (Accession XM_085112) is another VGAM2684 host target gene. LOC145368 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145368, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145368 BINDING SITE, designated SEQ ID:37827, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, also designated SEQ ID:5395.

[90227] Another function of VGAM2684 is therefore inhibition of LOC145368 (Accession XM_085112). Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145368. LOC150423 (Accession XM_086912) is another VGAM2684 host target gene. LOC150423 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC150423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150423 BINDING SITE, designated SEQ ID:38967, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, also designated SEQ ID:5395.

[90228] Another function of VGAM2684 is therefore inhibition of LOC150423 (Accession XM_086912). Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150423. LOC152343 (Accession XM_087441) is another VGAM2684 host target gene. LOC152343 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152343, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152343 BINDING SITE, designated SEQ ID:39261, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, also designated SEQ ID:5395.

[90229] Another function of VGAM2684 is therefore inhibition of LOC152343 (Accession XM_087441). Accordingly, utilities

of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152343. LOC197358 (Accession XM_113872) is another VGAM2684 host target gene. LOC197358 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197358, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197358 BINDING SITE, designated SEQ ID:42506, to the nucleotide sequence of VGAM2684 RNA, herein designated VGAM RNA, also designated SEQ ID:5395.

[90230] Another function of VGAM2684 is therefore inhibition of LOC197358 (Accession XM_113872). Accordingly, utilities of VGAM2684 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197358. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2685 (VGAM2685) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90231] VGAM2685 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2685 was detected is described hereinabove with reference to Figs. 1-8.

[90232] VGAM2685 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 5-Ld. VGAM2685 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90233] VGAM2685 gene encodes a VGAM2685 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2685 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2685 precursor RNA is designated SEQ ID:2671, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2671 is located at position 1580 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 5-Ld.

[90234] VGAM2685 precursor RNA folds onto itself, forming VGAM2685 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90235] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2685 folded precursor RNA into VGAM2685 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2685 RNA is designated SEQ ID:5396, and is provided hereinbelow with reference to the sequence listing part.

[90236] VGAM2685 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2685 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[90237] VGAM2685 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2685 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2685 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90238] The complementary binding of VGAM2685 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2685 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2685 host target RNA into VGAM2685 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90239] It is appreciated that VGAM2685 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2685 host target genes. The mRNA of each one of this plurality of VGAM2685 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2685 RNA, herein designated VGAM RNA, and which when bound by VGAM2685 RNA causes inhibition of translation of respective one or more VGAM2685 host target proteins.

[90240] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2685 gene, herein designated VGAM GENE, on one or more VGAM2685 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90241] It is yet further appreciated that a function of VGAM2685 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2685 include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 5-Ld. Specific functions, and accordingly utilities, of VGAM2685 correlate with, and may be deduced from, the identity of the host target genes which VGAM2685 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90242] Nucleotide sequences of the VGAM2685 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2685 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2685 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2685 are further described hereinbelow with reference to Table 1.

[90243] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2685 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2685 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90244] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2685 gene, herein designated VGAM is inhibition of expression of VGAM2685 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2685 correlate with, and may be deduced from, the identity of the target genes which VGAM2685 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90245] Melanoma Antigen, Family B, 4 (MAGEB4, Accession NM_002367) is a VGAM2685 host target gene. MAGEB4

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAGEB4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAGEB4 BINDING SITE, designated SEQ ID:8176, to the nucleotide sequence of VGAM2685 RNA, herein designated VGAM RNA, also designated SEQ ID:5396.

[90246] A function of VGAM2685 is therefore inhibition of Melanoma Antigen, Family B, 4 (MAGEB4, Accession NM_002367). Accordingly, utilities of VGAM2685 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGEB4. Claudin 1 (CLDN1, Accession NM_021101) is another VGAM2685 host target gene. CLDN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLDN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLDN1 BINDING SITE, designated SEQ ID:22083, to the nucleotide sequence of VGAM2685 RNA, herein designated VGAM RNA, also designated SEQ

ID:5396.

[90247] Another function of VGAM2685 is therefore inhibition of Claudin 1 (CLDN1, Accession NM_021101). Accordingly, utilities of VGAM2685 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN1. RNA Binding Motif Protein 7 (RBM7, Accession NM_016090) is another VGAM2685 host target gene. RBM7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBM7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBM7 BINDING SITE, designated SEQ ID:18178, to the nucleotide sequence of VGAM2685 RNA, herein designated VGAM RNA, also designated SEQ ID:5396.

[90248] Another function of VGAM2685 is therefore inhibition of RNA Binding Motif Protein 7 (RBM7, Accession NM_016090). Accordingly, utilities of VGAM2685 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBM7. LOC92497 (Accession XM_045436) is another VGAM2685 host target gene. LOC92497 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by LOC92497, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92497 BINDING SITE, designated SEQ ID:34460, to the nucleotide sequence of VGAM2685 RNA, herein designated VGAM RNA, also designated SEQ ID:5396.

[90249] Another function of VGAM2685 is therefore inhibition of LOC92497 (Accession XM_045436). Accordingly, utilities of VGAM2685 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92497. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2686 (VGAM2686) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90250] VGAM2686 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2686 was detected is described hereinabove with reference to Figs. 1-8.

[90251] VGAM2686 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Ophiostoma Novo-ulmi Mitovirus 5-Ld. VGAM2686 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90252] VGAM2686 gene encodes a VGAM2686 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2686 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2686 precursor RNA is designated SEQ ID:2672, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2672 is located at position 328 relative to the genome of Ophiostoma Novo-ulmi Mitovirus 5-Ld.

[90253] VGAM2686 precursor RNA folds onto itself, forming VGAM2686 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90254] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2686 folded precursor RNA into VGAM2686 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2686 RNA is designated SEQ ID:5397, and is provided hereinbelow with reference to the sequence listing part.

[90255] VGAM2686 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2686 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90256] VGAM2686 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2686 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2686 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90257] The complementary binding of VGAM2686 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2686 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2686

host target RNA into VGAM2686 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90258] It is appreciated that VGAM2686 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2686 host target genes. The mRNA of each one of this plurality of VGAM2686 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2686 RNA, herein designated VGAM RNA, and which when bound by VGAM2686 RNA causes inhibition of translation of respective one or more VGAM2686 host target proteins.

[90259] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2686 gene, herein designated VGAM GENE, on one or more VGAM2686 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90260] It is yet further appreciated that a function of VGAM2686 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2686 include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 5-Ld. Specific functions, and accordingly utilities, of VGAM2686 correlate with, and may be deduced from, the identity of the host target genes which VGAM2686 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90261] Nucleotide sequences of the VGAM2686 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2686 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2686 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2686 are further

described hereinbelow with reference to Table 1.

[90262] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2686 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2686 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90263] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2686 gene, herein designated VGAM is inhibition of expression of VGAM2686 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2686 correlate with, and may be deduced from, the identity of the target genes which VGAM2686 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90264] Calnexin (CANX, Accession XM_113469) is a VGAM2686 host target gene. CANX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CANX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CANX BINDING SITE, desig-

nated SEQ ID:42277, to the nucleotide sequence of VGAM2686 RNA, herein designated VGAM RNA, also designated SEQ ID:5397.

[90265] A function of VGAM2686 is therefore inhibition of Calnexin (CANX, Accession XM_113469), a gene which may function as a chaperone in the endoplasmic reticulum, involved in the secretion of proteins from the ER to the outer cellular membrane. Accordingly, utilities of VGAM2686 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CANX. The function of CANX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM116.Nuclear Receptor Coactivator 6 Interacting Protein (NCOA6IP, Accession NM_024831) is another VGAM2686 host target gene. NCOA6IP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NCOA6IP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA6IP BINDING SITE, designated SEQ ID:24227, to the nucleotide sequence of VGAM2686 RNA, herein designated VGAM

RNA, also designated SEQ ID:5397.

[90266] Another function of VGAM2686 is therefore inhibition of Nuclear Receptor Coactivator 6 Interacting Protein (NCOA6IP, Accession NM_024831). Accordingly, utilities of VGAM2686 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6IP. EPLIN (Accession NM_016357) is another VGAM2686 host target gene. EPLIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPLIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPLIN BINDING SITE, designated SEQ ID:18497, to the nucleotide sequence of VGAM2686 RNA, herein designated VGAM RNA, also designated SEQ ID:5397.

[90267] Another function of VGAM2686 is therefore inhibition of EPLIN (Accession NM_016357). Accordingly, utilities of VGAM2686 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPLIN. LOC253970 (Accession XM_172910) is another VGAM2686 host target gene. LOC253970 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC253970, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253970 BINDING SITE, designated SEQ ID:46172, to the nucleotide sequence of VGAM2686 RNA, herein designated VGAM RNA, also designated SEQ ID:5397.

[90268] Another function of VGAM2686 is therefore inhibition of LOC253970 (Accession XM_172910). Accordingly, utilities of VGAM2686 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253970. LOC57826 (Accession NM_021183) is another VGAM2686 host target gene. LOC57826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57826 BINDING SITE, designated SEQ ID:22162, to the nucleotide sequence of VGAM2686 RNA, herein designated VGAM RNA, also designated SEQ ID:5397.

[90269] Another function of VGAM2686 is therefore inhibition of LOC57826 (Accession NM_021183). Accordingly, utilities

of VGAM2686 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57826. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2687 (VGAM2687) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90270] VGAM2687 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2687 was detected is described hereinabove with reference to Figs. 1-8.

[90271] VGAM2687 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Southern Bean Mosaic Virus. VGAM2687 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90272] VGAM2687 gene encodes a VGAM2687 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2687 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2687 precursor RNA is designated SEQ ID:2673, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2673 is located at position 820 relative to the genome of Southern Bean Mosaic Virus.

[90273] VGAM2687 precursor RNA folds onto itself, forming VGAM2687 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90274] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2687 folded precursor RNA into VGAM2687 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2687 RNA is designated SEQ ID:5398, and

is provided hereinbelow with reference to the sequence listing part.

[90275] VGAM2687 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2687 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90276] VGAM2687 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2687 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2687 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90277] The complementary binding of VGAM2687 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2687 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2687 host target RNA into VGAM2687 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90278] It is appreciated that VGAM2687 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2687 host target genes. The mRNA of each one of this plurality of VGAM2687 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2687 RNA, herein designated VGAM RNA, and which when bound by VGAM2687 RNA causes inhibition of translation of respective one or more VGAM2687 host target proteins.

[90279] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2687 gene, herein designated VGAM GENE, on one or more VGAM2687 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90280] It is yet further appreciated that a function of VGAM2687 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2687 include diagnosis, prevention and treatment of viral infection by Southern Bean Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2687 correlate with, and may be deduced from, the identity of the host target genes which VGAM2687 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90281] Nucleotide sequences of the VGAM2687 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2687 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2687 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2687 are further described hereinbelow with reference to Table 1.

[90282] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2687 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2687 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90283] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2687 gene, herein designated VGAM is inhibition of expression of VGAM2687 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2687 correlate with, and may be deduced from, the identity of the target genes which VGAM2687 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90284] Fanconi Anemia, Complementation Group F (FANCF, Accession NM_022725) is a VGAM2687 host target gene. FANCF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FANCF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FANCF BINDING SITE, designated SEQ ID:22924, to the nucleotide sequence of VGAM2687 RNA, herein designated VGAM RNA, also designated SEQ ID:5398.

[90285] A function of VGAM2687 is therefore inhibition of Fanconi Anemia, Complementation Group F (FANCF, Accession NM_022725). Accordingly, utilities of VGAM2687 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCF. FLJ10895

(Accession NM_019084) is another VGAM2687 host target gene. FLJ10895 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10895 BINDING SITE, designated SEQ ID:21157, to the nucleotide sequence of VGAM2687 RNA, herein designated VGAM RNA, also designated SEQ ID:5398.

[90286] Another function of VGAM2687 is therefore inhibition of FLJ10895 (Accession NM_019084). Accordingly, utilities of VGAM2687 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10895. Glutamic Pyruvate Transaminase (alanine aminotransferase) 2 (GPT2, Accession NM_133443) is another VGAM2687 host target gene. GPT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPT2 BINDING SITE, designated SEQ ID:28521, to the nucleotide se-

quence of VGAM2687 RNA, herein designated VGAM RNA, also designated SEQ ID:5398.

[90287] Another function of VGAM2687 is therefore inhibition of Glutamic Pyruvate Transaminase (alanine aminotransferase) 2 (GPT2, Accession NM_133443). Accordingly, utilities of VGAM2687 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPT2. KIAA1676 (Accession XM_167612) is another VGAM2687 host target gene. KIAA1676 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1676 BINDING SITE, designated SEQ ID:44728, to the nucleotide sequence of VGAM2687 RNA, herein designated VGAM RNA, also designated SEQ ID:5398.

[90288] Another function of VGAM2687 is therefore inhibition of KIAA1676 (Accession XM_167612). Accordingly, utilities of VGAM2687 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1676. LOC200609 (Accession XM_117256) is another VGAM2687 host target gene. LOC200609 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200609, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200609 BINDING SITE, designated SEQ ID:43332, to the nucleotide sequence of VGAM2687 RNA, herein designated VGAM RNA, also designated SEQ ID:5398.

[90289] Another function of VGAM2687 is therefore inhibition of LOC200609 (Accession XM_117256). Accordingly, utilities of VGAM2687 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200609. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2688 (VGAM2688) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90290] VGAM2688 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2688 was detected is described hereinabove with reference to Figs. 1-8.

[90291] VGAM2688 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Southern Bean Mosaic Virus. VGAM2688 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90292] VGAM2688 gene encodes a VGAM2688 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2688 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2688 precursor RNA is designated SEQ ID:2674, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2674 is located at position 2629 relative to the genome of Southern Bean Mosaic Virus.

[90293] VGAM2688 precursor RNA folds onto itself, forming VGAM2688 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[90294] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2688 folded precursor RNA into VGAM2688 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2688 RNA is designated SEQ ID:5399, and is provided hereinbelow with reference to the sequence listing part.

[90295] VGAM2688 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2688 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90296] VGAM2688 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2688 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2688 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2688 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90297] The complementary binding of VGAM2688 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2688 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2688 host target RNA into VGAM2688 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90298] It is appreciated that VGAM2688 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2688 host target genes. The mRNA of each one of this plurality of VGAM2688 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2688 RNA, herein designated VGAM RNA, and which when bound by VGAM2688 RNA causes inhibition of translation of respective one or more VGAM2688 host target proteins.

[90299] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2688 gene, herein designated VGAM GENE, on one or more VGAM2688 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90300] It is yet further appreciated that a function of VGAM2688 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2688 include diagnosis, prevention and treatment of viral infection by Southern Bean Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2688 correlate with, and may be deduced from, the identity of the host target genes which VGAM2688 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90301] Nucleotide sequences of the VGAM2688 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2688 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2688 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2688 are further described hereinbelow with reference to Table 1.

[90302] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2688 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2688 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90303] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2688 gene, herein designated VGAM is inhibition of expression of VGAM2688 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2688 correlate with, and may be deduced from, the identity of the target genes which VGAM2688 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90304] Coagulation Factor II (thrombin) Receptor-like 3 (F2RL3, Accession NM_003950) is a VGAM2688 host target gene. F2RL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by F2RL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of F2RL3 BINDING SITE, designated SEQ ID:10080, to the nucleotide sequence of VGAM2688 RNA, herein designated VGAM RNA, also designated SEQ ID:5399.

[90305] A function of VGAM2688 is therefore inhibition of Coagulation Factor II (thrombin) Receptor-like 3 (F2RL3, Accession NM_003950), a gene which Protease-activated receptor 4; G protein-coupled receptor that increases phosphoinositide hydrolysis. Accordingly, utilities of VGAM2688 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL3. The function of F2RL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM193.FLJ10520 (Accession NM_018124) is another VGAM2688 host target gene. FLJ10520 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:19903, to the nucleotide

sequence of VGAM2688 RNA, herein designated VGAM RNA, also designated SEQ ID:5399.

[90306] Another function of VGAM2688 is therefore inhibition of FLJ10520 (Accession NM_018124). Accordingly, utilities of VGAM2688 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520. KIAA0451 (Accession NM_014826) is another VGAM2688 host target gene. KIAA0451 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0451, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0451 BINDING SITE, designated SEQ ID:16808, to the nucleotide sequence of VGAM2688 RNA, herein designated VGAM RNA, also designated SEQ ID:5399.

[90307] Another function of VGAM2688 is therefore inhibition of KIAA0451 (Accession NM_014826). Accordingly, utilities of VGAM2688 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0451. Splicing Factor, Arginine/serine-rich 11 (SFRS11, Accession NM_004768) is another VGAM2688 host target gene. SFRS11 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by SFRS11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS11 BINDING SITE, designated SEQ ID:11157, to the nucleotide sequence of VGAM2688 RNA, herein designated VGAM RNA, also designated SEQ ID:5399.

[90308] Another function of VGAM2688 is therefore inhibition of Splicing Factor, Arginine/serine-rich 11 (SFRS11, Accession NM_004768). Accordingly, utilities of VGAM2688 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS11. LOC149271 (Accession XM_086475) is another VGAM2688 host target gene. LOC149271 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149271 BINDING SITE, designated SEQ ID:38675, to the nucleotide sequence of VGAM2688 RNA, herein designated VGAM RNA, also designated SEQ ID:5399.

[90309] Another function of VGAM2688 is therefore inhibition of LOC149271 (Accession XM_086475). Accordingly, utilities of VGAM2688 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149271. LOC255196 (Accession XM_173157) is another VGAM2688 host target gene. LOC255196 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255196 BINDING SITE, designated SEQ ID:46411, to the nucleotide sequence of VGAM2688 RNA, herein designated VGAM RNA, also designated SEQ ID:5399.

[90310] Another function of VGAM2688 is therefore inhibition of LOC255196 (Accession XM_173157). Accordingly, utilities of VGAM2688 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255196. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2689 (VGAM2689) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[90311] VGAM2689 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2689 was detected is described hereinabove with reference to Figs. 1-8.

[90312] VGAM2689 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Southern Bean Mosaic Virus. VGAM2689 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90313] VGAM2689 gene encodes a VGAM2689 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2689 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2689 precursor RNA is designated SEQ ID:2675, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2675 is located at position 649 relative to the genome of Southern Bean Mosaic Virus.

[90314] VGAM2689 precursor RNA folds onto itself, forming VGAM2689 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90315] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2689 folded precursor RNA into VGAM2689 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2689 RNA is designated SEQ ID:5400, and is provided hereinbelow with reference to the sequence listing part.

[90316] VGAM2689 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2689 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90317] VGAM2689 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2689 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2689 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90318] The complementary binding of VGAM2689 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2689 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2689 host target RNA into VGAM2689 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90319] It is appreciated that VGAM2689 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2689 host target genes. The mRNA of each one of this plurality of VGAM2689 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2689 RNA, herein designated VGAM RNA, and which when bound by VGAM2689 RNA causes inhibition of translation of respective one or more VGAM2689 host target proteins.

[90320] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2689 gene, herein designated VGAM GENE, on one or more VGAM2689 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90321] It is yet further appreciated that a function of VGAM2689 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of viral infection by Southern Bean Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2689 correlate with, and may be deduced from, the identity of the host target genes which VGAM2689 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[90322] Nucleotide sequences of the VGAM2689 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2689 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2689 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2689 are further described hereinbelow with reference to Table 1.

[90323] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2689 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2689 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90324] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2689 gene, herein designated VGAM is inhibition of expression of VGAM2689 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2689 correlate with, and may be deduced from, the identity of the target genes which VGAM2689 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90325] E1A Binding Protein P300 (EP300, Accession NM_001429) is a VGAM2689 host target gene. EP300 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EP300, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EP300 BINDING SITE, designated SEQ ID:7148, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90326] A function of VGAM2689 is therefore inhibition of E1A Binding Protein P300 (EP300, Accession NM_001429), a gene which may have a function in cell cycle regulation. Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EP300. The function of EP300 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.Heme Oxygenase (decycling) 1 (HMOX1, Accession NM_002133) is another VGAM2689 host target gene. HMOX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMOX1, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMOX1 BINDING SITE, designated SEQ ID:7910, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90327] Another function of VGAM2689 is therefore inhibition of Heme Oxygenase (decycling) 1 (HMOX1, Accession NM_002133). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMOX1. Retinoid X Receptor, Alpha (RXRA, Accession NM_002957) is another VGAM2689 host target gene. RXRA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RXRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RXRA BINDING SITE, designated SEQ ID:8867, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90328] Another function of VGAM2689 is therefore inhibition of Retinoid X Receptor, Alpha (RXRA, Accession NM_002957),

a gene which activates genes required for vitamin A metabolism, binds 9-cis retinoic acid. Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RXRA. The function of RXRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM349.Tumor Necrosis Factor (ligand) Superfamily, Member 15 (TNFSF15, Accession NM_005118) is another VGAM2689 host target gene. TNFSF15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFSF15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF15 BINDING SITE, designated SEQ ID:11601, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90329] Another function of VGAM2689 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 15 (TNFSF15, Accession NM_005118), a gene which acts as an autocrine factor to induce apoptosis in endothelial cells. Accordingly, utilities of VGAM2689 include diagno-

sis, prevention and treatment of diseases and clinical conditions associated with TNFSF15. The function of TNFSF15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM350.Vesicle Amine Transport Protein 1 Homolog (T californica) (VAT1, Accession NM_006373) is another VGAM2689 host target gene. VAT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VAT1 BINDING SITE, designated SEQ ID:13067, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90330] Another function of VGAM2689 is therefore inhibition of Vesicle Amine Transport Protein 1 Homolog (T californica) (VAT1, Accession NM_006373), a gene which is a membrane protein of cholinergic synaptic vesicles. Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VAT1. The function of VAT1 and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM212.Diacylglycerol Kinase, Zeta 104kDa (DGKZ, Accession NM_003646) is another VGAM2689 host target gene. DGKZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGKZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKZ BINDING SITE, designated SEQ ID:9720, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90331] Another function of VGAM2689 is therefore inhibition of Diacylglycerol Kinase, Zeta 104kDa (DGKZ, Accession NM_003646). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKZ. DKFZP434F0318 (Accession NM_030817) is another VGAM2689 host target gene. DKFZP434F0318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F0318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE, designated SEQ ID:25140, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90332] Another function of VGAM2689 is therefore inhibition of DKFZP434F0318 (Accession NM_030817). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F0318. FLJ20034 (Accession NM_017630) is another VGAM2689 host target gene. FLJ20034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20034 BINDING SITE, designated SEQ ID:19131, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90333] Another function of VGAM2689 is therefore inhibition of FLJ20034 (Accession NM_017630). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20034. FLJ20188 (Accession NM_017703) is another

VGAM2689 host target gene. FLJ20188 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20188, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20188 BINDING SITE, designated SEQ ID:19276, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90334] Another function of VGAM2689 is therefore inhibition of FLJ20188 (Accession NM_017703). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20188. KIAA1317 (Accession XM_098368) is another VGAM2689 host target gene. KIAA1317 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1317 BINDING SITE, designated SEQ ID:41626, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90335] Another function of VGAM2689 is therefore inhibition of KIAA1317 (Accession XM_098368). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1317. KIAA1813 (Accession XM_046743) is another VGAM2689 host target gene. KIAA1813 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1813 BINDING SITE, designated SEQ ID:34811, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90336] Another function of VGAM2689 is therefore inhibition of KIAA1813 (Accession XM_046743). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1813. Keratin Associated Protein 1-5 (KRTAP1-5, Accession NM_031957) is another VGAM2689 host target gene. KRTAP1-5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KRTAP1-5, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KRTAP1-5 BINDING SITE, designated SEQ ID:25698, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90337] Another function of VGAM2689 is therefore inhibition of Keratin Associated Protein 1-5 (KRTAP1-5, Accession NM_031957). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KRTAP1-5. MAGE-E1 (Accession NM_030801) is another VGAM2689 host target gene. MAGE-E1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAGE-E1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAGE-E1 BINDING SITE, designated SEQ ID:25104, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90338] Another function of VGAM2689 is therefore inhibition of MAGE-E1 (Accession NM_030801). Accordingly, utilities of

VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGE-E1. moblak (Accession NM_130807) is another VGAM2689 host target gene. moblak BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by moblak, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of moblak BINDING SITE, designated SEQ ID:28306, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90339] Another function of VGAM2689 is therefore inhibition of moblak (Accession NM_130807). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with moblak. Myosin, Heavy Polypeptide 10, Non-muscle (MYH10, Accession XM_044702) is another VGAM2689 host target gene. MYH10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYH10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of MYH10 BINDING SITE, designated SEQ ID:34262, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90340] Another function of VGAM2689 is therefore inhibition of Myosin, Heavy Polypeptide 10, Non-muscle (MYH10, Accession XM_044702). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYH10. TBC1 Domain Family, Member 2 (TBC1D2, Accession NM_018421) is another VGAM2689 host target gene. TBC1D2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TBC1D2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBC1D2 BINDING SITE, designated SEQ ID:20465, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90341] Another function of VGAM2689 is therefore inhibition of TBC1 Domain Family, Member 2 (TBC1D2, Accession NM_018421). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TBC1D2. Tyrosine Kinase, Non-receptor, 1 (TNK1, Accession NM_003985) is another VGAM2689 host target gene. TNK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNK1 BINDING SITE, designated SEQ ID:10135, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90342] Another function of VGAM2689 is therefore inhibition of Tyrosine Kinase, Non-receptor, 1 (TNK1, Accession NM_003985). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNK1. LOC146774 (Accession XM_085584) is another VGAM2689 host target gene. LOC146774 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146774, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146774 BINDING SITE, desig-

nated SEQ ID:38235, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90343] Another function of VGAM2689 is therefore inhibition of LOC146774 (Accession XM_085584). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146774. LOC150290 (Accession XM_086863) is another VGAM2689 host target gene. LOC150290 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150290, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150290 BINDING SITE, designated SEQ ID:38931, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90344] Another function of VGAM2689 is therefore inhibition of LOC150290 (Accession XM_086863). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150290. LOC155064 (Accession XM_088128) is another VGAM2689 host target gene. LOC155064 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC155064, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155064 BINDING SITE, designated SEQ ID:39528, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90345] Another function of VGAM2689 is therefore inhibition of LOC155064 (Accession XM_088128). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155064. LOC256477 (Accession XM_173324) is another VGAM2689 host target gene. LOC256477 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256477, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256477 BINDING SITE, designated SEQ ID:46535, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90346] Another function of VGAM2689 is therefore inhibition of

LOC256477 (Accession XM_173324). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256477. LOC257465 (Accession XM_088384) is another VGAM2689 host target gene. LOC257465 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257465 BINDING SITE, designated SEQ ID:39666, to the nucleotide sequence of VGAM2689 RNA, herein designated VGAM RNA, also designated SEQ ID:5400.

[90347] Another function of VGAM2689 is therefore inhibition of LOC257465 (Accession XM_088384). Accordingly, utilities of VGAM2689 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257465. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2690 (VGAM2690) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[90348] VGAM2690 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2690 was detected is described hereinabove with reference to Figs. 1-8.

[90349] VGAM2690 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea Operculella Granulovirus. VGAM2690 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90350] VGAM2690 gene encodes a VGAM2690 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2690 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2690 precursor RNA is designated SEQ ID:2676, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2676 is located at position 69388 relative to the genome of Phthorimaea Operculella Granulovirus.

[90351] VGAM2690 precursor RNA folds onto itself, forming VGAM2690 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90352] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2690 folded precursor RNA into VGAM2690 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2690 RNA is designated SEQ ID:5401, and is provided hereinbelow with reference to the sequence listing part.

[90353] VGAM2690 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2690 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90354] VGAM2690 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2690 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2690 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[90355] The complementary binding of VGAM2690 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2690 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2690 host target RNA into VGAM2690 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90356] It is appreciated that VGAM2690 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2690 host target genes. The mRNA of each one of this plurality of VGAM2690 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2690 RNA, herein designated VGAM RNA, and which when bound by VGAM2690 RNA causes inhibition of translation of respective one or more VGAM2690 host target proteins.

[90357] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2690 gene, herein designated VGAM GENE, on one

or more VGAM2690 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90358] It is yet further appreciated that a function of VGAM2690 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2690 include diagnosis, prevention and treatment of viral infection by Phthorimaea Operculella Granulovirus. Specific functions, and accordingly utilities, of VGAM2690 correlate with, and may be deduced from, the identity of the host target genes which VGAM2690 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90359] Nucleotide sequences of the VGAM2690 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2690 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2690 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2690 are further described hereinbelow with reference to Table 1.

[90360] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2690 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2690 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90361] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2690 gene, herein designated VGAM is inhibition of expression of VGAM2690 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2690 correlate with, and may be deduced from, the identity of the target genes which VGAM2690 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90362] COX11 Homolog, Cytochrome C Oxidase Assembly Protein

(yeast) (COX11, Accession NM_004375) is a VGAM2690 host target gene. COX11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COX11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COX11 BINDING SITE, designated SEQ ID:10596, to the nucleotide sequence of VGAM2690 RNA, herein designated VGAM RNA, also designated SEQ ID:5401.

[90363] A function of VGAM2690 is therefore inhibition of COX11 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX11, Accession NM_004375). Accordingly, utilities of VGAM2690 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COX11. CEGP1 (Accession NM_020974) is another VGAM2690 host target gene. CEGP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CEGP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CEGP1 BINDING SITE, designated SEQ ID:21958, to the nucleotide sequence of VGAM2690 RNA,

herein designated VGAM RNA, also designated SEQ ID:5401.

[90364] Another function of VGAM2690 is therefore inhibition of CEGP1 (Accession NM_020974). Accordingly, utilities of VGAM2690 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEGP1. KIAA1061 (Accession XM_048786) is another VGAM2690 host target gene. KIAA1061 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1061, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1061 BINDING SITE, designated SEQ ID:35264, to the nucleotide sequence of VGAM2690 RNA, herein designated VGAM RNA, also designated SEQ ID:5401.

[90365] Another function of VGAM2690 is therefore inhibition of KIAA1061 (Accession XM_048786). Accordingly, utilities of VGAM2690 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1061. KIAA1211 (Accession XM_044178) is another VGAM2690 host target gene. KIAA1211 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1211, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1211 BINDING SITE, designated SEQ ID:34159, to the nucleotide sequence of VGAM2690 RNA, herein designated VGAM RNA, also designated SEQ ID:5401.

[90366] Another function of VGAM2690 is therefore inhibition of KIAA1211 (Accession XM_044178). Accordingly, utilities of VGAM2690 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1211. LOC163231 (Accession XM_092094) is another VGAM2690 host target gene. LOC163231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163231 BINDING SITE, designated SEQ ID:40093, to the nucleotide sequence of VGAM2690 RNA, herein designated VGAM RNA, also designated SEQ ID:5401.

[90367] Another function of VGAM2690 is therefore inhibition of LOC163231 (Accession XM_092094). Accordingly, utilities

of VGAM2690 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163231. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2691 (VGAM2691) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90368] VGAM2691 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2691 was detected is described hereinabove with reference to Figs. 1-8.

[90369] VGAM2691 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea Operculella Granulovirus. VGAM2691 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90370] VGAM2691 gene encodes a VGAM2691 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2691 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2691 precursor RNA is designated SEQ ID:2677, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2677 is located at position 68718 relative to the genome of Phthorimaea Operculella Granulovirus.

[90371] VGAM2691 precursor RNA folds onto itself, forming VGAM2691 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90372] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2691 folded precursor RNA into VGAM2691 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2691 RNA is designated SEQ ID:5402, and

is provided hereinbelow with reference to the sequence listing part.

[90373] VGAM2691 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2691 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90374] VGAM2691 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2691 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2691 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90375] The complementary binding of VGAM2691 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2691 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2691 host target RNA into VGAM2691 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90376] It is appreciated that VGAM2691 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2691 host target genes. The mRNA of each one of this plurality of VGAM2691 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2691 RNA, herein designated VGAM RNA, and which when bound by VGAM2691 RNA causes inhibition of translation of respective one or more VGAM2691 host target proteins.

[90377] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2691 gene, herein designated VGAM GENE, on one or more VGAM2691 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90378] It is yet further appreciated that a function of VGAM2691 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2691 include diagnosis, prevention and treatment of viral infection by Phthorimaea Operculella Granulovirus. Specific functions, and accordingly utilities, of VGAM2691 correlate with, and may be deduced from, the identity of the host target genes which VGAM2691 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90379] Nucleotide sequences of the VGAM2691 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2691 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2691 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2691 are further described hereinbelow with reference to Table 1.

[90380] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2691 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2691 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90381] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2691 gene, herein designated VGAM is inhibition of expression of VGAM2691 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2691 correlate with, and may be deduced from, the identity of the target genes which VGAM2691 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90382] Reserved (C8orf13, Accession XM_088377) is a VGAM2691 host target gene. C8orf13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C8orf13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C8orf13 BINDING SITE, designated SEQ ID:39651, to the nucleotide sequence of VGAM2691 RNA, herein designated VGAM RNA, also designated SEQ ID:5402.

[90383] A function of VGAM2691 is therefore inhibition of Reserved (C8orf13, Accession XM_088377). Accordingly, utilities of VGAM2691 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf13. PP35 (Accession NM_007016) is another VGAM2691 host target gene. PP35 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by PP35, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP35 BINDING SITE, designated SEQ ID:13871, to the nucleotide sequence of VGAM2691 RNA, herein designated VGAM RNA, also designated SEQ ID:5402.

[90384] Another function of VGAM2691 is therefore inhibition of PP35 (Accession NM_007016). Accordingly, utilities of VGAM2691 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP35. LOC200014 (Accession XM_114087) is another VGAM2691 host target gene. LOC200014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200014 BINDING SITE, designated SEQ ID:42686, to the nucleotide sequence of VGAM2691 RNA, herein designated VGAM RNA, also designated SEQ ID:5402.

[90385] Another function of VGAM2691 is therefore inhibition of

LOC200014 (Accession XM_114087). Accordingly, utilities of VGAM2691 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200014. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2692 (VGAM2692) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90386] VGAM2692 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2692 was detected is described hereinabove with reference to Figs. 1-8.

[90387] VGAM2692 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea Operculella Granulovirus. VGAM2692 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90388] VGAM2692 gene encodes a VGAM2692 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2692 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2692 precursor RNA is designated SEQ ID:2678, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2678 is located at position 70677 relative to the genome of Phthorimaea Operculella Granulovirus.

[90389] VGAM2692 precursor RNA folds onto itself, forming VGAM2692 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90390] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2692 folded precursor RNA into VGAM2692 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide se-

quence of VGAM2692 RNA is designated SEQ ID:5403, and is provided hereinbelow with reference to the sequence listing part.

[90391] VGAM2692 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2692 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90392] VGAM2692 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2692 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2692 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90393] The complementary binding of VGAM2692 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2692 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2692 host target RNA into VGAM2692 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90394] It is appreciated that VGAM2692 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2692 host target genes. The mRNA of each one of this plurality of VGAM2692 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2692 RNA, herein designated VGAM RNA, and which when bound by VGAM2692 RNA causes inhibition of translation of respective one or more VGAM2692 host target proteins.

[90395] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2692 gene, herein designated VGAM GENE, on one or more VGAM2692 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90396] It is yet further appreciated that a function of VGAM2692

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of viral infection by Phthorimaea Operculella Granulovirus. Specific functions, and accordingly utilities, of VGAM2692 correlate with, and may be deduced from, the identity of the host target genes which VGAM2692 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90397] Nucleotide sequences of the VGAM2692 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2692 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2692 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2692 are further described hereinbelow with reference to Table 1.

[90398] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2692 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2692 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90399] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2692 gene, herein designated VGAM is inhibition of expression of VGAM2692 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2692 correlate with, and may be deduced from, the identity of the target genes which VGAM2692 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90400] F-box and WD-40 Domain Protein 1B (FBXW1B, Accession NM_012300) is a VGAM2692 host target gene. FBXW1B BINDING SITE1 through FBXW1B BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FBXW1B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXW1B BINDING SITE1 through FBXW1B BINDING SITE3, designated SEQ ID:14667, SEQ ID:27369 and SEQ ID:27379 respectively, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90401] A function of VGAM2692 is therefore inhibition of F-box and WD-40 Domain Protein 1B (FBXW1B, Accession NM_012300), a gene which somehow is involved in the

process of neuronal cell differentiation or brain development. Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW1B. The function of FBXW1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.Chromosome 1 Open Reading Frame 17 (C1orf17, Accession XM_042965) is another VGAM2692 host target gene. C1orf17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf17 BINDING SITE, designated SEQ ID:33856, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90402] Another function of VGAM2692 is therefore inhibition of Chromosome 1 Open Reading Frame 17 (C1orf17, Accession XM_042965). Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf17. DK-

FZp434A2417 (Accession XM_038526) is another VGAM2692 host target gene. DKFZp434A2417 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434A2417, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434A2417 BINDING SITE, designated SEQ ID:32866, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90403] Another function of VGAM2692 is therefore inhibition of DKFZp434A2417 (Accession XM_038526). Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434A2417. FLJ10607 (Accession XM_085119) is another VGAM2692 host target gene. FLJ10607 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10607, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10607 BINDING SITE, designated SEQ ID:37836, to the

nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90404] Another function of VGAM2692 is therefore inhibition of FLJ10607 (Accession XM_085119). Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10607. FLJ20202 (Accession NM_017709) is another VGAM2692 host target gene. FLJ20202 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20202 BINDING SITE, designated SEQ ID:19290, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90405] Another function of VGAM2692 is therefore inhibition of FLJ20202 (Accession NM_017709). Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20202. FLJ31101 (Accession NM_017964) is another VGAM2692 host target gene. FLJ31101 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ31101, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ31101 BINDING SITE, designated SEQ ID:19688, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90406] Another function of VGAM2692 is therefore inhibition of FLJ31101 (Accession NM_017964). Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31101. KIAA0979 (Accession NM_015032) is another VGAM2692 host target gene. KIAA0979 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0979, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0979 BINDING SITE, designated SEQ ID:17390, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90407] Another function of VGAM2692 is therefore inhibition of KIAA0979 (Accession NM_015032). Accordingly, utilities

of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0979. Neuron Navigator 3 (NAV3, Accession NM_014903) is another VGAM2692 host target gene. NAV3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAV3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAV3 BINDING SITE, designated SEQ ID:17092, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90408] Another function of VGAM2692 is therefore inhibition of Neuron Navigator 3 (NAV3, Accession NM_014903). Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAV3. p21(CDKN1A)-activated Kinase 7 (PAK7, Accession XM_045653) is another VGAM2692 host target gene. PAK7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAK7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of PAK7 BINDING SITE, designated SEQ ID:34512, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90409] Another function of VGAM2692 is therefore inhibition of p21(CDKN1A)-activated Kinase 7 (PAK7, Accession XM_045653). Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAK7. SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003) is another VGAM2692 host target gene. SEC14L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC14L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC14L1 BINDING SITE, designated SEQ ID:8907, to the nucleotide sequence of VGAM2692 RNA, herein designated VGAM RNA, also designated SEQ ID:5403.

[90410] Another function of VGAM2692 is therefore inhibition of SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003). Accordingly, utilities of VGAM2692 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with SEC14L1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2693 (VGAM2693) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90411] VGAM2693 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2693 was detected is described hereinabove with reference to Figs. 1-8.

[90412] VGAM2693 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea Operculella Granulovirus. VGAM2693 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90413] VGAM2693 gene encodes a VGAM2693 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2693 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2693 precursor RNA is designated SEQ ID:2679, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2679 is located at position 70243 relative to the genome of Phthorimaea Operculella Granulovirus.

[90414] VGAM2693 precursor RNA folds onto itself, forming VGAM2693 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90415] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2693 folded precursor RNA into VGAM2693 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2693 RNA is designated SEQ ID:5404, and is provided hereinbelow with reference to the sequence listing part.

[90416] VGAM2693 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2693 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90417] VGAM2693 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2693 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2693 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90418] The complementary binding of VGAM2693 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2693 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2693 host target RNA into VGAM2693 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90419] It is appreciated that VGAM2693 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2693 host target genes. The mRNA of each one of this plurality of VGAM2693 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2693 RNA, herein designated VGAM RNA, and which when bound by VGAM2693 RNA causes

inhibition of translation of respective one or more VGAM2693 host target proteins.

[90420] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2693 gene, herein designated VGAM GENE, on one or more VGAM2693 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90421] It is yet further appreciated that a function of VGAM2693 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2693 include diagnosis, prevention and

treatment of viral infection by Phthorimaea Operculella Granulovirus. Specific functions, and accordingly utilities, of VGAM2693 correlate with, and may be deduced from, the identity of the host target genes which VGAM2693 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90422] Nucleotide sequences of the VGAM2693 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2693 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2693 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2693 are further described hereinbelow with reference to Table 1.

[90423] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2693 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2693 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90424] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2693 gene, herein designated VGAM is inhibition of expression of VGAM2693 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2693 correlate with, and may be deduced from, the identity of the target genes which VGAM2693 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90425] Archain 1 (ARCN1, Accession NM_001655) is a VGAM2693 host target gene. ARCN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARCN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARCN1 BINDING SITE, designated SEQ ID:7365, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90426] A function of VGAM2693 is therefore inhibition of Archain 1 (ARCN1, Accession NM_001655), a gene which plays a fundamental role in eukaryotic cell biology. Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARCN1. The function of ARCN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM1226.UDP-Gal:betaGlcNAc Beta 1,3-galactosyltransferase, Polypeptide 2 (B3GALT2, Accession NM_003783) is another VGAM2693 host target gene. B3GALT2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by B3GALT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B3GALT2 BINDING SITE, designated SEQ ID:9869, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90427] Another function of VGAM2693 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,3-galactosyltransferase, Polypeptide 2 (B3GALT2, Accession NM_003783). Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GALT2. Ectodermal-neural Cortex (with BTB-like domain) (ENC1, Accession NM_003633) is another VGAM2693 host target gene. ENC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENC1 BINDING SITE, designated SEQ ID:9695, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90428] Another function of VGAM2693 is therefore inhibition of Ectodermal-neural Cortex (with BTB-like domain) (ENC1, Accession NM_003633), a gene which is an actin-binding protein involved in the regulation of neuronal process formation and in differentiation of neural crest cells. Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENC1. The function of ENC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM233.Epidermal Growth Factor Receptor Pathway Substrate 8 (EPS8, Accession NM_004447) is another VGAM2693 host target gene. EPS8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPS8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPS8

BINDING SITE, designated SEQ ID:10741, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90429] Another function of VGAM2693 is therefore inhibition of Epidermal Growth Factor Receptor Pathway Substrate 8 (EPS8, Accession NM_004447), a gene which has a role in normal and neoplastic cell proliferation; contains an SH3 motif. Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPS8. The function of EPS8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1533.Fatty Acid Binding Protein 2, Intestinal (FABP2, Accession NM_000134) is another VGAM2693 host target gene. FABP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FABP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FABP2 BINDING SITE, designated SEQ ID:5621, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90430] Another function of VGAM2693 is therefore inhibition of Fatty Acid Binding Protein 2, Intestinal (FABP2, Accession NM_000134), a gene which may have a role in dietary fat uptake or processing. Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FABP2. The function of FABP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM951.Lipoprotein Lipase (LPL, Accession NM_000237) is another VGAM2693 host target gene. LPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LPL BINDING SITE, designated SEQ ID:5748, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90431] Another function of VGAM2693 is therefore inhibition of Lipoprotein Lipase (LPL, Accession NM_000237), a gene which is the hydrolysis of triglycerides of circulating chylomicrons and very low density lipoproteins (vldl). the en-

zyme functions in the presence of apolipoprotein c-2 on the luminal surface of vascular. Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPL. The function of LPL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Nuclear Receptor Subfamily 4, Group A, Member 2 (NR4A2, Accession NM_006186) is another VGAM2693 host target gene. NR4A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NR4A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR4A2 BINDING SITE, designated SEQ ID:12853, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90432] Another function of VGAM2693 is therefore inhibition of Nuclear Receptor Subfamily 4, Group A, Member 2 (NR4A2, Accession NM_006186), a gene which may be a general coactivator of transcription. Accordingly, utilities of VGAM2693 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with NR4A2. The function of NR4A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM127.Parkinson Disease (autosomal recessive, juvenile) 2, Parkin (PARK2, Accession NM_004562) is another VGAM2693 host target gene. PARK2 BINDING SITE1 through PARK2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PARK2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PARK2 BINDING SITE1 through PARK2 BINDING SITE3, designated SEQ ID:10902, SEQ ID:15149 and SEQ ID:15156 respectively, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90433] Another function of VGAM2693 is therefore inhibition of Parkinson Disease (autosomal recessive, juvenile) 2, Parkin (PARK2, Accession NM_004562). Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PARK2. Ubiquitin-conjugating Enzyme E2 Variant 1 (UBE2V1, Ac-

cession NM_021988) is another VGAM2693 host target gene. UBE2V1 BINDING SITE1 through UBE2V1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by UBE2V1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2V1 BINDING SITE1 through UBE2V1 BINDING SITE3, designated SEQ ID:22517, SEQ ID:9365 and SEQ ID:17886 respectively, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90434] Another function of VGAM2693 is therefore inhibition of Ubiquitin-conjugating Enzyme E2 Variant 1 (UBE2V1, Accession NM_021988), a gene which may play a role in signaling for DNA repair. Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2V1. The function of UBE2V1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM155.KIAA0335 (Accession NM_014803) is another VGAM2693 host target gene. KIAA0335 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0335, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0335 BINDING SITE, designated SEQ ID:16728, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90435] Another function of VGAM2693 is therefore inhibition of KIAA0335 (Accession NM_014803). Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0335. Neuropilin (NRP) and Tolloid (TLL)-like 1 (NETO1, Accession NM_138966) is another VGAM2693 host target gene. NETO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NETO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NETO1 BINDING SITE, designated SEQ ID:29068, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90436] Another function of VGAM2693 is therefore inhibition of Neuropilin (NRP) and Tolloid (TLL)-like 1 (NETO1, Accession NM_138966). Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NETO1. NTT73 (Accession NM_018057) is another VGAM2693 host target gene. NTT73 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTT73, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTT73 BINDING SITE, designated SEQ ID:19821, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90437] Another function of VGAM2693 is therefore inhibition of NTT73 (Accession NM_018057). Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTT73. R3H Domain (binds single-stranded nucleic acids) Containing (R3HDM, Accession NM_015361) is another VGAM2693 host target gene. R3HDM BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by R3HDM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of R3HDM BINDING SITE, designated SEQ ID:17658, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90438] Another function of VGAM2693 is therefore inhibition of R3H Domain (binds single-stranded nucleic acids) Containing (R3HDM, Accession NM_015361). Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with R3HDM. Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202) is another VGAM2693 host target gene. SS18L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS18L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS18L1 BINDING SITE, designated SEQ ID:32557, to the nucleotide sequence of VGAM2693 RNA, herein designated VGAM RNA, also designated SEQ ID:5404.

[90439] Another function of VGAM2693 is therefore inhibition of Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202). Accordingly, utilities of VGAM2693 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SS18L1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2694 (VGAM2694) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90440] VGAM2694 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2694 was detected is described hereinabove with reference to Figs. 1-8.

[90441] VGAM2694 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Phthorimaea Operculella Granulovirus. VGAM2694 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90442] VGAM2694 gene encodes a VGAM2694 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2694 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2694 precursor RNA is designated SEQ ID:2680, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2680 is located at position 71428 relative to the genome of Phthorimaea Operculella Granulovirus.

[90443] VGAM2694 precursor RNA folds onto itself, forming VGAM2694 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90444] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2694 folded precursor RNA into VGAM2694 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2694 RNA is designated SEQ ID:5405, and is provided hereinbelow with reference to the sequence listing part.

[90445] VGAM2694 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2694 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90446] VGAM2694 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2694 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2694 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90447] The complementary binding of VGAM2694 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2694 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2694 host target RNA into VGAM2694 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90448] It is appreciated that VGAM2694 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2694 host target genes. The mRNA of

each one of this plurality of VGAM2694 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2694 RNA, herein designated VGAM RNA, and which when bound by VGAM2694 RNA causes inhibition of translation of respective one or more VGAM2694 host target proteins.

[90449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2694 gene, herein designated VGAM GENE, on one or more VGAM2694 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[90450] It is yet further appreciated that a function of VGAM2694 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of viral infection by Phthorimaea Operculella Granulovirus. Specific functions, and accordingly utilities, of VGAM2694 correlate with, and may be deduced from, the identity of the host target genes which VGAM2694 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90451] Nucleotide sequences of the VGAM2694 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2694 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2694 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2694 are further described hereinbelow with reference to Table 1.

[90452] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2694 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2694 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90453] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2694 gene, herein designated VGAM is inhibition of expression of VGAM2694 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2694 correlate with, and may be deduced from, the identity of the target genes which VGAM2694 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90454] ADP-ribosylation Factor-like 4 (ARL4, Accession NM_005738) is a VGAM2694 host target gene. ARL4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARL4 BINDING SITE, designated SEQ ID:12299, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90455] A function of VGAM2694 is therefore inhibition of ADP-ribosylation Factor-like 4 (ARL4, Accession NM_005738), a gene which may be required for the progression of cells

through meiosis. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARL4. The function of ARL4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1050.Moesin (MSN, Accession XM_013042) is another VGAM2694 host target gene. MSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSN BINDING SITE, designated SEQ ID:30227, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90456] Another function of VGAM2694 is therefore inhibition of Moesin (MSN, Accession XM_013042), a gene which may have a role linking the cytoskeleton to the plasma membrane. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSN. The function of MSN and its association with various diseases and clinical conditions,

has been established by previous studies, as described hereinabove with reference to VGAM248.Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071) is another VGAM2694 host target gene. NCOA6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NCOA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE, designated SEQ ID:15285, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90457] Another function of VGAM2694 is therefore inhibition of Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071), a gene which activates gene transcription through ligand-dependent association with coactivators. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6. The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.Norrie Disease (pseudoglioma) (NDP, Accession NM_000266) is

another VGAM2694 host target gene. NDP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDP BINDING SITE, designated SEQ ID:5805, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90458] Another function of VGAM2694 is therefore inhibition of Norrie Disease (pseudoglioma) (NDP, Accession NM_000266), a gene which may be involved in a pathway that regulates neural cell differentiation and proliferation. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDP. The function of NDP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM113.Soc-2 Suppressor of Clear Homolog (C. elegans) (SHOC2, Accession NM_007373) is another VGAM2694 host target gene. SHOC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

SHOC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHOC2 BINDING SITE, designated SEQ ID:14305, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90459] Another function of VGAM2694 is therefore inhibition of Soc-2 Suppressor of Clear Homolog (C. elegans) (SHOC2, Accession NM_007373), a gene which may be a regulator of the let-60 ras pathway. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHOC2. The function of SHOC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM464.Sarcospan (Kras oncogene-associated gene) (SSPN, Accession NM_005086) is another VGAM2694 host target gene. SSPN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of SSPN BINDING SITE, designated SEQ ID:11536, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90460] Another function of VGAM2694 is therefore inhibition of Sarcospan (Kras oncogene-associated gene) (SSPN, Accession NM_005086), a gene which spans the muscle plasma membrane and forms a link between the f-actin cytoskeleton and the extracellular matrix. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSPN. The function of SSPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM996.SUV39H2 (Accession NM_024670) is another VGAM2694 host target gene. SUV39H2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUV39H2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUV39H2 BINDING SITE, designated SEQ ID:23977, to the nucleotide sequence of VGAM2694 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5405.

[90461] Another function of VGAM2694 is therefore inhibition of SUV39H2 (Accession NM_024670), a gene which is involved in gene repression and the modification of position-effect- variegation. Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUV39H2. The function of SUV39H2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM424.Tripartite Motif-containing 37 (TRIM37, Accession NM_015294) is another VGAM2694 host target gene. TRIM37 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM37, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM37 BINDING SITE, designated SEQ ID:17616, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90462] Another function of VGAM2694 is therefore inhibition of Tripartite Motif-containing 37 (TRIM37, Accession

NM_015294). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM37. Zinc Finger Protein 137 (clone pHZ-30) (ZNF137, Accession NM_003438) is another VGAM2694 host target gene. ZNF137 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF137, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF137 BINDING SITE, designated SEQ ID:9495, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90463] Another function of VGAM2694 is therefore inhibition of Zinc Finger Protein 137 (clone pHZ-30) (ZNF137, Accession NM_003438). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF137. ATPase, Class V, Type 10D (ATP10D, Accession XM_054907) is another VGAM2694 host target gene. ATP10D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP10D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP10D BINDING SITE, designated SEQ ID:36203, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90464] Another function of VGAM2694 is therefore inhibition of ATPase, Class V, Type 10D (ATP10D, Accession XM_054907). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP10D. Chromosome 2 Open Reading Frame 6 (C2orf6, Accession NM_018221) is another VGAM2694 host target gene. C2orf6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C2orf6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C2orf6 BINDING SITE, designated SEQ ID:20143, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90465] Another function of VGAM2694 is therefore inhibition of Chromosome 2 Open Reading Frame 6 (C2orf6, Accession NM_018221). Accordingly, utilities of VGAM2694 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with C2orf6. ELL2 (Accession NM_012081) is another VGAM2694 host target gene. ELL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELL2 BINDING SITE, designated SEQ ID:14370, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90466] Another function of VGAM2694 is therefore inhibition of ELL2 (Accession NM_012081). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELL2. FUS Interacting Protein (serine-arginine rich) 1 (FUSIP1, Accession NM_006625) is another VGAM2694 host target gene. FUSIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FUSIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FUSIP1 BINDING SITE, designated SEQ

ID:13412, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90467] Another function of VGAM2694 is therefore inhibition of FUS Interacting Protein (serine-arginine rich) 1 (FUSIP1, Accession NM_006625). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUSIP1. KIAA0495 (Accession XM_031397) is another VGAM2694 host target gene. KIAA0495 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0495 BINDING SITE, designated SEQ ID:31365, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90468] Another function of VGAM2694 is therefore inhibition of KIAA0495 (Accession XM_031397). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0495. NET-6 (Accession NM_014399) is another

VGAM2694 host target gene. NET-6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NET-6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NET-6 BINDING SITE, designated SEQ ID:15743, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90469] Another function of VGAM2694 is therefore inhibition of NET-6 (Accession NM_014399). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NET-6. LOC150517 (Accession XM_086936) is another VGAM2694 host target gene. LOC150517 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150517, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150517 BINDING SITE, designated SEQ ID:38986, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90470] Another function of VGAM2694 is therefore inhibition of LOC150517 (Accession XM_086936). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150517. LOC253228 (Accession XM_171113) is another VGAM2694 host target gene. LOC253228 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253228 BINDING SITE, designated SEQ ID:45914, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90471] Another function of VGAM2694 is therefore inhibition of LOC253228 (Accession XM_171113). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253228. LOC256946 (Accession XM_170543) is another VGAM2694 host target gene. LOC256946 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256946, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256946 BINDING SITE, designated SEQ ID:45362, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90472] Another function of VGAM2694 is therefore inhibition of LOC256946 (Accession XM_170543). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256946. LOC56959 (Accession XM_088578) is another VGAM2694 host target gene. LOC56959 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC56959, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56959 BINDING SITE, designated SEQ ID:39838, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90473] Another function of VGAM2694 is therefore inhibition of LOC56959 (Accession XM_088578). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC56959. LOC93550 (Accession XM_051999) is another VGAM2694 host target gene. LOC93550 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93550, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93550 BINDING SITE, designated SEQ ID:35932, to the nucleotide sequence of VGAM2694 RNA, herein designated VGAM RNA, also designated SEQ ID:5405.

[90474] Another function of VGAM2694 is therefore inhibition of LOC93550 (Accession XM_051999). Accordingly, utilities of VGAM2694 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93550. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2695 (VGAM2695) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90475] VGAM2695 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2695 was detected is described hereinabove with reference to Figs. 1-8.

[90476] VGAM2695 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fringilla Coelebs Papillomavirus (FPV). VGAM2695 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90477] VGAM2695 gene encodes a VGAM2695 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2695 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2695 precursor RNA is designated SEQ ID:2681, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2681 is located at position 1921 relative to the genome of Fringilla Coelebs Papillomavirus (FPV).

[90478] VGAM2695 precursor RNA folds onto itself, forming VGAM2695 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90479] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2695 folded precursor RNA into VGAM2695 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2695 RNA is designated SEQ ID:5406, and is provided hereinbelow with reference to the sequence listing part.

[90480] VGAM2695 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2695 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90481] VGAM2695 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2695 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2695 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90482] The complementary binding of VGAM2695 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2695 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2695 host target RNA into VGAM2695 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90483] It is appreciated that VGAM2695 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2695 host target genes. The mRNA of each one of this plurality of VGAM2695 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2695 RNA, herein designated VGAM RNA, and which when bound by VGAM2695 RNA causes inhibition of translation of respective one or more VGAM2695 host target proteins.

[90484] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2695 gene, herein designated VGAM GENE, on one or more VGAM2695 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90485] It is yet further appreciated that a function of VGAM2695 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2695 include diagnosis, prevention and treatment of viral infection by Fringilla Coelebs Papillomavirus (FPV). Specific functions, and accordingly utilities, of VGAM2695 correlate with, and may be deduced from, the identity of the host target genes which VGAM2695 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90486] Nucleotide sequences of the VGAM2695 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2695 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2695 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2695 are further described hereinbelow with reference to Table 1.

[90487] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2695 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2695 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90488] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2695 gene, herein designated VGAM is inhibition of expression of VGAM2695 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2695 correlate with, and may be deduced from, the identity of the target genes which VGAM2695 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90489] V-yes-1 Yamaguchi Sarcoma Viral Oncogene Homolog 1 (YES1, Accession NM_005433) is a VGAM2695 host target gene. YES1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

YES1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YES1 BINDING SITE, designated SEQ ID:11912, to the nucleotide sequence of VGAM2695 RNA, herein designated VGAM RNA, also designated SEQ ID:5406.

[90490] A function of VGAM2695 is therefore inhibition of V-yes-1 Yamaguchi Sarcoma Viral Oncogene Homolog 1 (YES1, Accession NM_005433), a gene which is a putative protein-tyrosine kinase. Accordingly, utilities of VGAM2695 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YES1. The function of YES1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.KIAA0721 (Accession NM_021648) is another VGAM2695 host target gene. KIAA0721 BINDING SITE1 and KIAA0721 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0721, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0721 BINDING SITE1 and KIAA0721

BINDING SITE2, designated SEQ ID:22317 and SEQ ID:45924 respectively, to the nucleotide sequence of VGAM2695 RNA, herein designated VGAM RNA, also designated SEQ ID:5406.

[90491] Another function of VGAM2695 is therefore inhibition of KIAA0721 (Accession NM_021648). Accordingly, utilities of VGAM2695 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0721. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2696 (VGAM2696) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90492] VGAM2696 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2696 was detected is described hereinabove with reference to Figs. 1-8.

[90493] VGAM2696 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Paprika Mild Mottle Virus. VGAM2696 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[90494] VGAM2696 gene encodes a VGAM2696 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2696 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2696 precursor RNA is designated SEQ ID:2682, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2682 is located at position 4675 relative to the genome of Paprika Mild Mottle Virus.

[90495] VGAM2696 precursor RNA folds onto itself, forming VGAM2696 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90496] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2696 folded precursor RNA into VGAM2696 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2696 RNA is designated SEQ ID:5407, and is provided hereinbelow with reference to the sequence listing part.

[90497] VGAM2696 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2696 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90498] VGAM2696 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2696 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2696 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90499] The complementary binding of VGAM2696 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2696 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2696 host target RNA into VGAM2696 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90500] It is appreciated that VGAM2696 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2696 host target genes. The mRNA of each one of this plurality of VGAM2696 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2696 RNA, herein designated VGAM RNA, and which when bound by VGAM2696 RNA causes inhibition of translation of respective one or more VGAM2696 host target proteins.

[90501] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2696 gene, herein designated VGAM GENE, on one or more VGAM2696 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90502] It is yet further appreciated that a function of VGAM2696 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of viral infection by Paprika Mild Mottle Virus. Specific functions, and accordingly utilities, of VGAM2696 correlate with, and may be deduced from, the identity of the host target genes which VGAM2696 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90503] Nucleotide sequences of the VGAM2696 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2696 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2696 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2696 are further described hereinbelow with reference to Table 1.

[90504] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2696 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2696 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90505] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2696 gene, herein designated VGAM is inhibition of expression of VGAM2696 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2696 correlate with, and may be deduced from, the identity of the target genes which VGAM2696 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90506] Inhibitor of Growth Family, Member 1 (ING1, Accession NM_005537) is a VGAM2696 host target gene. ING1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ING1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ING1 BINDING SITE, designated SEQ ID:12061, to the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, also designated SEQ ID:5407.

[90507] A function of VGAM2696 is therefore inhibition of Inhibitor of Growth Family, Member 1 (ING1, Accession NM_005537), a gene which acts as a potent growth regulator in normal and in established cells. Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ING1. The function of ING1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM170.Mitogen-activated Protein Kinase Kinase Kinase 9 (MAP3K9, Accession XM_027237) is another VGAM2696 host target gene. MAP3K9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K9 BINDING SITE, designated SEQ ID:30460, to the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, also designated SEQ ID:5407.

[90508] Another function of VGAM2696 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 9 (MAP3K9, Accession XM_027237), a gene which is a

MIXED-LINEAGE KINASE 1. Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K9. The function of MAP3K9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1601.Purinergic Receptor P2Y, G-protein Coupled, 1 (P2RY1, Accession NM_002563) is another VGAM2696 host target gene. P2RY1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P2RY1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RY1 BINDING SITE, designated SEQ ID:8412, to the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, also designated SEQ ID:5407.

[90509] Another function of VGAM2696 is therefore inhibition of Purinergic Receptor P2Y, G-protein Coupled, 1 (P2RY1, Accession NM_002563), a gene which plays an essential role in thrombotic states. Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RY1.

The function of P2RY1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 8 (SLC7A8, Accession NM_012244) is another VGAM2696 host target gene. SLC7A8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC7A8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC7A8 BINDING SITE, designated SEQ ID:14551, to the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, also designated SEQ ID:5407.

[90510] Another function of VGAM2696 is therefore inhibition of Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 8 (SLC7A8, Accession NM_012244), a gene which helps mediate transport of large and small neutral amino acids. Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A8. The function of SLC7A8 and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1263.Chromosome 20 Open Reading Frame 12 (C20orf12, Accession NM_018152) is another VGAM2696 host target gene. C20orf12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf12 BINDING SITE, designated SEQ ID:19960, to the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, also designated SEQ ID:5407.

[90511] Another function of VGAM2696 is therefore inhibition of Chromosome 20 Open Reading Frame 12 (C20orf12, Accession NM_018152). Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf12. Collectin Sub-family Member 10 (C-type lectin) (COLEC10, Accession NM_006438) is another VGAM2696 host target gene. COLEC10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COLEC10, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COLEC10 BINDING SITE, designated SEQ ID:13144, to the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, also designated SEQ ID:5407.

[90512] Another function of VGAM2696 is therefore inhibition of Collectin Sub-family Member 10 (C-type lectin) (COLEC10, Accession NM_006438). Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC10. Zinc Finger Protein 387 (ZNF387, Accession NM_014682) is another VGAM2696 host target gene. ZNF387 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF387 BINDING SITE, designated SEQ ID:16175, to the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, also designated SEQ ID:5407.

[90513] Another function of VGAM2696 is therefore inhibition of

Zinc Finger Protein 387 (ZNF387, Accession NM_014682). Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF387. LOC133584 (Accession XM_059661) is another VGAM2696 host target gene. LOC133584 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC133584, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133584 BINDING SITE, designated SEQ ID:37044, to the nucleotide sequence of VGAM2696 RNA, herein designated VGAM RNA, also designated SEQ ID:5407.

[90514] Another function of VGAM2696 is therefore inhibition of LOC133584 (Accession XM_059661). Accordingly, utilities of VGAM2696 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133584. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2697 (VGAM2697) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[90515] VGAM2697 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2697 was detected is described hereinabove with reference to Figs. 1-8.

[90516] VGAM2697 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Paprika Mild Mottle Virus. VGAM2697 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90517] VGAM2697 gene encodes a VGAM2697 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2697 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2697 precursor RNA is designated SEQ ID:2683, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2683 is located at position 891 relative to the genome of Paprika Mild Mottle Virus.

[90518] VGAM2697 precursor RNA folds onto itself, forming VGAM2697 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90519] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2697 folded precursor RNA into VGAM2697 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2697 RNA is designated SEQ ID:5408, and is provided hereinbelow with reference to the sequence listing part.

[90520] VGAM2697 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2697 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90521] VGAM2697 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2697 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2697 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90522] The complementary binding of VGAM2697 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2697 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2697 host target RNA into VGAM2697 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90523] It is appreciated that VGAM2697 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2697 host target genes. The mRNA of each one of this plurality of VGAM2697 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2697 RNA, herein designated VGAM RNA, and which when bound by VGAM2697 RNA causes inhibition of translation of respective one or more VGAM2697 host target proteins.

[90524] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2697 gene, herein designated VGAM GENE, on one or more VGAM2697 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90525] It is yet further appreciated that a function of VGAM2697 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of viral infection by Paprika Mild Mottle Virus. Specific functions, and accordingly utilities, of VGAM2697 correlate with, and may be deduced from, the identity of the host target genes which VGAM2697 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[90526] Nucleotide sequences of the VGAM2697 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2697 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2697 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2697 are further described hereinbelow with reference to Table 1.

[90527] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2697 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2697 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90528] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2697 gene, herein designated VGAM is inhibition of expression of VGAM2697 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2697 correlate with, and may be deduced from, the identity of the target genes which VGAM2697 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90529] B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898) is a VGAM2697 host target gene. BCL11B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL11B BINDING SITE, designated SEQ ID:23171, to the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, also designated SEQ ID:5408.

[90530] A function of VGAM2697 is therefore inhibition of B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898). Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL11B. Integrin, Alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) (ITGAV, Accession NM_002210) is another VGAM2697 host target gene. ITGAV BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAV, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of ITGAV BINDING SITE, designated SEQ ID:7975, to the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, also designated SEQ ID:5408.

[90531] Another function of VGAM2697 is therefore inhibition of Integrin, Alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) (ITGAV, Accession NM_002210), a gene which is a member of the integrin family of cell-surface proteins. Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAV. The function of ITGAV and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM20.Spondin 1, (f-spondin) Extracellular Matrix Protein (SPON1, Accession XM_031184) is another VGAM2697 host target gene. SPON1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPON1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPON1 BINDING SITE, designated SEQ ID:31298, to the nucleotide sequence of VGAM2697 RNA,

herein designated VGAM RNA, also designated SEQ ID:5408.

[90532] Another function of VGAM2697 is therefore inhibition of Spondin 1, (f-spondin) Extracellular Matrix Protein (SPON1, Accession XM_031184). Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPON1. Activity-dependent Neuroprotector (ADNP, Accession NM_015339) is another VGAM2697 host target gene. ADNP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADNP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADNP BINDING SITE, designated SEQ ID:17646, to the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, also designated SEQ ID:5408.

[90533] Another function of VGAM2697 is therefore inhibition of Activity-dependent Neuroprotector (ADNP, Accession NM_015339). Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADNP. ATP6M8-9 (Accession NM_005765) is another VGAM2697 host target

gene. ATP6M8-9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP6M8-9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP6M8-9 BINDING SITE, designated SEQ ID:12328, to the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, also designated SEQ ID:5408.

[90534] Another function of VGAM2697 is therefore inhibition of ATP6M8-9 (Accession NM_005765). Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6M8-9. KIAA0830 (Accession XM_045759) is another VGAM2697 host target gene. KIAA0830 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0830 BINDING SITE, designated SEQ ID:34545, to the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, also designated SEQ ID:5408.

[90535] Another function of VGAM2697 is therefore inhibition of KIAA0830 (Accession XM_045759). Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0830. LOC135932 (Accession XM_072433) is another VGAM2697 host target gene. LOC135932 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC135932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135932 BINDING SITE, designated SEQ ID:37498, to the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, also designated SEQ ID:5408.

[90536] Another function of VGAM2697 is therefore inhibition of LOC135932 (Accession XM_072433). Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135932. LOC154760 (Accession XM_098603) is another VGAM2697 host target gene. LOC154760 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154760, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154760 BINDING SITE, designated SEQ ID:41724, to the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, also designated SEQ ID:5408.

[90537] Another function of VGAM2697 is therefore inhibition of LOC154760 (Accession XM_098603). Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154760. LOC91266 (Accession XM_037268) is another VGAM2697 host target gene. LOC91266 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91266 BINDING SITE, designated SEQ ID:32605, to the nucleotide sequence of VGAM2697 RNA, herein designated VGAM RNA, also designated SEQ ID:5408.

[90538] Another function of VGAM2697 is therefore inhibition of LOC91266 (Accession XM_037268). Accordingly, utilities of VGAM2697 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC91266. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2698 (VGAM2698) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90539] VGAM2698 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2698 was detected is described hereinabove with reference to Figs. 1-8.

[90540] VGAM2698 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Paprika Mild Mottle Virus. VGAM2698 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90541] VGAM2698 gene encodes a VGAM2698 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2698 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2698 precursor RNA is designated SEQ ID:2684, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2684 is located at position 1275 relative to the genome of Paprika Mild Mottle Virus.

[90542] VGAM2698 precursor RNA folds onto itself, forming VGAM2698 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90543] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2698 folded precursor RNA into VGAM2698 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2698 RNA is designated SEQ ID:5409, and is provided hereinbelow with reference to the sequence listing part.

[90544] VGAM2698 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2698 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90545] VGAM2698 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2698 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2698 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90546] The complementary binding of VGAM2698 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2698 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2698 host target RNA into VGAM2698 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90547] It is appreciated that VGAM2698 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2698 host target genes. The mRNA of each one of this plurality of VGAM2698 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2698 RNA, herein designated VGAM RNA, and which when bound by VGAM2698 RNA causes

inhibition of translation of respective one or more VGAM2698 host target proteins.

[90548] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2698 gene, herein designated VGAM GENE, on one or more VGAM2698 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90549] It is yet further appreciated that a function of VGAM2698 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2698 include diagnosis, prevention and

treatment of viral infection by Paprika Mild Mottle Virus. Specific functions, and accordingly utilities, of VGAM2698 correlate with, and may be deduced from, the identity of the host target genes which VGAM2698 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90550] Nucleotide sequences of the VGAM2698 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2698 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2698 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2698 are further described hereinbelow with reference to Table 1.

[90551] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2698 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2698 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90552] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2698 gene, herein designated VGAM is inhibition of expression of VGAM2698 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2698 correlate with, and may be deduced from, the identity of the target genes which VGAM2698 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90553] Adrenergic, Beta-3-, Receptor (ADRB3, Accession NM_000025) is a VGAM2698 host target gene. ADRB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADRB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADRB3 BINDING SITE, designated SEQ ID:5462, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90554] A function of VGAM2698 is therefore inhibition of Adrenergic, Beta-3-, Receptor (ADRB3, Accession NM_000025), a gene which stimulates adenylyl cyclase activity and regulates lipolysis. Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADRB3. The function of ADRB3 and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to VGAM179.Arginine Vasopressin Receptor 1A (AVPR1A, Accession NM_000706) is another VGAM2698 host target gene. AVPR1A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AVPR1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AVPR1A BINDING SITE, designated SEQ ID:6374, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90555] Another function of VGAM2698 is therefore inhibition of Arginine Vasopressin Receptor 1A (AVPR1A, Accession NM_000706), a gene which mediates cell contraction and proliferation, platelet aggregation, release of coagulation factor, and glycogenolysis. Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AVPR1A. The function of AVPR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM549.B-cell CLL/lymphoma 2 (BCL2, Ac-

cession NM_000633) is another VGAM2698 host target gene. BCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL2 BINDING SITE, designated SEQ ID:6253, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90556] Another function of VGAM2698 is therefore inhibition of B-cell CLL/lymphoma 2 (BCL2, Accession NM_000633). Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL2. B-cell CLL/lymphoma 7A (BCL7A, Accession NM_020993) is another VGAM2698 host target gene. BCL7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL7A BINDING SITE, designated SEQ ID:21991, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5409.

[90557] Another function of VGAM2698 is therefore inhibition of B-cell CLL/lymphoma 7A (BCL7A, Accession NM_020993). Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL7A. V-myc Myelocytomatosis Viral Oncogene Homolog 2 (avian) (MYCL2, Accession NM_005377) is another VGAM2698 host target gene. MYCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYCL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYCL2 BINDING SITE, designated SEQ ID:11857, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90558] Another function of VGAM2698 is therefore inhibition of V-myc Myelocytomatosis Viral Oncogene Homolog 2 (avian) (MYCL2, Accession NM_005377). Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYCL2. Synapsin III (SYN3, Accession NM_133632) is

another VGAM2698 host target gene. SYN3 BINDING SITE1 through SYN3 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SYN3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYN3 BINDING SITE1 through SYN3 BINDING SITE3, designated SEQ ID:28593, SEQ ID:28595 and SEQ ID:9584 respectively, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90559] Another function of VGAM2698 is therefore inhibition of Synapsin III (SYN3, Accession NM_133632), a gene which may be involved in the regulation of neurotransmitter release and synaptogenesis. Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYN3. The function of SYN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM925.FLJ31952 (Accession NM_144682) is another VGAM2698 host target gene. FLJ31952 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ31952, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ31952 BINDING SITE, designated SEQ ID:29498, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90560] Another function of VGAM2698 is therefore inhibition of FLJ31952 (Accession NM_144682). Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31952. HSOBRGRP (Accession NM_017526) is another VGAM2698 host target gene. HSOBRGRP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSOBRGRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSOBRGRP BINDING SITE, designated SEQ ID:18970, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90561] Another function of VGAM2698 is therefore inhibition of HSOBRGRP (Accession NM_017526). Accordingly, utilities

of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSOBRGRP. Myelin Transcription Factor 1-like (MYT1L, Accession XM_039762) is another VGAM2698 host target gene. MYT1L BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MYT1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYT1L BINDING SITE, designated SEQ ID:33184, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90562] Another function of VGAM2698 is therefore inhibition of Myelin Transcription Factor 1-like (MYT1L, Accession XM_039762). Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYT1L. TUSP (Accession NM_020245) is another VGAM2698 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21535, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90563] Another function of VGAM2698 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. LOC145225 (Accession XM_096741) is another VGAM2698 host target gene. LOC145225 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145225, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145225 BINDING SITE, designated SEQ ID:40525, to the nucleotide sequence of VGAM2698 RNA, herein designated VGAM RNA, also designated SEQ ID:5409.

[90564] Another function of VGAM2698 is therefore inhibition of LOC145225 (Accession XM_096741). Accordingly, utilities of VGAM2698 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145225. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2699 (VGAM2699) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90565] VGAM2699 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2699 was detected is described hereinabove with reference to Figs. 1-8.

[90566] VGAM2699 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Paprika Mild Mottle Virus. VGAM2699 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90567] VGAM2699 gene encodes a VGAM2699 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2699 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2699 precursor RNA is designated SEQ ID:2685, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2685 is located at position 2770 relative to the genome of Paprika Mild Mottle Virus.

[90568] VGAM2699 precursor RNA folds onto itself, forming VGAM2699 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90569] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2699 folded precursor RNA into VGAM2699 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2699 RNA is designated SEQ ID:5410, and is provided hereinbelow with reference to the sequence listing part.

[90570] VGAM2699 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2699 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90571] VGAM2699 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2699 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2699 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2699 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90572] The complementary binding of VGAM2699 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2699 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2699 host target RNA into VGAM2699 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90573] It is appreciated that VGAM2699 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2699 host target genes. The mRNA of each one of this plurality of VGAM2699 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2699 RNA, herein designated VGAM RNA, and which when bound by VGAM2699 RNA causes inhibition of translation of respective one or more

VGAM2699 host target proteins.

[90574] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2699 gene, herein designated VGAM GENE, on one or more VGAM2699 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90575] It is yet further appreciated that a function of VGAM2699 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of viral infection by Paprika Mild Mottle Virus.

Specific functions, and accordingly utilities, of VGAM2699 correlate with, and may be deduced from, the identity of the host target genes which VGAM2699 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90576] Nucleotide sequences of the VGAM2699 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2699 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2699 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2699 are further described hereinbelow with reference to Table 1.

[90577] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2699 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2699 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90578] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2699 gene, herein designated VGAM is inhibition of expression of VGAM2699 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2699 correlate with, and may be deduced from, the identity of the target genes which VGAM2699 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90579] ATPase, Na+/K+ Transporting, Alpha 2 (+) Polypeptide (ATP1A2, Accession NM_000702) is a VGAM2699 host target gene. ATP1A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP1A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1A2 BINDING SITE, designated SEQ ID:6365, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90580] A function of VGAM2699 is therefore inhibition of ATPase, Na+/K+ Transporting, Alpha 2 (+) Polypeptide (ATP1A2, Accession NM_000702). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1A2. Caspase 8, Apoptosis-related Cysteine Protease (CASP8, Accession NM_033357) is another VGAM2699 host target gene. CASP8 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by CASP8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:27208, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90581] Another function of VGAM2699 is therefore inhibition of Caspase 8, Apoptosis-related Cysteine Protease (CASP8, Accession NM_033357), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor-induced apoptosis. Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP8. The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM145.Chloride Channel 3 (CLCN3, Accession NM_001829) is another VGAM2699 host target gene. CLCN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLCN3, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLCN3 BINDING SITE, designated SEQ ID:7565, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90582] Another function of VGAM2699 is therefore inhibition of Chloride Channel 3 (CLCN3, Accession NM_001829), a gene which play a role in the neural cell function through regulation of membrane excitability. Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN3. The function of CLCN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1332.Collagen-like Tail Subunit (single strand of homotrimer) of Asymmetric Acetylcholinesterase (COLQ, Accession NM_005677) is another VGAM2699 host target gene. COLQ BINDING SITE1 through COLQ BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COLQ, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of COLQ BINDING SITE1 through COLQ BINDING SITE6, designated SEQ ID:12231, SEQ ID:27851, SEQ ID:27854, SEQ ID:27857, SEQ ID:27860 and SEQ ID:27863 respectively, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90583] Another function of VGAM2699 is therefore inhibition of Collagen-like Tail Subunit (single strand of homotrimer) of Asymmetric Acetylcholinesterase (COLQ, Accession NM_005677). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLQ. Islet Cell Autoantigen 1, 69kDa (ICA1, Accession NM_022308) is another VGAM2699 host target gene. ICA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICA1 BINDING SITE, designated SEQ ID:22739, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90584] Another function of VGAM2699 is therefore inhibition of

Islet Cell Autoantigen 1, 69kDa (ICA1, Accession NM_022308), a gene which Islet cell autoantigen 1. Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICA1. The function of ICA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.RNA Binding Motif Protein, X Chromosome (RBMX, Accession XM_042968) is another VGAM2699 host target gene. RBMX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBMX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBMX BINDING SITE, designated SEQ ID:33858, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90585] Another function of VGAM2699 is therefore inhibition of RNA Binding Motif Protein, X Chromosome (RBMX, Accession XM_042968), a gene which binds rna as a component of the ribonucleosome. Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with RBMX. The function of RBMX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1043.Zinc Finger Protein 255 (ZNF255, Accession NM_005774) is another VGAM2699 host target gene. ZNF255 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF255 BINDING SITE, designated SEQ ID:12348, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90586] Another function of VGAM2699 is therefore inhibition of Zinc Finger Protein 255 (ZNF255, Accession NM_005774). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF255. Zinc Finger Protein 268 (ZNF268, Accession XM_031851) is another VGAM2699 host target gene. ZNF268 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by ZNF268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF268 BINDING SITE, designated SEQ ID:31501, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90587] Another function of VGAM2699 is therefore inhibition of Zinc Finger Protein 268 (ZNF268, Accession XM_031851). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF268. Chromosome 20 Open Reading Frame 97 (C20orf97, Accession NM_021158) is another VGAM2699 host target gene. C20orf97 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf97, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf97 BINDING SITE, designated SEQ ID:22139, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90588] Another function of VGAM2699 is therefore inhibition of

Chromosome 20 Open Reading Frame 97 (C20orf97, Accession NM_021158). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf97. Reserved (C8orf13, Accession XM_088377) is another VGAM2699 host target gene. C8orf13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C8orf13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C8orf13 BINDING SITE, designated SEQ ID:39652, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90589] Another function of VGAM2699 is therefore inhibition of Reserved (C8orf13, Accession XM_088377). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf13. FLJ13224 (Accession NM_024799) is another VGAM2699 host target gene. FLJ13224 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13224, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13224 BINDING SITE, designated SEQ ID:24178, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90590] Another function of VGAM2699 is therefore inhibition of FLJ13224 (Accession NM_024799). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13224. FLJ20209 (Accession XM_098142) is another VGAM2699 host target gene. FLJ20209 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20209, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20209 BINDING SITE, designated SEQ ID:41404, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90591] Another function of VGAM2699 is therefore inhibition of FLJ20209 (Accession XM_098142). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20209. KIAA0217 (Accession XM_040265) is another VGAM2699 host target gene. KIAA0217 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0217 BINDING SITE, designated SEQ ID:33281, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90592] Another function of VGAM2699 is therefore inhibition of KIAA0217 (Accession XM_040265). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0217. KIAA0980 (Accession NM_025176) is another VGAM2699 host target gene. KIAA0980 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0980, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0980 BINDING SITE, designated SEQ ID:24811, to the nucleotide sequence of VGAM2699 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5410.

[90593] Another function of VGAM2699 is therefore inhibition of KIAA0980 (Accession NM_025176). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0980. KIAA1130 (Accession XM_031104) is another VGAM2699 host target gene. KIAA1130 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1130, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1130 BINDING SITE, designated SEQ ID:31286, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90594] Another function of VGAM2699 is therefore inhibition of KIAA1130 (Accession XM_031104). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1130. KIAA1204 (Accession XM_045011) is another VGAM2699 host target gene. KIAA1204 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1204, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1204 BINDING SITE, designated SEQ ID:34314, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90595] Another function of VGAM2699 is therefore inhibition of KIAA1204 (Accession XM_045011). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1204. KIAA1281 (Accession XM_114432) is another VGAM2699 host target gene. KIAA1281 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1281, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1281 BINDING SITE, designated SEQ ID:42962, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90596] Another function of VGAM2699 is therefore inhibition of KIAA1281 (Accession XM_114432). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1281. KIAA1727 (Accession XM_034262) is another VGAM2699 host target gene. KIAA1727 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1727, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1727 BINDING SITE, designated SEQ ID:32029, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90597] Another function of VGAM2699 is therefore inhibition of KIAA1727 (Accession XM_034262). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1727. KIAA1879 (Accession XM_056635) is another VGAM2699 host target gene. KIAA1879 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1879, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1879 BINDING SITE, designated SEQ ID:36416, to the

nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90598] Another function of VGAM2699 is therefore inhibition of KIAA1879 (Accession XM_056635). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1879. KIAA1938 (Accession XM_166407) is another VGAM2699 host target gene. KIAA1938 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1938, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1938 BINDING SITE, designated SEQ ID:44278, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90599] Another function of VGAM2699 is therefore inhibition of KIAA1938 (Accession XM_166407). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1938. Nuclear Receptor Subfamily 6, Group A, Member 1 (NR6A1, Accession NM_033335) is another VGAM2699 host target gene. NR6A1 BINDING SITE1

through NR6A1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NR6A1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR6A1 BINDING SITE1 through NR6A1 BINDING SITE3, designated SEQ ID:27186, SEQ ID:27180 and SEQ ID:7232 respectively, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90600] Another function of VGAM2699 is therefore inhibition of Nuclear Receptor Subfamily 6, Group A, Member 1 (NR6A1, Accession NM_033335). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR6A1. RNAC (Accession NM_005772) is another VGAM2699 host target gene. RNAC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNAC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNAC BINDING SITE, designated SEQ ID:12345, to the nucleotide sequence of VGAM2699 RNA,

herein designated VGAM RNA, also designated SEQ ID:5410.

[90601] Another function of VGAM2699 is therefore inhibition of RNAC (Accession NM_005772). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNAC. U5-116KD (Accession NM_004247) is another VGAM2699 host target gene. U5-116KD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by U5-116KD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of U5-116KD BINDING SITE, designated SEQ ID:10436, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90602] Another function of VGAM2699 is therefore inhibition of U5-116KD (Accession NM_004247). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U5-116KD. LOC146909 (Accession XM_085634) is another VGAM2699 host target gene. LOC146909 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC146909, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE, designated SEQ ID:38272, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90603] Another function of VGAM2699 is therefore inhibition of LOC146909 (Accession XM_085634). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909. LOC152445 (Accession XM_098231) is another VGAM2699 host target gene. LOC152445 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:41510, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90604] Another function of VGAM2699 is therefore inhibition of LOC152445 (Accession XM_098231). Accordingly, utilities

of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445. LOC158476 (Accession XM_098955) is another VGAM2699 host target gene. LOC158476 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158476, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158476 BINDING SITE, designated SEQ ID:41998, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90605] Another function of VGAM2699 is therefore inhibition of LOC158476 (Accession XM_098955). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158476. LOC223009 (Accession XM_170214) is another VGAM2699 host target gene. LOC223009 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC223009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC223009 BINDING SITE, designated SEQ ID:45313, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90606] Another function of VGAM2699 is therefore inhibition of LOC223009 (Accession XM_170214). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC223009. LOC256158 (Accession XM_175125) is another VGAM2699 host target gene. LOC256158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256158 BINDING SITE, designated SEQ ID:46618, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90607] Another function of VGAM2699 is therefore inhibition of LOC256158 (Accession XM_175125). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256158. LOC257444 (Accession XM_088028) is another VGAM2699 host target gene. LOC257444 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257444, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257444 BINDING SITE, designated SEQ ID:39479, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90608] Another function of VGAM2699 is therefore inhibition of LOC257444 (Accession XM_088028). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257444. LOC56267 (Accession NM_019610) is another VGAM2699 host target gene. LOC56267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56267 BINDING SITE, designated SEQ ID:21229, to the nucleotide sequence of VGAM2699 RNA, herein designated VGAM RNA, also designated SEQ ID:5410.

[90609] Another function of VGAM2699 is therefore inhibition of

LOC56267 (Accession NM_019610). Accordingly, utilities of VGAM2699 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56267. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2700 (VGAM2700) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90610] VGAM2700 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2700 was detected is described hereinabove with reference to Figs. 1-8.

[90611] VGAM2700 gene, herein designated VGAM GENE, is a viral gene contained in the genome of La Crosse Virus. VGAM2700 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90612] VGAM2700 gene encodes a VGAM2700 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2700 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2700 precursor RNA is designated SEQ ID:2686, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2686 is located at position 1021 relative to the genome of La Crosse Virus.

[90613] VGAM2700 precursor RNA folds onto itself, forming VGAM2700 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90614] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2700 folded precursor RNA into VGAM2700 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2700 RNA is designated SEQ ID:5411, and is provided hereinbelow with reference to the sequence listing part.

[90615] VGAM2700 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2700 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90616] VGAM2700 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2700 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2700 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90617] The complementary binding of VGAM2700 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2700 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2700 host target RNA into VGAM2700 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90618] It is appreciated that VGAM2700 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2700 host target genes. The mRNA of each one of this plurality of VGAM2700 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2700 RNA, herein designated VGAM RNA, and which when bound by VGAM2700 RNA causes inhibition of translation of respective one or more VGAM2700 host target proteins.

[90619] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2700 gene, herein designated VGAM GENE, on one or more VGAM2700 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90620] It is yet further appreciated that a function of VGAM2700

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2700 include diagnosis, prevention and treatment of viral infection by La Crosse Virus. Specific functions, and accordingly utilities, of VGAM2700 correlate with, and may be deduced from, the identity of the host target genes which VGAM2700 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90621] Nucleotide sequences of the VGAM2700 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2700 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2700 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2700 are further described hereinbelow with reference to Table 1.

[90622] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2700 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2700 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90623] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2700 gene, herein designated VGAM is inhibition of expression of VGAM2700 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2700 correlate with, and may be deduced from, the identity of the target genes which VGAM2700 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90624] Gap Junction Protein, Alpha 1, 43kDa (connexin 43) (GJA1, Accession NM_000165) is a VGAM2700 host target gene. GJA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GJA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GJA1 BINDING SITE, designated SEQ ID:5679, to the nucleotide sequence of VGAM2700 RNA, herein designated VGAM RNA, also designated SEQ ID:5411.

[90625] A function of VGAM2700 is therefore inhibition of Gap Junction Protein, Alpha 1, 43kDa (connexin 43) (GJA1, Accession NM_000165), a gene which may act in synchronizing heart contraction and embryonic development. Accordingly, utilities of VGAM2700 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with GJA1. The function of GJA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.RAB Interacting Factor (RABIF, Accession NM_002871) is another VGAM2700 host target gene. RABIF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RABIF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RABIF BINDING SITE, designated SEQ ID:8780, to the nucleotide sequence of VGAM2700 RNA, herein designated VGAM RNA, also designated SEQ ID:5411.

[90626] Another function of VGAM2700 is therefore inhibition of RAB Interacting Factor (RABIF, Accession NM_002871), a gene which is involved in the regulation of intracellular vesicular transport. Accordingly, utilities of VGAM2700 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABIF. The function of RABIF and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to VGAM1633.Chromosome 20 Open Reading Frame 108 (C20orf108, Accession NM_080821) is another VGAM2700 host target gene. C20orf108 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf108, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf108 BINDING SITE, designated SEQ ID:28089, to the nucleotide sequence of VGAM2700 RNA, herein designated VGAM RNA, also designated SEQ ID:5411.

[90627] Another function of VGAM2700 is therefore inhibition of Chromosome 20 Open Reading Frame 108 (C20orf108, Accession NM_080821). Accordingly, utilities of VGAM2700 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf108. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2701 (VGAM2701) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[90628] VGAM2701 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2701 was detected is described hereinabove with reference to Figs. 1-8.

[90629] VGAM2701 gene, herein designated VGAM GENE, is a viral gene contained in the genome of La Crosse Virus. VGAM2701 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90630] VGAM2701 gene encodes a VGAM2701 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2701 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2701 precursor RNA is designated SEQ ID:2687, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2687 is located at position 4064 relative to the genome of La Crosse Virus.

[90631] VGAM2701 precursor RNA folds onto itself, forming VGAM2701 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90632] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2701 folded precursor RNA into VGAM2701 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2701 RNA is designated SEQ ID:5412, and is provided hereinbelow with reference to the sequence listing part.

[90633] VGAM2701 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2701 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90634] VGAM2701 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2701 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2701 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[90635] The complementary binding of VGAM2701 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2701 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2701 host target RNA into VGAM2701 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90636] It is appreciated that VGAM2701 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2701 host target genes. The mRNA of each one of this plurality of VGAM2701 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2701 RNA, herein designated VGAM RNA, and which when bound by VGAM2701 RNA causes inhibition of translation of respective one or more VGAM2701 host target proteins.

[90637] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2701 gene, herein designated VGAM GENE, on one

or more VGAM2701 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90638] It is yet further appreciated that a function of VGAM2701 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2701 include diagnosis, prevention and treatment of viral infection by La Crosse Virus. Specific functions, and accordingly utilities, of VGAM2701 correlate with, and may be deduced from, the identity of the host target genes which VGAM2701 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90639] Nucleotide sequences of the VGAM2701 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2701 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2701 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2701 are further described hereinbelow with reference to Table 1.

[90640] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2701 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2701 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90641] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2701 gene, herein designated VGAM is inhibition of expression of VGAM2701 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2701 correlate with, and may be deduced from, the identity of the target genes which VGAM2701 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90642] Fibroblast Growth Factor 5 (FGF5, Accession NM_004464)

is a VGAM2701 host target gene. FGF5 BINDING SITE1 and FGF5 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FGF5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE1 and FGF5 BINDING SITE2, designated SEQ ID:10771 and SEQ ID:26998 respectively, to the nucleotide sequence of VGAM2701 RNA, herein designated VGAM RNA, also designated SEQ ID:5412.

[90643] A function of VGAM2701 is therefore inhibition of Fibroblast Growth Factor 5 (FGF5, Accession NM_004464), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of VGAM2701 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5. The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM276.LOC90333 (Accession XM_030958) is another VGAM2701 host target gene. LOC90333 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90333, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90333 BINDING SITE, designated SEQ ID:31221, to the nucleotide sequence of VGAM2701 RNA, herein designated VGAM RNA, also designated SEQ ID:5412.

[90644] Another function of VGAM2701 is therefore inhibition of LOC90333 (Accession XM_030958). Accordingly, utilities of VGAM2701 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90333. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2702 (VGAM2702) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90645] VGAM2702 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2702 was detected is described hereinabove with reference to Figs. 1-8.

[90646] VGAM2702 gene, herein designated VGAM GENE, is a viral gene contained in the genome of La Crosse Virus.

VGAM2702 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90647] VGAM2702 gene encodes a VGAM2702 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2702 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2702 precursor RNA is designated SEQ ID:2688, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2688 is located at position 4272 relative to the genome of La Crosse Virus.

[90648] VGAM2702 precursor RNA folds onto itself, forming VGAM2702 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90649] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2702 folded precursor RNA into VGAM2702 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2702 RNA is designated SEQ ID:5413, and is provided hereinbelow with reference to the sequence listing part.

[90650] VGAM2702 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2702 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90651] VGAM2702 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2702 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2702 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90652] The complementary binding of VGAM2702 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2702 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2702 host target RNA into VGAM2702 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90653] It is appreciated that VGAM2702 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2702 host target genes. The mRNA of each one of this plurality of VGAM2702 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2702 RNA, herein designated VGAM RNA, and which when bound by VGAM2702 RNA causes inhibition of translation of respective one or more VGAM2702 host target proteins.

[90654] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2702 gene, herein designated VGAM GENE, on one or more VGAM2702 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90655] It is yet further appreciated that a function of VGAM2702 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of viral infection by La Crosse Virus. Specific functions, and accordingly utilities, of VGAM2702 correlate with, and may be deduced from, the identity of the host target genes which VGAM2702 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90656] Nucleotide sequences of the VGAM2702 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2702 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2702 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2702 are further described hereinbelow with reference to Table 1.

[90657] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2702 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2702 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90658] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2702 gene, herein designated VGAM is inhibition of expression of VGAM2702 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2702 correlate with, and may be deduced from, the identity of the target genes which VGAM2702 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90659] Hormonally Upregulated Neu-associated Kinase (HUNK, Accession NM_014586) is a VGAM2702 host target gene. HUNK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HUNK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HUNK BINDING SITE, designated SEQ ID:15944,

to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, also designated SEQ ID:5413.

[90660] A function of VGAM2702 is therefore inhibition of Hormonally Upregulated Neu-associated Kinase (HUNK, Accession NM_014586). Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUNK. Hyaluronan Binding Protein 2 (HABP2, Accession NM_004132) is another VGAM2702 host target gene. HABP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HABP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HABP2 BINDING SITE, designated SEQ ID:10341, to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, also designated SEQ ID:5413.

[90661] Another function of VGAM2702 is therefore inhibition of Hyaluronan Binding Protein 2 (HABP2, Accession NM_004132). Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HABP2. KIAA1023 (Accession NM_017604) is another VGAM2702 host target

gene. KIAA1023 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1023, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1023 BINDING SITE, designated SEQ ID:19085, to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, also designated SEQ ID:5413.

[90662] Another function of VGAM2702 is therefore inhibition of KIAA1023 (Accession NM_017604). Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1023. Olfactory Receptor, Family 2, Subfamily C, Member 3 (OR2C3, Accession XM_060575) is another VGAM2702 host target gene. OR2C3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OR2C3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OR2C3 BINDING SITE, designated SEQ ID:37176, to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA,

also designated SEQ ID:5413.

[90663] Another function of VGAM2702 is therefore inhibition of Olfactory Receptor, Family 2, Subfamily C, Member 3 (OR2C3, Accession XM_060575). Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR2C3. TERA (Accession NM_021238) is another VGAM2702 host target gene. TERA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TERA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TERA BINDING SITE, designated SEQ ID:22203, to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, also designated SEQ ID:5413.

[90664] Another function of VGAM2702 is therefore inhibition of TERA (Accession NM_021238). Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERA. LOC147949 (Accession XM_085973) is another VGAM2702 host target gene. LOC147949 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC147949, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147949 BINDING SITE, designated SEQ ID:38422, to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, also designated SEQ ID:5413.

[90665] Another function of VGAM2702 is therefore inhibition of LOC147949 (Accession XM_085973). Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147949. LOC155179 (Accession XM_088169) is another VGAM2702 host target gene. LOC155179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155179 BINDING SITE, designated SEQ ID:39553, to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, also designated SEQ ID:5413.

[90666] Another function of VGAM2702 is therefore inhibition of LOC155179 (Accession XM_088169). Accordingly, utilities

of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155179. LOC158267 (Accession XM_088528) is another VGAM2702 host target gene. LOC158267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158267 BINDING SITE, designated SEQ ID:39790, to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, also designated SEQ ID:5413.

[90667] Another function of VGAM2702 is therefore inhibition of LOC158267 (Accession XM_088528). Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158267. LOC90161 (Accession XM_029551) is another VGAM2702 host target gene. LOC90161 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90161, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC90161 BINDING SITE, designated SEQ ID:30901, to the nucleotide sequence of VGAM2702 RNA, herein designated VGAM RNA, also designated SEQ ID:5413.

[90668] Another function of VGAM2702 is therefore inhibition of LOC90161 (Accession XM_029551). Accordingly, utilities of VGAM2702 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90161. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2703 (VGAM2703) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90669] VGAM2703 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2703 was detected is described hereinabove with reference to Figs. 1-8.

[90670] VGAM2703 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mamestra Configurata Nucleopolyhedrovirus B. VGAM2703 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90671] VGAM2703 gene encodes a VGAM2703 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2703 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2703 precursor RNA is designated SEQ ID:2689, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2689 is located at position 133043 relative to the genome of Mamestra Configurata Nucleopolyhedrovirus B.

[90672] VGAM2703 precursor RNA folds onto itself, forming VGAM2703 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90673] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2703 folded precursor RNA into VGAM2703 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2703 RNA is designated SEQ ID:5414, and is provided hereinbelow with reference to the sequence listing part.

[90674] VGAM2703 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2703 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90675] VGAM2703 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2703 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2703 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90676] The complementary binding of VGAM2703 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2703 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2703 host target RNA into VGAM2703 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90677] It is appreciated that VGAM2703 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2703 host target genes. The mRNA of each one of this plurality of VGAM2703 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2703 RNA, herein designated VGAM RNA, and which when bound by VGAM2703 RNA causes inhibition of translation of respective one or more VGAM2703 host target proteins.

[90678] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2703 gene, herein designated VGAM GENE, on one or more VGAM2703 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90679] It is yet further appreciated that a function of VGAM2703 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2703 include diagnosis, prevention and treatment of viral infection by Mamestra Configurata Nucleopolyhedrovirus B. Specific functions, and accordingly utilities, of VGAM2703 correlate with, and may be deduced from, the identity of the host target genes which VGAM2703 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90680] Nucleotide sequences of the VGAM2703 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2703 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2703 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2703 are further described hereinbelow with reference to Table 1.

[90681] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2703 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2703 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90682] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2703 gene, herein designated VGAM is inhibition of expression of VGAM2703 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2703 correlate with, and may be deduced from, the identity of the target genes which VGAM2703 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90683] Chromosome 5 Open Reading Frame 3 (C5orf3, Accession NM_018691) is a VGAM2703 host target gene. C5orf3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5orf3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf3 BINDING SITE, designated SEQ ID:20763, to the nucleotide sequence of VGAM2703 RNA, herein designated VGAM RNA, also designated SEQ ID:5414.

[90684] A function of VGAM2703 is therefore inhibition of Chro-

mosome 5 Open Reading Frame 3 (C5orf3, Accession NM_018691). Accordingly, utilities of VGAM2703 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf3. FLJ21870 (Accession NM_023016) is another VGAM2703 host target gene. FLJ21870 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21870, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21870 BINDING SITE, designated SEQ ID:23281, to the nucleotide sequence of VGAM2703 RNA, herein designated VGAM RNA, also designated SEQ ID:5414.

[90685] Another function of VGAM2703 is therefore inhibition of FLJ21870 (Accession NM_023016). Accordingly, utilities of VGAM2703 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21870. MGC2452 (Accession NM_032644) is another VGAM2703 host target gene. MGC2452 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC2452, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2452 BINDING SITE, designated SEQ ID:26364, to the nucleotide sequence of VGAM2703 RNA, herein designated VGAM RNA, also designated SEQ ID:5414.

[90686] Another function of VGAM2703 is therefore inhibition of MGC2452 (Accession NM_032644). Accordingly, utilities of VGAM2703 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2452. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2704 (VGAM2704) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90687] VGAM2704 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2704 was detected is described hereinabove with reference to Figs. 1-8.

[90688] VGAM2704 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mamestra Configurata Nucleopolyhedrovirus B. VGAM2704 host target gene,

herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90689] VGAM2704 gene encodes a VGAM2704 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2704 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2704 precursor RNA is designated SEQ ID:2690, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2690 is located at position 133581 relative to the genome of Mamestra Configurata Nucleopolyhedrovirus B.

[90690] VGAM2704 precursor RNA folds onto itself, forming VGAM2704 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90691] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2704 folded precursor RNA into VGAM2704

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of VGAM2704 RNA is designated SEQ ID:5415, and is provided hereinbelow with reference to the sequence listing part.

[90692] VGAM2704 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2704 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90693] VGAM2704 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2704 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2704 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90694] The complementary binding of VGAM2704 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2704 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2704 host target RNA into VGAM2704 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[90695] It is appreciated that VGAM2704 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2704 host target genes. The mRNA of each one of this plurality of VGAM2704 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2704 RNA, herein designated VGAM RNA, and which when bound by VGAM2704 RNA causes inhibition of translation of respective one or more VGAM2704 host target proteins.

[90696] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2704 gene, herein designated VGAM GENE, on one or more VGAM2704 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90697] It is yet further appreciated that a function of VGAM2704 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2704 include diagnosis, prevention and treatment of viral infection by Mamestra Configurata Nucleopolyhedrovirus B. Specific functions, and accordingly utilities, of VGAM2704 correlate with, and may be deduced from, the identity of the host target genes which VGAM2704 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90698] Nucleotide sequences of the VGAM2704 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2704 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2704 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2704 are further described hereinbelow with reference to Table 1.

[90699] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2704 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2704 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90700] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2704 gene, herein designated VGAM is inhibition of expression of VGAM2704 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2704 correlate with, and may be deduced from, the identity of the target genes which VGAM2704 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90701] Calumenin (CALU, Accession NM_001219) is a VGAM2704 host target gene. CALU BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CALU, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CALU BINDING SITE, designated SEQ ID:6888, to the nucleotide sequence of VGAM2704 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5415.

[90702] A function of VGAM2704 is therefore inhibition of Calumenin (CALU, Accession NM_001219), a gene which binds 7 calcium ions with a low affinity with unidtified function. Accordingly, utilities of VGAM2704 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALU. The function of CALU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM253.LAG1 Longevity Assurance Homolog 2 (S. cerevisiae) (LASS2, Accession XM_041889) is another VGAM2704 host target gene. LASS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LASS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LASS2 BINDING SITE, designated SEQ ID:33624, to the nucleotide sequence of VGAM2704 RNA, herein designated VGAM RNA, also designated SEQ ID:5415.

[90703] Another function of VGAM2704 is therefore inhibition of LAG1 Longevity Assurance Homolog 2 (S. cerevisiae)

(LASS2, Accession XM_041889). Accordingly, utilities of VGAM2704 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LASS2. LOC51339 (Accession NM_016651) is another VGAM2704 host target gene. LOC51339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51339, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51339 BINDING SITE, designated SEQ ID:18769, to the nucleotide sequence of VGAM2704 RNA, herein designated VGAM RNA, also designated SEQ ID:5415.

[90704] Another function of VGAM2704 is therefore inhibition of LOC51339 (Accession NM_016651). Accordingly, utilities of VGAM2704 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51339. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2705 (VGAM2705) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[90705] VGAM2705 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2705 was detected is described hereinabove with reference to Figs. 1-8.

[90706] VGAM2705 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis Zea Virus 1 (HZV-1). VGAM2705 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90707] VGAM2705 gene encodes a VGAM2705 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2705 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2705 precursor RNA is designated SEQ ID:2691, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2691 is located at position 81066 relative to the genome of Heliothis Zea Virus 1 (HZV-1).

[90708] VGAM2705 precursor RNA folds onto itself, forming VGAM2705 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90709] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2705 folded precursor RNA into VGAM2705 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2705 RNA is designated SEQ ID:5416, and is provided hereinbelow with reference to the sequence listing part.

[90710] VGAM2705 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2705 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90711] VGAM2705 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2705 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2705 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90712] The complementary binding of VGAM2705 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2705 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2705 host target RNA into VGAM2705 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90713] It is appreciated that VGAM2705 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2705 host target genes. The mRNA of each one of this plurality of VGAM2705 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2705 RNA, herein designated VGAM RNA, and which when bound by VGAM2705 RNA causes inhibition of translation of respective one or more VGAM2705 host target proteins.

[90714] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2705 gene, herein designated VGAM GENE, on one or more VGAM2705 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90715] It is yet further appreciated that a function of VGAM2705 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of viral infection by Heliothis Zea Virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2705 correlate with, and may be deduced from, the identity of the host target genes which VGAM2705 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90716] Nucleotide sequences of the VGAM2705 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2705 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2705 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2705 are further described hereinbelow with reference to Table 1.

[90717] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2705 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2705 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90718] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2705 gene, herein designated VGAM is inhibition of expression of VGAM2705 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2705 correlate with, and may be deduced from, the identity of the target genes which VGAM2705 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90719] Adenosine Monophosphate Deaminase (isoform E) (AMPD3, Accession NM_000480) is a VGAM2705 host target gene. AMPD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AMPD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AMPD3 BINDING SITE, designated SEQ ID:6089, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90720] A function of VGAM2705 is therefore inhibition of Adenosine Monophosphate Deaminase (isoform E) (AMPD3, Accession NM_000480), a gene which plays a critical role in energy metabolism. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMPD3. The function of AMPD3 has been established by previous studies. Yamada et al. (1992) determined the nucleotide sequence of erythrocyte cDNA. The 3.7-kb cDNA contained an open reading frame of 2,301 bp that encodes 767 amino acids to form an 89-kD protein. Whereas both the AMPD1 and AMPD2 genes are situated in the 1p21-p13 region of chromosome 1, Eddy et al. (1993) demonstrated that the AMPD3 gene is located on chromosome 11 in the region pter-p13. Sermsuvitayawong et al. (1997) demonstrated that the Ampd3 gene is located on mouse chromosome 7 in a region of conserved linkage homology with human 11p. The mouse homolog, however, has a different gene structure in the 5-prime region, the gene products are reported to be immunologically distinct, and Sermsuvitayawong et al. (1997) referred to the Ampd3 gene as the heart-type AMPD. Ogasawara et al. (1987) observed 6 related individuals with complete deficiency of erythrocyte

AMP deaminase. All were healthy and had no hematologic disorders. The deficiency was limited to isozyme E, which is the red cell type. The deficiency was inherited as an autosomal recessive trait as demonstrated by the fact that both parents had partial deficiency in each case in which this could be studied and all children of completely deficient individuals were partially deficient. The frequency of the mutant gene was surprisingly high; heterozygotes had a frequency of about 1 in 30 in Japan, Seoul, and Taipei. The ATP level was approximately 50% higher in AMP-deficient red cells compared to the level in the control cells. Degradation of adenine nucleotide was slower in the deficient erythrocytes than in the control erythrocytes. Yamada et al. (1994) stated that AMPD3 deficiency had been found in Europe and that the frequency in northern Poland was almost the same as that in east Asia.

[90721] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[90722] Ogasawara, N.; Goto, H.; Yamada, Y.; Nishigaki, I.; Itoh, T.; Hasegawa, I.; Park, K. S. : Deficiency of AMP deaminase in erythrocytes. Hum. Genet. 75: 15-18, 1987. ; and

[90723] Yamada, Y.; Goto, H.; Ogasawara, N. : A point mutation

responsible for human erythrocyte AMP deaminase deficiency. Hum. Molec. Genet. 3: 331-334, 1994.

[90724] Further studies establishing the function and utilities of AMPD3 are found in John Hopkins OMIM database record ID 102772, and in sited publications numbered 12767-12771 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Bassoon (presynaptic cytomatrix protein) (BSN, Accession NM_003458) is another VGAM2705 host target gene. BSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BSN BINDING SITE, designated SEQ ID:9519, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90725] Another function of VGAM2705 is therefore inhibition of Bassoon (presynaptic cytomatrix protein) (BSN, Accession NM_003458), a gene which may be involved in cytomatrix organization at the site of neurotransmitter release. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with BSN. The function of BSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM638.Nuclear Protein, Ataxia-telangiectasia Locus (NPAT, Accession XM_040846) is another VGAM2705 host target gene. NPAT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPAT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPAT BINDING SITE, designated SEQ ID:33388, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90726] Another function of VGAM2705 is therefore inhibition of Nuclear Protein, Ataxia-telangiectasia Locus (NPAT, Accession XM_040846), a gene which is expressed in all tissues. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPAT. The function of NPAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM376.Otoraplin

(OTOR, Accession NM_020157) is another VGAM2705 host target gene. OTOR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OTOR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OTOR BINDING SITE, designated SEQ ID:21367, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90727] Another function of VGAM2705 is therefore inhibition of Otoraplin (OTOR, Accession NM_020157), a gene which plays a role in the early chondrogenesis of the periotic mesenchyme. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTOR. The function of OTOR has been established by previous studies. During large-scale analysis of human fetal cochlea EST sequences, Robertson et al. (2000) identified a novel gene, designated OTOR. They also isolated orthologous genes in mouse, chicken, and bullfrog by screening inner ear cDNA libraries. Rendtorff et al. (2001) independently identified OTOR, which they called MIA-like (MIAL), during a search

for cochlea-specific EST clusters. Cohen-Salmon et al. (2000) cloned the mouse Otor gene, which they called fibrocyte-derived protein (Fdp), using a subtracted mouse cochlea cDNA library and 5-prime RACE. Human OTOR encodes a 128-amino acid protein with a predicted secretion signal peptide. The protein shares high sequence identity with the mouse (90%), chicken (80%), and bullfrog (60%) orthologs and with the related human CDRAP/MIA protein (OMIM Ref. No. 601340) (43%). By expressing OTOR in mammalian cell cultures, Rendtorff et al. (2001) showed that OTOR is translated as an approximately 15-kD polypeptide that is assembled into a covalently linked homodimer, modified by sulfation, and secreted from the cells via the Golgi apparatus. By Northern blot analysis, Robertson et al. (2000) detected expression of a major 1.1-kb and minor 1.8- and 4-kb OTOR transcripts in human cochlea. Using RT-PCR and in situ hybridization, Rendtorff et al. (2001) detected OTOR expression specific to a cell layer beneath the sensory epithelium of cochlea and vestibule of human fetal inner ear. Rendtorff et al. (2001) reported a frequent polymorphism in the translation initiation codon of OTOR (ACG instead of ATG). Of 505 unrelated individuals analyzed, 9.5% were ACG/ATG

heterozygous. The ACG allele failed to direct synthesis of the OTOR protein in transfected cells. Rendtorff et al. (2001) concluded that OTOR may contribute to inner ear dysfunction in humans.

[90728] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[90729] Rendtorff, N. D.; Frodin, M.; Attie-Bitach, T.; Vekemans, M.; Tommerup, N. : Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation. Genomics 71: 40-52, 2001. ; and

[90730] Robertson, N. G.; Heller, S.; Lin, J. S.; Resendes, B. L.; Weremowicz, S.; Denis, C. S.; Bell, A. M.; Hudspeth, A. J.; Morton, C. C. : A novel conserved cochlear gene, OTOR: identificati.

[90731] Further studies establishing the function and utilities of OTOR are found in John Hopkins OMIM database record ID 606067, and in sited publications numbered 4496-4498 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Synaptotagmin I (SYT1, Accession NM_005639) is another VGAM2705 host

target gene. SYT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYT1 BINDING SITE, designated SEQ ID:12171, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90732] Another function of VGAM2705 is therefore inhibition of Synaptotagmin I (SYT1, Accession NM_005639), a gene which may have a regulatory role in the membrane interactions during trafficking of synaptic vesicles at the active zone of the synapse. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT1. The function of SYT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM739.T, Brachyury Homolog (mouse) (T, Accession NM_003181) is another VGAM2705 host target gene. T BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by T, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of T BINDING SITE, designated SEQ ID:9154, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90733] Another function of VGAM2705 is therefore inhibition of T, Brachyury Homolog (mouse) (T, Accession NM_003181), a gene which is a potent transcription factor. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with T. The function of T and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1083.V-yes-1 Yamaguchi Sarcoma Viral Oncogene Homolog 1 (YES1, Accession NM_005433) is another VGAM2705 host target gene. YES1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YES1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YES1 BINDING SITE, designated SEQ ID:11916, to the nucleotide sequence of

VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90734] Another function of VGAM2705 is therefore inhibition of V-yes-1 Yamaguchi Sarcoma Viral Oncogene Homolog 1 (YES1, Accession NM_005433), a gene which is a putative protein-tyrosine kinase. Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YES1. The function of YES1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Rho Guanine Nucleotide Exchange Factor (GEF) 10 (ARHGEF10, Accession XM_017169) is another VGAM2705 host target gene. ARHGEF10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGEF10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF10 BINDING SITE, designated SEQ ID:30305, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90735] Another function of VGAM2705 is therefore inhibition of

Rho Guanine Nucleotide Exchange Factor (GEF) 10 (ARHGEF10, Accession XM_017169). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF10. CD109 (Accession NM_133493) is another VGAM2705 host target gene. CD109 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD109, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD109 BINDING SITE, designated SEQ ID:28572, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90736] Another function of VGAM2705 is therefore inhibition of CD109 (Accession NM_133493). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD109. FLJ12934 (Accession NM_022899) is another VGAM2705 host target gene. FLJ12934 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12934 BINDING SITE, designated SEQ ID:23177, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90737] Another function of VGAM2705 is therefore inhibition of FLJ12934 (Accession NM_022899). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12934. KIAA0014 (Accession NM_014665) is another VGAM2705 host target gene. KIAA0014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0014 BINDING SITE, designated SEQ ID:16117, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90738] Another function of VGAM2705 is therefore inhibition of KIAA0014 (Accession NM_014665). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0014. KIAA0092 (Accession NM_014679) is another VGAM2705 host target gene. KIAA0092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0092 BINDING SITE, designated SEQ ID:16157, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90739] Another function of VGAM2705 is therefore inhibition of KIAA0092 (Accession NM_014679). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0092. KIAA0318 (Accession XM_044334) is another VGAM2705 host target gene. KIAA0318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0318 BINDING SITE, designated SEQ ID:34185, to the nucleotide sequence of VGAM2705 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5416.

[90740] Another function of VGAM2705 is therefore inhibition of KIAA0318 (Accession XM_044334). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0318. KIAA1219 (Accession XM_028835) is another VGAM2705 host target gene. KIAA1219 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1219 BINDING SITE, designated SEQ ID:30760, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90741] Another function of VGAM2705 is therefore inhibition of KIAA1219 (Accession XM_028835). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1219. Low Density Lipoprotein-related Protein 1B (deleted in tumors) (LRP1B, Accession NM_018557) is another VGAM2705 host target gene. LRP1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LRP1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRP1B BINDING SITE, designated SEQ ID:20640, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90742] Another function of VGAM2705 is therefore inhibition of Low Density Lipoprotein-related Protein 1B (deleted in tumors) (LRP1B, Accession NM_018557). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP1B. TRIP-Br2 (Accession NM_014755) is another VGAM2705 host target gene. TRIP-Br2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP-Br2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:16487, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90743] Another function of VGAM2705 is therefore inhibition of

TRIP-Br2 (Accession NM_014755). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP-Br2. Tubulin, Gamma Complex Associated Protein 3 (TUBGCP3, Accession NM_006322) is another VGAM2705 host target gene. TUBGCP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUBGCP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUBGCP3 BINDING SITE, designated SEQ ID:13013, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90744] Another function of VGAM2705 is therefore inhibition of Tubulin, Gamma Complex Associated Protein 3 (TUBGCP3, Accession NM_006322). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUBGCP3. LOC158014 (Accession XM_088442) is another VGAM2705 host target gene. LOC158014 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158014, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158014 BINDING SITE, designated SEQ ID:39696, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90745] Another function of VGAM2705 is therefore inhibition of LOC158014 (Accession XM_088442). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158014. LOC202908 (Accession XM_114602) is another VGAM2705 host target gene. LOC202908 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202908, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202908 BINDING SITE, designated SEQ ID:42996, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90746] Another function of VGAM2705 is therefore inhibition of LOC202908 (Accession XM_114602). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC202908. LOC90719 (Accession XM_033704) is another VGAM2705 host target gene. LOC90719 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90719 BINDING SITE, designated SEQ ID:31948, to the nucleotide sequence of VGAM2705 RNA, herein designated VGAM RNA, also designated SEQ ID:5416.

[90747] Another function of VGAM2705 is therefore inhibition of LOC90719 (Accession XM_033704). Accordingly, utilities of VGAM2705 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90719. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2706 (VGAM2706) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90748] VGAM2706 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2706 was detected is described hereinabove with reference to Figs. 1-8.

[90749] VGAM2706 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis Zea Virus 1 (HZV-1). VGAM2706 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90750] VGAM2706 gene encodes a VGAM2706 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2706 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2706 precursor RNA is designated SEQ ID:2692, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2692 is located at position 84781 relative to the genome of Heliothis Zea Virus 1 (HZV-1).

[90751] VGAM2706 precursor RNA folds onto itself, forming VGAM2706 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90752] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2706 folded precursor RNA into VGAM2706 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2706 RNA is designated SEQ ID:5417, and is provided hereinbelow with reference to the sequence listing part.

[90753] VGAM2706 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2706 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90754] VGAM2706 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2706 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2706 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90755] The complementary binding of VGAM2706 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2706 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2706 host target RNA into VGAM2706 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90756] It is appreciated that VGAM2706 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2706 host target genes. The mRNA of each one of this plurality of VGAM2706 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2706 RNA, herein designated VGAM RNA, and which when bound by VGAM2706 RNA causes inhibition of translation of respective one or more VGAM2706 host target proteins.

[90757] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2706 gene, herein designated VGAM GENE, on one or more VGAM2706 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90758] It is yet further appreciated that a function of VGAM2706 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of viral infection by Heliothis Zea Virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2706 correlate with, and may be deduced from, the identity of the host target genes which VGAM2706 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90759] Nucleotide sequences of the VGAM2706 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2706 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2706 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2706 are further described hereinbelow with reference to Table 1.

[90760] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2706 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2706 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90761] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2706 gene, herein designated VGAM is inhibition of expression of VGAM2706 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2706 correlate with, and may be deduced from, the identity of the target genes which VGAM2706 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90762] Dachshund Homolog (Drosophila) (DACH, Accession NM_080759) is a VGAM2706 host target gene. DACH BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by DACH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DACH BINDING SITE, designated SEQ ID:28035, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90763] A function of VGAM2706 is therefore inhibition of Dachshund Homolog (Drosophila) (DACH, Accession NM_080759), a gene which regulates early progenitor cell proliferation during retinogenesis and pituitary development . Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DACH. The function of DACH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM260.Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155) is another VGAM2706 host target gene. SERPINB9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINB9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE, designated SEQ ID:10362, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90764] Another function of VGAM2706 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB9. The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM60.Chromosome 20 Open Reading Frame 139 (C20orf139, Accession XM_097749) is another VGAM2706 host target gene. C20orf139 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of C20orf139 BINDING SITE, designated SEQ ID:41107, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90765] Another function of VGAM2706 is therefore inhibition of Chromosome 20 Open Reading Frame 139 (C20orf139, Accession XM_097749). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf139. FLJ13769 (Accession NM_025012) is another VGAM2706 host target gene. FLJ13769 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13769 BINDING SITE, designated SEQ ID:24590, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90766] Another function of VGAM2706 is therefore inhibition of FLJ13769 (Accession NM_025012). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13769. FLJ32734 (Accession NM_144681) is another VGAM2706 host target gene. FLJ32734 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ32734, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32734 BINDING SITE, designated SEQ ID:29496, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90767] Another function of VGAM2706 is therefore inhibition of FLJ32734 (Accession NM_144681). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32734. KIAA0494 (Accession NM_014774) is another VGAM2706 host target gene. KIAA0494 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0494, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0494 BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of VGAM2706 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5417.

[90768] Another function of VGAM2706 is therefore inhibition of KIAA0494 (Accession NM_014774). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0494. KIAA1775 (Accession NM_033100) is another VGAM2706 host target gene. KIAA1775 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1775, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1775 BINDING SITE, designated SEQ ID:26942, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90769] Another function of VGAM2706 is therefore inhibition of KIAA1775 (Accession NM_033100). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1775. MGC2749 (Accession NM_024069) is another VGAM2706 host target gene. MGC2749 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2749, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2749 BINDING SITE, designated SEQ ID:23499, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90770] Another function of VGAM2706 is therefore inhibition of MGC2749 (Accession NM_024069). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2749. MGC3178 (Accession NM_030810) is another VGAM2706 host target gene. MGC3178 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3178 BINDING SITE, designated SEQ ID:25131, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90771] Another function of VGAM2706 is therefore inhibition of MGC3178 (Accession NM_030810). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC3178. LOC146229 (Accession XM_085387) is another VGAM2706 host target gene. LOC146229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE, designated SEQ ID:38111, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90772] Another function of VGAM2706 is therefore inhibition of LOC146229 (Accession XM_085387). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229. LOC147040 (Accession XM_085689) is another VGAM2706 host target gene. LOC147040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147040 BINDING SITE, designated SEQ ID:38287, to

the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90773] Another function of VGAM2706 is therefore inhibition of LOC147040 (Accession XM_085689). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147040. LOC154881 (Accession XM_088063) is another VGAM2706 host target gene. LOC154881 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154881, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154881 BINDING SITE, designated SEQ ID:39496, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90774] Another function of VGAM2706 is therefore inhibition of LOC154881 (Accession XM_088063). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154881. LOC155036 (Accession XM_098651) is another VGAM2706 host target gene. LOC155036 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC155036, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155036 BINDING SITE, designated SEQ ID:41753, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90775] Another function of VGAM2706 is therefore inhibition of LOC155036 (Accession XM_098651). Accordingly, utilities of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155036. LOC253681 (Accession XM_170830) is another VGAM2706 host target gene. LOC253681 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253681, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253681 BINDING SITE, designated SEQ ID:45605, to the nucleotide sequence of VGAM2706 RNA, herein designated VGAM RNA, also designated SEQ ID:5417.

[90776] Another function of VGAM2706 is therefore inhibition of LOC253681 (Accession XM_170830). Accordingly, utilities

of VGAM2706 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253681. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2707 (VGAM2707) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90777] VGAM2707 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2707 was detected is described hereinabove with reference to Figs. 1-8.

[90778] VGAM2707 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis Zea Virus 1 (HZV-1). VGAM2707 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90779] VGAM2707 gene encodes a VGAM2707 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2707 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2707 precursor RNA is designated SEQ ID:2693, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2693 is located at position 85718 relative to the genome of Heliothis Zea Virus 1 (HZV-1).

[90780] VGAM2707 precursor RNA folds onto itself, forming VGAM2707 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90781] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2707 folded precursor RNA into VGAM2707 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2707 RNA is designated SEQ ID:5418, and

is provided hereinbelow with reference to the sequence listing part.

[90782] VGAM2707 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2707 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90783] VGAM2707 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2707 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2707 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90784] The complementary binding of VGAM2707 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2707 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2707 host target RNA into VGAM2707 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90785] It is appreciated that VGAM2707 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2707 host target genes. The mRNA of each one of this plurality of VGAM2707 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2707 RNA, herein designated VGAM RNA, and which when bound by VGAM2707 RNA causes inhibition of translation of respective one or more VGAM2707 host target proteins.

[90786] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2707 gene, herein designated VGAM GENE, on one or more VGAM2707 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90787] It is yet further appreciated that a function of VGAM2707 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of viral infection by Heliothis Zea Virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2707 correlate with, and may be deduced from, the identity of the host target genes which VGAM2707 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90788] Nucleotide sequences of the VGAM2707 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2707 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2707 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2707 are further described hereinbelow with reference to Table 1.

[90789] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2707 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2707 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90790] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2707 gene, herein designated VGAM is inhibition of expression of VGAM2707 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2707 correlate with, and may be deduced from, the identity of the target genes which VGAM2707 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90791] Transmembrane, Prostate Androgen Induced RNA (TMEPAI, Accession NM_020182) is a VGAM2707 host target gene. TMEPAI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMEPAI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMEPAI BINDING SITE, designated SEQ ID:21404, to the nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, also designated SEQ ID:5418.

[90792] A function of VGAM2707 is therefore inhibition of Transmembrane, Prostate Androgen Induced RNA (TMEPAI, Accession NM_020182). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEPAI. FLJ13769

(Accession NM_025012) is another VGAM2707 host target gene. FLJ13769 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13769 BINDING SITE, designated SEQ ID:24598, to the nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, also designated SEQ ID:5418.

[90793] Another function of VGAM2707 is therefore inhibition of FLJ13769 (Accession NM_025012). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13769. KIAA1915 (Accession XM_055481) is another VGAM2707 host target gene. KIAA1915 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1915, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1915 BINDING SITE, designated SEQ ID:36272, to the nucleotide sequence of VGAM2707 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5418.

[90794] Another function of VGAM2707 is therefore inhibition of KIAA1915 (Accession XM_055481). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1915. MGC12217 (Accession NM_032771) is another VGAM2707 host target gene. MGC12217 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC12217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12217 BINDING SITE, designated SEQ ID:26516, to the nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, also designated SEQ ID:5418.

[90795] Another function of VGAM2707 is therefore inhibition of MGC12217 (Accession NM_032771). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12217. LOC152503 (Accession XM_098238) is another VGAM2707 host target gene. LOC152503 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152503, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152503 BINDING SITE, designated SEQ ID:41516, to the nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, also designated SEQ ID:5418.

[90796] Another function of VGAM2707 is therefore inhibition of LOC152503 (Accession XM_098238). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152503. LOC153914 (Accession XM_087799) is another VGAM2707 host target gene. LOC153914 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153914, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153914 BINDING SITE, designated SEQ ID:39436, to the nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, also designated SEQ ID:5418.

[90797] Another function of VGAM2707 is therefore inhibition of LOC153914 (Accession XM_087799). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC153914. LOC253430 (Accession XM_171385) is another VGAM2707 host target gene. LOC253430 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253430, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253430 BINDING SITE, designated SEQ ID:46044, to the nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, also designated SEQ ID:5418.

[90798] Another function of VGAM2707 is therefore inhibition of LOC253430 (Accession XM_171385). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253430. LOC91496 (Accession XM_038788) is another VGAM2707 host target gene. LOC91496 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91496, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91496 BINDING SITE, designated SEQ ID:32921, to the

nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, also designated SEQ ID:5418.

[90799] Another function of VGAM2707 is therefore inhibition of LOC91496 (Accession XM_038788). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91496. LOC92096 (Accession XM_042812) is another VGAM2707 host target gene. LOC92096 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92096, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92096 BINDING SITE, designated SEQ ID:33777, to the nucleotide sequence of VGAM2707 RNA, herein designated VGAM RNA, also designated SEQ ID:5418.

[90800] Another function of VGAM2707 is therefore inhibition of LOC92096 (Accession XM_042812). Accordingly, utilities of VGAM2707 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92096. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2708 (VGAM2708) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90801] VGAM2708 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2708 was detected is described hereinabove with reference to Figs. 1-8.

[90802] VGAM2708 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis Zea Virus 1 (HZV-1). VGAM2708 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90803] VGAM2708 gene encodes a VGAM2708 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2708 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2708 precursor RNA is designated SEQ ID:2694, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2694 is located at position 91200 relative to the genome of Heliothis Zea Virus 1 (HZV-1).

[90804] VGAM2708 precursor RNA folds onto itself, forming VGAM2708 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90805] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2708 folded precursor RNA into VGAM2708 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2708 RNA is designated SEQ ID:5419, and is provided hereinbelow with reference to the sequence listing part.

[90806] VGAM2708 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2708 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2708 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90807] VGAM2708 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2708 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2708 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2708 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2708 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90808] The complementary binding of VGAM2708 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2708 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2708 host target RNA into VGAM2708 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90809] It is appreciated that VGAM2708 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2708 host target genes. The mRNA of each one of this plurality of VGAM2708 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2708 RNA, herein designated VGAM RNA, and which when bound by VGAM2708 RNA causes inhibition of translation of respective one or more VGAM2708 host target proteins.

[90810] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2708 gene, herein designated VGAM GENE, on one or more VGAM2708 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90811] It is yet further appreciated that a function of VGAM2708 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2708 include diagnosis, prevention and treatment of viral infection by Heliothis Zea Virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2708 correlate with, and may be deduced from, the

identity of the host target genes which VGAM2708 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90812] Nucleotide sequences of the VGAM2708 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2708 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2708 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2708 are further described hereinbelow with reference to Table 1.

[90813] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2708 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2708 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90814] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2708 gene, herein designated VGAM is inhibition of expression of VGAM2708 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2708 correlate with, and may be deduced from, the identity of the target genes which VGAM2708

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90815] Radixin (RDX, Accession NM_002906) is a VGAM2708 host target gene. RDX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RDX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RDX BINDING SITE, designated SEQ ID:8811, to the nucleotide sequence of VGAM2708 RNA, herein designated VGAM RNA, also designated SEQ ID:5419.

[90816] A function of VGAM2708 is therefore inhibition of Radixin (RDX, Accession NM_002906), a gene which plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane. Accordingly, utilities of VGAM2708 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RDX. The function of RDX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM290.V-akt Murine Thymoma Viral Oncogene Homolog 3 (protein kinase B, gamma) (AKT3, Accession NM_005465) is another VGAM2708 host target gene.

AKT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKT3 BINDING SITE, designated SEQ ID:11959, to the nucleotide sequence of VGAM2708 RNA, herein designated VGAM RNA, also designated SEQ ID:5419.

[90817] Another function of VGAM2708 is therefore inhibition of V-akt Murine Thymoma Viral Oncogene Homolog 3 (protein kinase B, gamma) (AKT3, Accession NM_005465). Accordingly, utilities of VGAM2708 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKT3. KIAA1091 (Accession XM_045750) is another VGAM2708 host target gene. KIAA1091 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1091, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1091 BINDING SITE, designated SEQ ID:34540, to the nucleotide sequence of VGAM2708 RNA, herein designated VGAM RNA, also designated SEQ

ID:5419.

[90818] Another function of VGAM2708 is therefore inhibition of KIAA1091 (Accession XM_045750). Accordingly, utilities of VGAM2708 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1091. MO25 (Accession NM_016289) is another VGAM2708 host target gene. MO25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MO25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MO25 BINDING SITE, designated SEQ ID:18418, to the nucleotide sequence of VGAM2708 RNA, herein designated VGAM RNA, also designated SEQ ID:5419.

[90819] Another function of VGAM2708 is therefore inhibition of MO25 (Accession NM_016289). Accordingly, utilities of VGAM2708 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MO25. LOC155061 (Accession XM_088139) is another VGAM2708 host target gene. LOC155061 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155061, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155061 BINDING SITE, designated SEQ ID:39538, to the nucleotide sequence of VGAM2708 RNA, herein designated VGAM RNA, also designated SEQ ID:5419.

[90820] Another function of VGAM2708 is therefore inhibition of LOC155061 (Accession XM_088139). Accordingly, utilities of VGAM2708 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155061. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2709 (VGAM2709) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90821] VGAM2709 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2709 was detected is described hereinabove with reference to Figs. 1-8.

[90822] VGAM2709 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis Zea Virus 1

(HZV-1). VGAM2709 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90823] VGAM2709 gene encodes a VGAM2709 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2709 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2709 precursor RNA is designated SEQ ID:2695, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2695 is located at position 89310 relative to the genome of Heliothis Zea Virus 1 (HZV-1).

[90824] VGAM2709 precursor RNA folds onto itself, forming VGAM2709 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90825] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2709 folded precursor RNA into VGAM2709 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2709 RNA is designated SEQ ID:5420, and is provided hereinbelow with reference to the sequence listing part.

[90826] VGAM2709 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2709 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90827] VGAM2709 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2709 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2709 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90828] The complementary binding of VGAM2709 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2709 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2709 host target RNA into VGAM2709 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90829] It is appreciated that VGAM2709 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2709 host target genes. The mRNA of each one of this plurality of VGAM2709 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2709 RNA, herein designated VGAM RNA, and which when bound by VGAM2709 RNA causes inhibition of translation of respective one or more VGAM2709 host target proteins.

[90830] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2709 gene, herein designated VGAM GENE, on one or more VGAM2709 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90831] It is yet further appreciated that a function of VGAM2709 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2709 include diagnosis, prevention and treatment of viral infection by Heliothis Zea Virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2709 correlate with, and may be deduced from, the identity of the host target genes which VGAM2709 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90832] Nucleotide sequences of the VGAM2709 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2709 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2709 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2709 are further described hereinbelow with reference to Table 1.

[90833] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2709 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2709 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90834] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2709 gene, herein designated VGAM is inhibition of expression of VGAM2709 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2709 correlate with, and may be deduced from, the identity of the target genes which VGAM2709 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90835] TOX (Accession NM_014729) is a VGAM2709 host target gene. TOX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOX BINDING SITE, designated SEQ ID:16328, to the nucleotide sequence of VGAM2709 RNA, herein

designated VGAM RNA, also designated SEQ ID:5420.

[90836] A function of VGAM2709 is therefore inhibition of TOX (Accession NM_014729). Accordingly, utilities of VGAM2709 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOX. FLJ14153 (Accession NM_022736) is another VGAM2709 host target gene. FLJ14153 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14153 BINDING SITE, designated SEQ ID:22941, to the nucleotide sequence of VGAM2709 RNA, herein designated VGAM RNA, also designated SEQ ID:5420.

[90837] Another function of VGAM2709 is therefore inhibition of FLJ14153 (Accession NM_022736). Accordingly, utilities of VGAM2709 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14153. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2710 (VGAM2710) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90838] VGAM2710 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2710 was detected is described hereinabove with reference to Figs. 1-8.

[90839] VGAM2710 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Heliothis Zea Virus 1 (HZV-1). VGAM2710 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90840] VGAM2710 gene encodes a VGAM2710 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2710 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2710 precursor RNA is designated SEQ ID:2696, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2696 is located at position 224367 relative to the genome of Heliothis Zea Virus 1 (HZV-1).

[90841] VGAM2710 precursor RNA folds onto itself, forming

VGAM2710 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90842] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2710 folded precursor RNA into VGAM2710 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM2710 RNA is designated SEQ ID:5421, and is provided hereinbelow with reference to the sequence listing part.

[90843] VGAM2710 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2710 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90844] VGAM2710 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2710 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2710 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90845] The complementary binding of VGAM2710 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2710 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2710 host target RNA into VGAM2710 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90846] It is appreciated that VGAM2710 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2710 host target genes. The mRNA of each one of this plurality of VGAM2710 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2710 RNA, herein designated VGAM RNA, and which when bound by VGAM2710 RNA causes inhibition of translation of respective one or more VGAM2710 host target proteins.

[90847] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2710 gene, herein designated VGAM GENE, on one or more VGAM2710 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90848] It is yet further appreciated that a function of VGAM2710 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2710 include diagnosis, prevention and treatment of viral infection by Heliothis Zea Virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGAM2710 correlate with, and may be deduced from, the identity of the host target genes which VGAM2710 binds

and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90849] Nucleotide sequences of the VGAM2710 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2710 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2710 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2710 are further described hereinbelow with reference to Table 1.

[90850] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2710 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2710 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90851] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2710 gene, herein designated VGAM is inhibition of expression of VGAM2710 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2710 correlate with, and may be deduced from, the identity of the target genes which VGAM2710 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[90852] Nijmegen Breakage Syndrome 1 (nibrin) (NBS1, Accession XM_045343) is a VGAM2710 host target gene. NBS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NBS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NBS1 BINDING SITE, designated SEQ ID:34434, to the nucleotide sequence of VGAM2710 RNA, herein designated VGAM RNA, also designated SEQ ID:5421.

[90853] A function of VGAM2710 is therefore inhibition of Nijmegen Breakage Syndrome 1 (nibrin) (NBS1, Accession XM_045343), a gene which may be involved in repair of DNA double-strand breaks. Accordingly, utilities of VGAM2710 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NBS1. The function of NBS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM450.FLJ20127 (Accession NM_017678) is another VGAM2710 host target gene. FLJ20127 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ20127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20127 BINDING SITE, designated SEQ ID:19220, to the nucleotide sequence of VGAM2710 RNA, herein designated VGAM RNA, also designated SEQ ID:5421.

[90854] Another function of VGAM2710 is therefore inhibition of FLJ20127 (Accession NM_017678). Accordingly, utilities of VGAM2710 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20127. LOC150503 (Accession XM_086933) is another VGAM2710 host target gene. LOC150503 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150503, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150503 BINDING SITE, designated SEQ ID:38985, to the nucleotide sequence of VGAM2710 RNA, herein designated VGAM RNA, also designated SEQ ID:5421.

[90855] Another function of VGAM2710 is therefore inhibition of LOC150503 (Accession XM_086933). Accordingly, utilities

of VGAM2710 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150503. LOC150504 (Accession XM_001732) is another VGAM2710 host target gene. LOC150504 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150504, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150504 BINDING SITE, designated SEQ ID:29850, to the nucleotide sequence of VGAM2710 RNA, herein designated VGAM RNA, also designated SEQ ID:5421.

[90856] Another function of VGAM2710 is therefore inhibition of LOC150504 (Accession XM_001732). Accordingly, utilities of VGAM2710 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150504. LOC221410 (Accession XM_166373) is another VGAM2710 host target gene. LOC221410 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221410, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC221410 BINDING SITE, designated SEQ ID:44194, to the nucleotide sequence of VGAM2710 RNA, herein designated VGAM RNA, also designated SEQ ID:5421.

[90857] Another function of VGAM2710 is therefore inhibition of LOC221410 (Accession XM_166373). Accordingly, utilities of VGAM2710 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221410. LOC90408 (Accession XM_031517) is another VGAM2710 host target gene. LOC90408 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90408 BINDING SITE, designated SEQ ID:31397, to the nucleotide sequence of VGAM2710 RNA, herein designated VGAM RNA, also designated SEQ ID:5421.

[90858] Another function of VGAM2710 is therefore inhibition of LOC90408 (Accession XM_031517). Accordingly, utilities of VGAM2710 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90408. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2711 (VGAM2711) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90859] VGAM2711 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2711 was detected is described hereinabove with reference to Figs. 1-8.

[90860] VGAM2711 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chikungunya Virus. VGAM2711 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90861] VGAM2711 gene encodes a VGAM2711 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2711 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2711 precursor RNA is designated SEQ ID:2697, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2697 is located at position 7022 relative to the

genome of Chikungunya Virus.

[90862] VGAM2711 precursor RNA folds onto itself, forming VGAM2711 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90863] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2711 folded precursor RNA into VGAM2711 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2711 RNA is designated SEQ ID:5422, and is provided hereinbelow with reference to the sequence listing part.

[90864] VGAM2711 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2711 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90865] VGAM2711 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2711 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2711 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90866] The complementary binding of VGAM2711 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2711 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2711 host target RNA into VGAM2711 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90867] It is appreciated that VGAM2711 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2711 host target genes. The mRNA of each one of this plurality of VGAM2711 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2711 RNA, herein designated VGAM RNA, and which when bound by VGAM2711 RNA causes inhibition of translation of respective one or more VGAM2711 host target proteins.

[90868] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2711 gene, herein designated VGAM GENE, on one or more VGAM2711 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90869] It is yet further appreciated that a function of VGAM2711 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of viral infection by Chikungunya Virus. Specific functions, and accordingly utilities, of VGAM2711 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2711 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90870] Nucleotide sequences of the VGAM2711 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2711 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2711 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2711 are further described hereinbelow with reference to Table 1.

[90871] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2711 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2711 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90872] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2711 gene, herein designated VGAM is inhibition of expression of VGAM2711 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2711 correlate with, and may be deduced

from, the identity of the target genes which VGAM2711 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90873] V-ets Erythroblastosis Virus E26 Oncogene Homolog 2 (avian) (ETS2, Accession NM_005239) is a VGAM2711 host target gene. ETS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ETS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ETS2 BINDING SITE, designated SEQ ID:11749, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90874] A function of VGAM2711 is therefore inhibition of V-ets Erythroblastosis Virus E26 Oncogene Homolog 2 (avian) (ETS2, Accession NM_005239), a gene which Transcription factor. Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ETS2. The function of ETS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM1958.Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_139125) is another VGAM2711 host target gene. MASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MASP1 BINDING SITE, designated SEQ ID:29159, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90875] Another function of VGAM2711 is therefore inhibition of Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_139125), a gene which a complement-dependent bactericidal factor . Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MASP1. The function of MASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM566.Translocase of Inner Mitochondrial Membrane

23 Homolog (yeast) (TIMM23, Accession XM_011891) is another VGAM2711 host target gene. TIMM23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIMM23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIMM23 BINDING SITE, designated SEQ ID:30199, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90876] Another function of VGAM2711 is therefore inhibition of Translocase of Inner Mitochondrial Membrane 23 Homolog (yeast) (TIMM23, Accession XM_011891), a gene which translocates nuclear-encoded proteins into the mitochondrion. Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIMM23. The function of TIMM23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Angiomotin (AMOT, Accession NM_133265) is another VGAM2711 host target gene. AMOT BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by AMOT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AMOT BINDING SITE, designated SEQ ID:28412, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90877] Another function of VGAM2711 is therefore inhibition of Angiomotin (AMOT, Accession NM_133265). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMOT. Centaurin, Alpha 2 (CENTA2, Accession NM_018404) is another VGAM2711 host target gene. CENTA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CENTA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENTA2 BINDING SITE, designated SEQ ID:20442, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90878] Another function of VGAM2711 is therefore inhibition of

Centaurin, Alpha 2 (CENTA2, Accession NM_018404). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENTA2. DKFZP434O047 (Accession NM_015594) is another VGAM2711 host target gene. DKFZP434O047 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434O047, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434O047 BINDING SITE, designated SEQ ID:17864, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90879] Another function of VGAM2711 is therefore inhibition of DKFZP434O047 (Accession NM_015594). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434O047. FLJ11078 (Accession NM_018316) is another VGAM2711 host target gene. FLJ11078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11078, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11078 BINDING SITE, designated SEQ ID:20309, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90880] Another function of VGAM2711 is therefore inhibition of FLJ11078 (Accession NM_018316). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11078. FLJ11274 (Accession NM_018375) is another VGAM2711 host target gene. FLJ11274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11274 BINDING SITE, designated SEQ ID:20401, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90881] Another function of VGAM2711 is therefore inhibition of FLJ11274 (Accession NM_018375). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ11274. FLJ21603 (Accession NM_024762) is another VGAM2711 host target gene. FLJ21603 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21603, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21603 BINDING SITE, designated SEQ ID:24119, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90882] Another function of VGAM2711 is therefore inhibition of FLJ21603 (Accession NM_024762). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21603. KIAA1077 (Accession XM_053496) is another VGAM2711 host target gene. KIAA1077 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1077 BINDING SITE, designated SEQ ID:36096, to the nucleotide sequence of VGAM2711 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5422.

[90883] Another function of VGAM2711 is therefore inhibition of KIAA1077 (Accession XM_053496). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1077. LOC150150 (Accession XM_097820) is another VGAM2711 host target gene. LOC150150 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150150, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150150 BINDING SITE, designated SEQ ID:41138, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90884] Another function of VGAM2711 is therefore inhibition of LOC150150 (Accession XM_097820). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150150. LOC254381 (Accession XM_173436) is another VGAM2711 host target gene. LOC254381 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254381, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254381 BINDING SITE, designated SEQ ID:46544, to the nucleotide sequence of VGAM2711 RNA, herein designated VGAM RNA, also designated SEQ ID:5422.

[90885] Another function of VGAM2711 is therefore inhibition of LOC254381 (Accession XM_173436). Accordingly, utilities of VGAM2711 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254381. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2712 (VGAM2712) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90886] VGAM2712 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2712 was detected is described hereinabove with reference to Figs. 1-8.

[90887] VGAM2712 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chikungunya Virus.

VGAM2712 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90888] VGAM2712 gene encodes a VGAM2712 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2712 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2712 precursor RNA is designated SEQ ID:2698, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2698 is located at position 2249 relative to the genome of Chikungunya Virus.

[90889] VGAM2712 precursor RNA folds onto itself, forming VGAM2712 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90890] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2712 folded precursor RNA into VGAM2712 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2712 RNA is designated SEQ ID:5423, and is provided hereinbelow with reference to the sequence listing part.

[90891] VGAM2712 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2712 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90892] VGAM2712 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2712 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2712 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90893] The complementary binding of VGAM2712 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2712 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2712 host target RNA into VGAM2712 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90894] It is appreciated that VGAM2712 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2712 host target genes. The mRNA of each one of this plurality of VGAM2712 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2712 RNA, herein designated VGAM RNA, and which when bound by VGAM2712 RNA causes inhibition of translation of respective one or more VGAM2712 host target proteins.

[90895] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2712 gene, herein designated VGAM GENE, on one or more VGAM2712 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90896] It is yet further appreciated that a function of VGAM2712 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of viral infection by Chikungunya Virus. Specific functions, and accordingly utilities, of VGAM2712 correlate with, and may be deduced from, the identity of the host target genes which VGAM2712 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90897] Nucleotide sequences of the VGAM2712 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2712 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2712 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2712 are further described hereinbelow with reference to Table 1.

[90898] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2712 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2712 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90899] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2712 gene, herein designated VGAM is inhibition of expression of VGAM2712 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2712 correlate with, and may be deduced from, the identity of the target genes which VGAM2712 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90900] Branched Chain Aminotransferase 1, Cytosolic (BCAT1, Accession XM_038659) is a VGAM2712 host target gene. BCAT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCAT1 BINDING SITE, designated SEQ

ID:32898, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90901] A function of VGAM2712 is therefore inhibition of Branched Chain Aminotransferase 1, Cytosolic (BCAT1, Accession XM_038659), a gene which catalyzes of the essential branched chain leucine, isoleucine, and valine. Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCAT1. The function of BCAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1367.Development and Differentiation Enhancing Factor 1 (DDEF1, Accession XM_005169) is another VGAM2712 host target gene. DDEF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDEF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDEF1 BINDING SITE, designated SEQ ID:29962, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ

ID:5423.

[90902] Another function of VGAM2712 is therefore inhibition of Development and Differentiation Enhancing Factor 1 (DDEF1, Accession XM_005169). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDEF1. Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411) is another VGAM2712 host target gene. HLCS BINDING SITE is HOST TARGET binding site found in the 3` un-translated region of mRNA encoded by HLCS, correspond-ing to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:5989, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90903] Another function of VGAM2712 is therefore inhibition of Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411). Accordingly, utilities of VGAM2712 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with HLCS. Phosphodiesterase 4B, CAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B, Accession NM_002600) is another VGAM2712 host target gene. PDE4B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4B BINDING SITE, designated SEQ ID:8465, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90904] Another function of VGAM2712 is therefore inhibition of Phosphodiesterase 4B, CAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B, Accession NM_002600), a gene which may be involved in mediating central nervous system effects of therapeutic agents ranging from antidepressants to antiasthmatic and anti-inflammatory agents. Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4B. The function of PDE4B and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM51.SH3-domain GRB2-like 2 (SH3GL2, Accession NM_003026) is another VGAM2712 host target gene. SH3GL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3GL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3GL2 BINDING SITE, designated SEQ ID:8965, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90905] Another function of VGAM2712 is therefore inhibition of SH3-domain GRB2-like 2 (SH3GL2, Accession NM_003026), a gene which plays a role in synaptic vesicle recycling, in particular in clathrin-mediated vesicle endocytosis. Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3GL2. The function of SH3GL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM982.Sarcospan (Kras oncogene-associated gene) (SSPN, Accession NM_005086) is another VGAM2712 host target gene. SSPN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSPN BINDING SITE, designated SEQ ID:11538, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90906] Another function of VGAM2712 is therefore inhibition of Sarcospan (Kras oncogene-associated gene) (SSPN, Accession NM_005086), a gene which spans the muscle plasma membrane and forms a link between the f-actin cytoskeleton and the extracellular matrix. Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSPN. The function of SSPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM996.Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283) is

another VGAM2712 host target gene. TACC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACC1 BINDING SITE, designated SEQ ID:12970, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90907] Another function of VGAM2712 is therefore inhibition of Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACC1. TRIM (Accession NM_016388) is another VGAM2712 host target gene. TRIM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM BINDING SITE, designated SEQ ID:18530, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ

ID:5423.

[90908] Another function of VGAM2712 is therefore inhibition of TRIM (Accession NM_016388), a gene which plays a role in recruiting signaling proteins to the plasma membrane upon T-cell receptor (TCR) complex activation in T cells. Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM. The function of TRIM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM227.Adaptor-related Protein Complex 1, Sigma 2 Subunit (AP1S2, Accession NM_003916) is another VGAM2712 host target gene. AP1S2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP1S2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP1S2 BINDING SITE, designated SEQ ID:10003, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90909] Another function of VGAM2712 is therefore inhibition of

Adaptor-related Protein Complex 1, Sigma 2 Subunit (AP1S2, Accession NM_003916). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S2. Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989) is another VGAM2712 host target gene. DIO2 BINDING SITE1 and DIO2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DIO2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIO2 BINDING SITE1 and DIO2 BINDING SITE2, designated SEQ ID:15165 and SEQ ID:6455 respectively, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90910] Another function of VGAM2712 is therefore inhibition of Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIO2. Erythrocyte Membrane Protein Band 4.1-like 1 (EPB41L1, Accession XM_047295) is another VGAM2712 host target gene.

EPB41L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPB41L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPB41L1 BINDING SITE, designated SEQ ID:34937, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90911] Another function of VGAM2712 is therefore inhibition of Erythrocyte Membrane Protein Band 4.1-like 1 (EPB41L1, Accession XM_047295). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB41L1. G Protein-coupled Receptor Kinase-interactor 2 (GIT2, Accession NM_014776) is another VGAM2712 host target gene. GIT2 BINDING SITE1 through GIT2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GIT2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GIT2 BINDING SITE1 through GIT2 BINDING SITE3, designated SEQ

ID:16599, SEQ ID:27681 and SEQ ID:27694 respectively, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90912] Another function of VGAM2712 is therefore inhibition of G Protein-coupled Receptor Kinase-interactor 2 (GIT2, Accession NM_014776). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GIT2. Neuronal Pentraxin Receptor (NPTXR, Accession NM_058178) is another VGAM2712 host target gene. NPTXR BINDING SITE1 and NPTXR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NPTXR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE1 and NPTXR BINDING SITE2, designated SEQ ID:27732 and SEQ ID:15584 respectively, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90913] Another function of VGAM2712 is therefore inhibition of Neuronal Pentraxin Receptor (NPTXR, Accession NM_058178). Accordingly, utilities of VGAM2712 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR. PSR (Accession XM_036784) is another VGAM2712 host target gene. PSR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSR BINDING SITE, designated SEQ ID:32498, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90914] Another function of VGAM2712 is therefore inhibition of PSR (Accession XM_036784). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSR. Solute Carrier Family 38, Member 4 (SLC38A4, Accession NM_018018) is another VGAM2712 host target gene. SLC38A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC38A4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC38A4 BINDING SITE, designated SEQ

ID:19757, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90915] Another function of VGAM2712 is therefore inhibition of Solute Carrier Family 38, Member 4 (SLC38A4, Accession NM_018018). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC38A4. LOC151414 (Accession XM_087197) is another VGAM2712 host target gene. LOC151414 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151414 BINDING SITE, designated SEQ ID:39108, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90916] Another function of VGAM2712 is therefore inhibition of LOC151414 (Accession XM_087197). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151414. LOC199704 (Accession XM_113994) is an-

other VGAM2712 host target gene. LOC199704 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199704 BINDING SITE, designated SEQ ID:42604, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90917] Another function of VGAM2712 is therefore inhibition of LOC199704 (Accession XM_113994). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199704. LOC201771 (Accession XM_046083) is another VGAM2712 host target gene. LOC201771 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201771, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201771 BINDING SITE, designated SEQ ID:34677, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90918] Another function of VGAM2712 is therefore inhibition of LOC201771 (Accession XM_046083). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201771. LOC206426 (Accession XM_116505) is another VGAM2712 host target gene. LOC206426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC206426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC206426 BINDING SITE, designated SEQ ID:43119, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90919] Another function of VGAM2712 is therefore inhibition of LOC206426 (Accession XM_116505). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC206426. LOC90843 (Accession XM_034430) is another VGAM2712 host target gene. LOC90843 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90843, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90843 BINDING SITE, designated SEQ ID:32117, to the nucleotide sequence of VGAM2712 RNA, herein designated VGAM RNA, also designated SEQ ID:5423.

[90920] Another function of VGAM2712 is therefore inhibition of LOC90843 (Accession XM_034430). Accordingly, utilities of VGAM2712 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90843. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2713 (VGAM2713) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90921] VGAM2713 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2713 was detected is described hereinabove with reference to Figs. 1-8.

[90922] VGAM2713 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mammalian Orthoreovirus 2. VGAM2713 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90923] VGAM2713 gene encodes a VGAM2713 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2713 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2713 precursor RNA is designated SEQ ID:2699, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2699 is located at position 1472 relative to the genome of Mammalian Orthoreovirus 2.

[90924] VGAM2713 precursor RNA folds onto itself, forming VGAM2713 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90925] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2713 folded precursor RNA into VGAM2713

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2713 RNA is designated SEQ ID:5424, and is provided hereinbelow with reference to the sequence listing part.

[90926] VGAM2713 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2713 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90927] VGAM2713 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2713 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2713 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90928] The complementary binding of VGAM2713 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2713 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2713 host target RNA into VGAM2713 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[90929] It is appreciated that VGAM2713 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2713 host target genes. The mRNA of each one of this plurality of VGAM2713 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2713 RNA, herein designated VGAM RNA, and which when bound by VGAM2713 RNA causes inhibition of translation of respective one or more VGAM2713 host target proteins.

[90930] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2713 gene, herein designated VGAM GENE, on one or more VGAM2713 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90931] It is yet further appreciated that a function of VGAM2713 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of viral infection by Mammalian Orthoreovirus 2. Specific functions, and accordingly utilities, of VGAM2713 correlate with, and may be deduced from, the identity of the host target genes which VGAM2713 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90932] Nucleotide sequences of the VGAM2713 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2713 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2713 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2713 are further described hereinbelow with reference to Table 1.

[90933] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2713 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2713 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90934] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2713 gene, herein designated VGAM is inhibition of expression of VGAM2713 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2713 correlate with, and may be deduced from, the identity of the target genes which VGAM2713 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90935] XT3 (Accession NM_020208) is a VGAM2713 host target gene. XT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XT3 BINDING SITE, designated SEQ ID:21447, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90936] A function of VGAM2713 is therefore inhibition of XT3 (Accession NM_020208), a gene which is a Kidney-specific orphan transporter. Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT3. The function of XT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM21.Bromodomain and PHD Finger Containing, 3 (BRPF3, Accession XM_166450) is another VGAM2713 host target gene. BRPF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRPF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRPF3 BINDING SITE, designated SEQ ID:44346, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90937] Another function of VGAM2713 is therefore inhibition of Bromodomain and PHD Finger Containing, 3 (BRPF3, Accession XM_166450). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with BRPF3. FLJ10661 (Accession NM_018172) is another VGAM2713 host target gene. FLJ10661 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10661, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10661 BINDING SITE, designated SEQ ID:19993, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90938] Another function of VGAM2713 is therefore inhibition of FLJ10661 (Accession NM_018172). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10661. FLJ11856 (Accession NM_024531) is another VGAM2713 host target gene. FLJ11856 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11856 BINDING SITE, designated SEQ ID:23735, to the nucleotide

sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90939] Another function of VGAM2713 is therefore inhibition of FLJ11856 (Accession NM_024531). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11856. GFR (Accession NM_012294) is another VGAM2713 host target gene. GFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GFR BINDING SITE, designated SEQ ID:14644, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90940] Another function of VGAM2713 is therefore inhibition of GFR (Accession NM_012294). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFR. Glutamate Receptor, Ionotropic, N-methyl-D-aspartate 3A (GRIN3A, Accession NM_133445) is another VGAM2713 host target gene. GRIN3A BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by GRIN3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRIN3A BINDING SITE, designated SEQ ID:28535, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90941] Another function of VGAM2713 is therefore inhibition of Glutamate Receptor, Ionotropic, N-methyl-D-aspartate 3A (GRIN3A, Accession NM_133445). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN3A. KIAA1219 (Accession XM_028835) is another VGAM2713 host target gene. KIAA1219 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1219 BINDING SITE, designated SEQ ID:30756, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90942] Another function of VGAM2713 is therefore inhibition of KIAA1219 (Accession XM_028835). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1219. LOC202934 (Accession XM_117486) is another VGAM2713 host target gene. LOC202934 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, designated SEQ ID:43452, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90943] Another function of VGAM2713 is therefore inhibition of LOC202934 (Accession XM_117486). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934. LOC255465 (Accession XM_173206) is another VGAM2713 host target gene. LOC255465 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255465, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255465 BINDING SITE, designated SEQ ID:46446, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90944] Another function of VGAM2713 is therefore inhibition of LOC255465 (Accession XM_173206). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255465. LOC51193 (Accession NM_016331) is another VGAM2713 host target gene. LOC51193 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51193 BINDING SITE, designated SEQ ID:18454, to the nucleotide sequence of VGAM2713 RNA, herein designated VGAM RNA, also designated SEQ ID:5424.

[90945] Another function of VGAM2713 is therefore inhibition of LOC51193 (Accession NM_016331). Accordingly, utilities of VGAM2713 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC51193. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2714 (VGAM2714) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90946] VGAM2714 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2714 was detected is described hereinabove with reference to Figs. 1-8.

[90947] VGAM2714 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mammalian Orthoreovirus 2. VGAM2714 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90948] VGAM2714 gene encodes a VGAM2714 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2714 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2714 precursor RNA is designated SEQ ID:2700, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2700 is located at position 1237 relative to the genome of Mammalian Orthoreovirus 2.

[90949] VGAM2714 precursor RNA folds onto itself, forming VGAM2714 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90950] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2714 folded precursor RNA into VGAM2714 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2714 RNA is designated SEQ ID:5425, and is provided hereinbelow with reference to the sequence listing part.

[90951] VGAM2714 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2714 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90952] VGAM2714 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2714 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2714 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90953] The complementary binding of VGAM2714 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2714 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2714 host target RNA into VGAM2714 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90954] It is appreciated that VGAM2714 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2714 host target genes. The mRNA of each one of this plurality of VGAM2714 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2714 RNA, herein designated VGAM RNA, and which when bound by VGAM2714 RNA causes

inhibition of translation of respective one or more VGAM2714 host target proteins.

[90955] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2714 gene, herein designated VGAM GENE, on one or more VGAM2714 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90956] It is yet further appreciated that a function of VGAM2714 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2714 include diagnosis, prevention and

treatment of viral infection by Mammalian Orthoreovirus 2. Specific functions, and accordingly utilities, of VGAM2714 correlate with, and may be deduced from, the identity of the host target genes which VGAM2714 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90957] Nucleotide sequences of the VGAM2714 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2714 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2714 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2714 are further described hereinbelow with reference to Table 1.

[90958] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2714 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2714 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90959] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2714 gene, herein designated VGAM is inhibition of expression of VGAM2714 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2714 correlate with, and may be deduced from, the identity of the target genes which VGAM2714 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90960] Aldehyde Dehydrogenase 3 Family, Member B2 (ALDH3B2, Accession NM_000695) is a VGAM2714 host target gene. ALDH3B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALDH3B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALDH3B2 BINDING SITE, designated SEQ ID:6356, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90961] A function of VGAM2714 is therefore inhibition of Aldehyde Dehydrogenase 3 Family, Member B2 (ALDH3B2, Accession NM_000695), a gene which may play a role in alcohol detoxitation. Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH3B2. The function of ALDH3B2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM251.BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 2 (BACH2, Accession NM_021813) is another VGAM2714 host target gene. BACH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BACH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BACH2 BINDING SITE, designated SEQ ID:22379, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90962] Another function of VGAM2714 is therefore inhibition of BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 2 (BACH2, Accession NM_021813), a gene which acts as repressor or activator, binds to maf recognition elements. Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BACH2. The function of BACH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM331.Complement Component 5 Receptor 1 (C5a ligand) (C5R1, Accession NM_001736) is another VGAM2714 host target gene. C5R1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5R1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5R1 BINDING SITE, designated SEQ ID:7471, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90963] Another function of VGAM2714 is therefore inhibition of Complement Component 5 Receptor 1 (C5a ligand) (C5R1, Accession NM_001736), a gene which has a nonredundant function and is required for mucosal host cell defense in the lung. Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5R1. The function of C5R1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM484.Collagen, Type VI, Alpha 2 (COL6A2, Accession NM_058175) is another VGAM2714 host target gene. COL6A2 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL6A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL6A2 BINDING SITE, designated SEQ ID:27727, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90964] Another function of VGAM2714 is therefore inhibition of Collagen, Type VI, Alpha 2 (COL6A2, Accession NM_058175). Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A2. Dihydrofolate Reductase (DHFR, Accession NM_000791) is another VGAM2714 host target gene. DHFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DHFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DHFR BINDING SITE, designated SEQ ID:6448, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90965] Another function of VGAM2714 is therefore inhibition of Dihydrofolate Reductase (DHFR, Accession NM_000791), a gene which converts dihydrofolate into tetrahydrofolate. Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHFR. The function of DHFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM826.Profilin 2 (PFN2, Accession NM_002628) is another VGAM2714 host target gene. PFN2 BINDING SITE1 and PFN2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PFN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFN2 BINDING SITE1 and PFN2 BINDING SITE2, designated SEQ ID:8487 and SEQ ID:27580 respectively, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90966] Another function of VGAM2714 is therefore inhibition of Profilin 2 (PFN2, Accession NM_002628). Accordingly, utilities of VGAM2714 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with PFN2. Cytochrome P450, Subfamily IIA (phenobarbital-inducible), Polypeptide 7 (CYP2A7, Accession NM_030589) is another VGAM2714 host target gene. CYP2A7 BINDING SITE1 and CYP2A7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CYP2A7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP2A7 BINDING SITE1 and CYP2A7 BINDING SITE2, designated SEQ ID:24957 and SEQ ID:39709 respectively, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90967] Another function of VGAM2714 is therefore inhibition of Cytochrome P450, Subfamily IIA (phenobarbital-inducible), Polypeptide 7 (CYP2A7, Accession NM_030589). Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2A7. MGC2452 (Accession NM_032644) is another VGAM2714 host target gene. MGC2452 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by MGC2452, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2452 BINDING SITE, designated SEQ ID:26367, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90968] Another function of VGAM2714 is therefore inhibition of MGC2452 (Accession NM_032644). Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2452. NESHBP (Accession NM_015429) is another VGAM2714 host target gene. NESHBP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NESHBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NESHBP BINDING SITE, designated SEQ ID:17727, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90969] Another function of VGAM2714 is therefore inhibition of NESHBP (Accession NM_015429). Accordingly, utilities of

VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NESHBP. LOC131034 (Accession NM_130808) is another VGAM2714 host target gene. LOC131034 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC131034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC131034 BINDING SITE, designated SEQ ID:28314, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90970] Another function of VGAM2714 is therefore inhibition of LOC131034 (Accession NM_130808). Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC131034. LOC196500 (Accession XM_113734) is another VGAM2714 host target gene. LOC196500 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196500, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC196500 BINDING SITE, designated SEQ ID:42386, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90971] Another function of VGAM2714 is therefore inhibition of LOC196500 (Accession XM_113734). Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196500. LOC256158 (Accession XM_175125) is another VGAM2714 host target gene. LOC256158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256158 BINDING SITE, designated SEQ ID:46620, to the nucleotide sequence of VGAM2714 RNA, herein designated VGAM RNA, also designated SEQ ID:5425.

[90972] Another function of VGAM2714 is therefore inhibition of LOC256158 (Accession XM_175125). Accordingly, utilities of VGAM2714 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256158. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2715 (VGAM2715) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[90973] VGAM2715 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2715 was detected is described hereinabove with reference to Figs. 1-8.

[90974] VGAM2715 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mammalian Orthoreovirus 2. VGAM2715 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[90975] VGAM2715 gene encodes a VGAM2715 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2715 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2715 precursor RNA is designated SEQ ID:2701, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2701 is located at position 1891 relative to the

genome of Mammalian Orthoreovirus 2.

[90976] VGAM2715 precursor RNA folds onto itself, forming VGAM2715 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[90977] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2715 folded precursor RNA into VGAM2715 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2715 RNA is designated SEQ ID:5426, and is provided hereinbelow with reference to the sequence listing part.

[90978] VGAM2715 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2715 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[90979] VGAM2715 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2715 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2715 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[90980] The complementary binding of VGAM2715 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2715 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2715 host target RNA into VGAM2715 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[90981] It is appreciated that VGAM2715 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2715 host target genes. The mRNA of each one of this plurality of VGAM2715 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2715 RNA, herein designated VGAM RNA, and which when bound by VGAM2715 RNA causes inhibition of translation of respective one or more VGAM2715 host target proteins.

[90982] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2715 gene, herein designated VGAM GENE, on one or more VGAM2715 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[90983] It is yet further appreciated that a function of VGAM2715 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of viral infection by Mammalian Orthoreovirus 2. Specific functions, and accordingly utilities, of

VGAM2715 correlate with, and may be deduced from, the identity of the host target genes which VGAM2715 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[90984] Nucleotide sequences of the VGAM2715 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2715 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2715 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2715 are further described hereinbelow with reference to Table 1.

[90985] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2715 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2715 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[90986] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2715 gene, herein designated VGAM is inhibition of expression of VGAM2715 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2715 correlate with, and may be deduced

from, the identity of the target genes which VGAM2715 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[90987] Adaptor-related Protein Complex 1, Beta 1 Subunit (AP1B1, Accession NM_001127) is a VGAM2715 host target gene. AP1B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP1B1 BINDING SITE, designated SEQ ID:6796, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90988] A function of VGAM2715 is therefore inhibition of Adaptor-related Protein Complex 1, Beta 1 Subunit (AP1B1, Accession NM_001127), a gene which plays a role in protein sorting in the late-golgi/trans-golgi network (tgn) and/or endosomes. Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1B1. The function of AP1B1 and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to VGAM1048.Collagen, Type VI, Alpha 2 (COL6A2, Accession NM_058175) is another VGAM2715 host target gene. COL6A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL6A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL6A2 BINDING SITE, designated SEQ ID:27724, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90989] Another function of VGAM2715 is therefore inhibition of Collagen, Type VI, Alpha 2 (COL6A2, Accession NM_058175). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A2. CREB Binding Protein (Rubinstein-Taybi syndrome) (CREBBP, Accession NM_004380) is another VGAM2715 host target gene. CREBBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CREBBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of CREBBP BINDING SITE, designated SEQ ID:10603, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90990] Another function of VGAM2715 is therefore inhibition of CREB Binding Protein (Rubinstein-Taybi syndrome) (CREBBP, Accession NM_004380). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CREBBP. V-erb-b2 Erythroblastic Leukemia Viral Oncogene Homolog 2, Neuro/glioblastoma Derived Oncogene Homolog (avian) (ERBB2, Accession NM_004448) is another VGAM2715 host target gene. ERBB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERBB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERBB2 BINDING SITE, designated SEQ ID:10744, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90991] Another function of VGAM2715 is therefore inhibition of

V-erb-b2 Erythroblastic Leukemia Viral Oncogene Homolog 2, Neuro/glioblastoma Derived Oncogene Homolog (avian) (ERBB2, Accession NM_004448), a gene which Tyrosine kinase receptor. Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERBB2. The function of ERBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1366.Fatty Acid Synthase (FASN, Accession NM_004104) is another VGAM2715 host target gene. FASN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FASN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FASN BINDING SITE, designated SEQ ID:10314, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90992] Another function of VGAM2715 is therefore inhibition of Fatty Acid Synthase (FASN, Accession NM_004104), a gene which catalyzes the formation of long-chain fatty acids from acetyl-coa, malonyl-coa and nadph. Accordingly,

utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FASN. The function of FASN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM477.Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209) is another VGAM2715 host target gene. ITGAL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGAL BINDING SITE, designated SEQ ID:7968, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90993] Another function of VGAM2715 is therefore inhibition of Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209), a gene which s a receptor for icam1, icam2, icam3 and icam4. it is involved in a variety of immune phenomena including leukocyte-endothelial

cell interaction, cytotoxic t-cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAL. The function of ITGAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Phosphomannomutase 2 (PMM2, Accession XM_050755) is another VGAM2715 host target gene. PMM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PMM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMM2 BINDING SITE, designated SEQ ID:35677, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90994] Another function of VGAM2715 is therefore inhibition of Phosphomannomutase 2 (PMM2, Accession XM_050755). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with PMM2. Apolipoprotein L, 4 (APOL4, Accession NM_030643) is another VGAM2715 host target gene. APOL4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APOL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APOL4 BINDING SITE, designated SEQ ID:24974, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90995] Another function of VGAM2715 is therefore inhibition of Apolipoprotein L, 4 (APOL4, Accession NM_030643). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL4. FLJ11106 (Accession NM_018324) is another VGAM2715 host target gene. FLJ11106 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11106 BINDING SITE, designated SEQ ID:20317, to the

nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90996] Another function of VGAM2715 is therefore inhibition of FLJ11106 (Accession NM_018324). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11106. FLJ20699 (Accession NM_017931) is another VGAM2715 host target gene. FLJ20699 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20699, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20699 BINDING SITE, designated SEQ ID:19617, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90997] Another function of VGAM2715 is therefore inhibition of FLJ20699 (Accession NM_017931). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20699. KIAA1028 (Accession XM_166324) is another VGAM2715 host target gene. KIAA1028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1028 BINDING SITE, designated SEQ ID:44158, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90998] Another function of VGAM2715 is therefore inhibition of KIAA1028 (Accession XM_166324). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1028. KIAA1161 (Accession XM_088501) is another VGAM2715 host target gene. KIAA1161 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1161, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1161 BINDING SITE, designated SEQ ID:39750, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[90999] Another function of VGAM2715 is therefore inhibition of KIAA1161 (Accession XM_088501). Accordingly, utilities

of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1161. KIAA1303 (Accession XM_038376) is another VGAM2715 host target gene. KIAA1303 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1303, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1303 BINDING SITE, designated SEQ ID:32832, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[91000] Another function of VGAM2715 is therefore inhibition of KIAA1303 (Accession XM_038376). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1303. KIAA1866 (Accession XM_027658) is another VGAM2715 host target gene. KIAA1866 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1866 BINDING SITE, designated SEQ ID:30555, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[91001] Another function of VGAM2715 is therefore inhibition of KIAA1866 (Accession XM_027658). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1866. PV1 (Accession NM_031310) is another VGAM2715 host target gene. PV1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PV1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PV1 BINDING SITE, designated SEQ ID:25349, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[91002] Another function of VGAM2715 is therefore inhibition of PV1 (Accession NM_031310). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PV1. SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003) is another VGAM2715 host target gene.

SEC14L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC14L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC14L1 BINDING SITE, designated SEQ ID:8901, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[91003] Another function of VGAM2715 is therefore inhibition of SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC14L1. LOC149832 (Accession XM_097733) is another VGAM2715 host target gene. LOC149832 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149832, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149832 BINDING SITE, designated SEQ ID:41078, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5426.

[91004] Another function of VGAM2715 is therefore inhibition of LOC149832 (Accession XM_097733). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149832. LOC151521 (Accession XM_098076) is another VGAM2715 host target gene. LOC151521 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151521, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151521 BINDING SITE, designated SEQ ID:41366, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[91005] Another function of VGAM2715 is therefore inhibition of LOC151521 (Accession XM_098076). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151521. LOC200325 (Accession XM_117223) is another VGAM2715 host target gene. LOC200325 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200325, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200325 BINDING SITE, designated SEQ ID:43287, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[91006] Another function of VGAM2715 is therefore inhibition of LOC200325 (Accession XM_117223). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200325. LOC90593 (Accession XM_032815) is another VGAM2715 host target gene. LOC90593 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90593, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90593 BINDING SITE, designated SEQ ID:31764, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[91007] Another function of VGAM2715 is therefore inhibition of LOC90593 (Accession XM_032815). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC90593. LOC93259 (Accession XM_050105) is another VGAM2715 host target gene. LOC93259 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93259 BINDING SITE, designated SEQ ID:35556, to the nucleotide sequence of VGAM2715 RNA, herein designated VGAM RNA, also designated SEQ ID:5426.

[91008] Another function of VGAM2715 is therefore inhibition of LOC93259 (Accession XM_050105). Accordingly, utilities of VGAM2715 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93259. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2716 (VGAM2716) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91009] VGAM2716 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2716 was detected is described hereinabove with reference to Figs. 1-8.

[91010] VGAM2716 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Tacaribe Virus. VGAM2716 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91011] VGAM2716 gene encodes a VGAM2716 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2716 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2716 precursor RNA is designated SEQ ID:2702, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2702 is located at position 2511 relative to the genome of Tacaribe Virus.

[91012] VGAM2716 precursor RNA folds onto itself, forming VGAM2716 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91013] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2716 folded precursor RNA into VGAM2716 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2716 RNA is designated SEQ ID:5427, and is provided hereinbelow with reference to the sequence listing part.

[91014] VGAM2716 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2716 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91015] VGAM2716 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2716 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2716 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91016] The complementary binding of VGAM2716 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2716 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2716 host target RNA into VGAM2716 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91017] It is appreciated that VGAM2716 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2716 host target genes. The mRNA of each one of this plurality of VGAM2716 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2716 RNA, herein designated VGAM RNA, and which when bound by VGAM2716 RNA causes inhibition of translation of respective one or more VGAM2716 host target proteins.

[91018] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2716 gene, herein designated VGAM GENE, on one or more VGAM2716 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91019] It is yet further appreciated that a function of VGAM2716 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of viral infection by Tacaribe Virus. Specific functions, and accordingly utilities, of VGAM2716 correlate with, and may be deduced from, the identity of the host target genes which VGAM2716 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91020] Nucleotide sequences of the VGAM2716 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2716 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2716 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2716 are further described hereinbelow with reference to Table 1.

[91021] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2716 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2716 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91022] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2716 gene, herein designated VGAM is inhibition of expression of VGAM2716 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2716 correlate with, and may be deduced from, the identity of the target genes which VGAM2716 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91023] Cadherin, EGF LAG Seven-pass G-type Receptor 2 (flamingo homolog, Drosophila) (CELSR2, Accession NM_001408) is a VGAM2716 host target gene. CELSR2

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CELSR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CELSR2 BINDING SITE, designated SEQ ID:7106, to the nucleotide sequence of VGAM2716 RNA, herein designated VGAM RNA, also designated SEQ ID:5427.

[91024] A function of VGAM2716 is therefore inhibition of Cadherin, EGF LAG Seven-pass G-type Receptor 2 (flamingo homolog, Drosophila) (CELSR2, Accession NM_001408), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CELSR2. The function of CELSR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM432.ERAP140 (Accession XM_059748) is another VGAM2716 host target gene. ERAP140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERAP140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of ERAP140 BINDING SITE, designated SEQ ID:37085, to the nucleotide sequence of VGAM2716 RNA, herein designated VGAM RNA, also designated SEQ ID:5427.

[91025] Another function of VGAM2716 is therefore inhibition of ERAP140 (Accession XM_059748). Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERAP140. FLJ13910 (Accession NM_022780) is another VGAM2716 host target gene. FLJ13910 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13910 BINDING SITE, designated SEQ ID:23055, to the nucleotide sequence of VGAM2716 RNA, herein designated VGAM RNA, also designated SEQ ID:5427.

[91026] Another function of VGAM2716 is therefore inhibition of FLJ13910 (Accession NM_022780). Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13910. HCA127 (Accession NM_018684) is another VGAM2716 host target gene. HCA127 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCA127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCA127 BINDING SITE, designated SEQ ID:20759, to the nucleotide sequence of VGAM2716 RNA, herein designated VGAM RNA, also designated SEQ ID:5427.

[91027] Another function of VGAM2716 is therefore inhibition of HCA127 (Accession NM_018684). Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCA127. KIAA1009 (Accession NM_014895) is another VGAM2716 host target gene. KIAA1009 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1009 BINDING SITE, designated SEQ ID:17052, to the nucleotide sequence of VGAM2716 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5427.

[91028] Another function of VGAM2716 is therefore inhibition of KIAA1009 (Accession NM_014895). Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1009. Kv6.3 (Accession NM_133490) is another VGAM2716 host target gene. Kv6.3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Kv6.3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Kv6.3 BINDING SITE, designated SEQ ID:28566, to the nucleotide sequence of VGAM2716 RNA, herein designated VGAM RNA, also designated SEQ ID:5427.

[91029] Another function of VGAM2716 is therefore inhibition of Kv6.3 (Accession NM_133490). Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Kv6.3. PRO0365 (Accession NM_014126) is another VGAM2716 host target gene. PRO0365 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0365, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0365 BINDING SITE, designated SEQ ID:15389, to the nucleotide sequence of VGAM2716 RNA, herein designated VGAM RNA, also designated SEQ ID:5427.

[91030] Another function of VGAM2716 is therefore inhibition of PRO0365 (Accession NM_014126). Accordingly, utilities of VGAM2716 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0365. LOC152742 (Accession XM_098259) is another VGAM2716 host target gene. LOC152742 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152742, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152742 BINDING SITE, designated SEQ ID:41544, to the nucleotide sequence of VGAM2716 RNA, herein designated VGAM RNA, also designated SEQ ID:5427.

[91031] Another function of VGAM2716 is therefore inhibition of LOC152742 (Accession XM_098259). Accordingly, utilities of VGAM2716 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC152742. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2717 (VGAM2717) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91032] VGAM2717 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2717 was detected is described hereinabove with reference to Figs. 1-8.

[91033] VGAM2717 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rachiplusia Ou Multiple Nucleopolyhedrovirus. VGAM2717 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91034] VGAM2717 gene encodes a VGAM2717 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2717 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2717 precursor RNA is desig-

nated SEQ ID:2703, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2703 is located at position 55572 relative to the genome of Rachiplusia Ou Multiple Nucleopolyhedrovirus.

[91035] VGAM2717 precursor RNA folds onto itself, forming VGAM2717 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91036] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2717 folded precursor RNA into VGAM2717 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2717 RNA is designated SEQ ID:5428, and is provided hereinbelow with reference to the sequence

listing part.

[91037] VGAM2717 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2717 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91038] VGAM2717 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2717 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2717 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91039] The complementary binding of VGAM2717 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2717 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2717 host target RNA into VGAM2717 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91040] It is appreciated that VGAM2717 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2717 host target genes. The mRNA of each one of this plurality of VGAM2717 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2717 RNA, herein designated VGAM

RNA, and which when bound by VGAM2717 RNA causes inhibition of translation of respective one or more VGAM2717 host target proteins.

[91041] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2717 gene, herein designated VGAM GENE, on one or more VGAM2717 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91042] It is yet further appreciated that a function of VGAM2717 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2717 include diagnosis, prevention and treatment of viral infection by Rachiplusia Ou Multiple Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGAM2717 correlate with, and may be deduced from, the identity of the host target genes which VGAM2717 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91043] Nucleotide sequences of the VGAM2717 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2717 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2717 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2717 are further described hereinbelow with reference to Table 1.

[91044] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2717 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2717 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91045] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2717 gene, herein designated VGAM is

inhibition of expression of VGAM2717 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2717 correlate with, and may be deduced from, the identity of the target genes which VGAM2717 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91046] Zinc Finger Protein 265 (ZNF265, Accession NM_005455) is a VGAM2717 host target gene. ZNF265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF265 BINDING SITE, designated SEQ ID:11940, to the nucleotide sequence of VGAM2717 RNA, herein designated VGAM RNA, also designated SEQ ID:5428.

[91047] A function of VGAM2717 is therefore inhibition of Zinc Finger Protein 265 (ZNF265, Accession NM_005455). Accordingly, utilities of VGAM2717 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF265. RNA Binding Motif Protein 9 (RBM9, Accession NM_014309) is another VGAM2717 host target gene. RBM9 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by RBM9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBM9 BINDING SITE, designated SEQ ID:15597, to the nucleotide sequence of VGAM2717 RNA, herein designated VGAM RNA, also designated SEQ ID:5428.

[91048] Another function of VGAM2717 is therefore inhibition of RNA Binding Motif Protein 9 (RBM9, Accession NM_014309). Accordingly, utilities of VGAM2717 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBM9. Transcription Factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1, Accession NM_003201) is another VGAM2717 host target gene. TCF6L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCF6L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF6L1 BINDING SITE, designated SEQ ID:9189, to the nucleotide sequence of VGAM2717 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5428.

[91049] Another function of VGAM2717 is therefore inhibition of Transcription Factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1, Accession NM_003201). Accordingly, utilities of VGAM2717 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF6L1. LOC120526 (Accession XM_058475) is another VGAM2717 host target gene. LOC120526 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120526, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120526 BINDING SITE, designated SEQ ID:36622, to the nucleotide sequence of VGAM2717 RNA, herein designated VGAM RNA, also designated SEQ ID:5428.

[91050] Another function of VGAM2717 is therefore inhibition of LOC120526 (Accession XM_058475). Accordingly, utilities of VGAM2717 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120526. LOC202266 (Accession XM_117373) is another VGAM2717 host target gene. LOC202266 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC202266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202266 BINDING SITE, designated SEQ ID:43420, to the nucleotide sequence of VGAM2717 RNA, herein designated VGAM RNA, also designated SEQ ID:5428.

[91051] Another function of VGAM2717 is therefore inhibition of LOC202266 (Accession XM_117373). Accordingly, utilities of VGAM2717 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202266. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2718 (VGAM2718) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91052] VGAM2718 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2718 was detected is described hereinabove with reference to Figs. 1-8.

[91053] VGAM2718 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Rachiplusia Ou Multiple Nucleopolyhedrovirus. VGAM2718 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91054] VGAM2718 gene encodes a VGAM2718 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2718 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2718 precursor RNA is designated SEQ ID:2704, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2704 is located at position 55389 relative to the genome of Rachiplusia Ou Multiple Nucleopolyhedrovirus.

[91055] VGAM2718 precursor RNA folds onto itself, forming VGAM2718 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91056] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2718 folded precursor RNA into VGAM2718 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2718 RNA is designated SEQ ID:5429, and is provided hereinbelow with reference to the sequence listing part.

[91057] VGAM2718 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2718 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91058] VGAM2718 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2718 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2718 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91059] The complementary binding of VGAM2718 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2718 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2718

host target RNA into VGAM2718 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91060] It is appreciated that VGAM2718 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2718 host target genes. The mRNA of each one of this plurality of VGAM2718 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2718 RNA, herein designated VGAM RNA, and which when bound by VGAM2718 RNA causes inhibition of translation of respective one or more VGAM2718 host target proteins.

[91061] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2718 gene, herein designated VGAM GENE, on one or more VGAM2718 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91062] It is yet further appreciated that a function of VGAM2718 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of viral infection by Rachiplusia Ou Multiple Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGAM2718 correlate with, and may be deduced from, the identity of the host target genes which VGAM2718 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91063] Nucleotide sequences of the VGAM2718 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2718 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2718 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2718 are further

described hereinbelow with reference to Table 1.

[91064] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2718 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2718 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91065] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2718 gene, herein designated VGAM is inhibition of expression of VGAM2718 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2718 correlate with, and may be deduced from, the identity of the target genes which VGAM2718 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91066] BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 2 (BACH2, Accession NM_021813) is a VGAM2718 host target gene. BACH2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BACH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of BACH2 BINDING SITE, designated SEQ ID:22383, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91067] A function of VGAM2718 is therefore inhibition of BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 2 (BACH2, Accession NM_021813), a gene which acts as repressor or activator, binds to maf recognition elements. Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BACH2. The function of BACH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM331.Kinesin Family Member 5C (KIF5C, Accession NM_004522) is another VGAM2718 host target gene. KIF5C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIF5C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIF5C BINDING SITE, designated SEQ ID:10857, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA,

also designated SEQ ID:5429.

[91068] Another function of VGAM2718 is therefore inhibition of Kinesin Family Member 5C (KIF5C, Accession NM_004522). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF5C. Phosphorylase Kinase, Alpha 2 (liver) (PHKA2, Accession NM_000292) is another VGAM2718 host target gene. PHKA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PHKA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PHKA2 BINDING SITE, designated SEQ ID:5836, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91069] Another function of VGAM2718 is therefore inhibition of Phosphorylase Kinase, Alpha 2 (liver) (PHKA2, Accession NM_000292). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHKA2. Bromodomain Containing 3 (BRD3, Accession NM_007371) is another VGAM2718 host target gene. BRD3 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by BRD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRD3 BINDING SITE, designated SEQ ID:14298, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91070] Another function of VGAM2718 is therefore inhibition of Bromodomain Containing 3 (BRD3, Accession NM_007371). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRD3. Chromosome 1 Open Reading Frame 28 (C1orf28, Accession NM_024529) is another VGAM2718 host target gene. C1orf28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf28 BINDING SITE, designated SEQ ID:23732, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91071] Another function of VGAM2718 is therefore inhibition of Chromosome 1 Open Reading Frame 28 (C1orf28, Accession NM_024529). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf28. DCOHM (Accession NM_032151) is another VGAM2718 host target gene. DCOHM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCOHM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCOHM BINDING SITE, designated SEQ ID:25846, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91072] Another function of VGAM2718 is therefore inhibition of DCOHM (Accession NM_032151). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCOHM. FLJ10726 (Accession NM_018195) is another VGAM2718 host target gene. FLJ10726 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10726, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10726 BINDING SITE, designated SEQ ID:20060, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91073] Another function of VGAM2718 is therefore inhibition of FLJ10726 (Accession NM_018195). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10726. FLJ20986 (Accession NM_024524) is another VGAM2718 host target gene. FLJ20986 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20986, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20986 BINDING SITE, designated SEQ ID:23730, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91074] Another function of VGAM2718 is therefore inhibition of FLJ20986 (Accession NM_024524). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20986. FLJ22004 (Accession NM_025181) is another VGAM2718 host target gene. FLJ22004 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22004, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22004 BINDING SITE, designated SEQ ID:24818, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91075] Another function of VGAM2718 is therefore inhibition of FLJ22004 (Accession NM_025181). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22004. FLJ23129 (Accession NM_024763) is another VGAM2718 host target gene. FLJ23129 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23129, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23129 BINDING SITE, designated SEQ ID:24120, to the nucleotide

sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91076] Another function of VGAM2718 is therefore inhibition of FLJ23129 (Accession NM_024763). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23129. KIAA0459 (Accession XM_027862) is another VGAM2718 host target gene. KIAA0459 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:30580, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91077] Another function of VGAM2718 is therefore inhibition of KIAA0459 (Accession XM_027862). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459. Mitogen-activated Protein Kinase Kinase Kinase Kinase 3 (MAP4K3, Accession NM_003618) is another VGAM2718 host target gene. MAP4K3 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP4K3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP4K3 BINDING SITE, designated SEQ ID:9684, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91078] Another function of VGAM2718 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase Kinase 3 (MAP4K3, Accession NM_003618). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP4K3. MGC2217 (Accession NM_024300) is another VGAM2718 host target gene. MGC2217 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2217 BINDING SITE, designated SEQ ID:23590, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91079] Another function of VGAM2718 is therefore inhibition of MGC2217 (Accession NM_024300). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2217. Protocadherin 17 (PCDH17, Accession NM_014459) is another VGAM2718 host target gene. PCDH17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDH17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH17 BINDING SITE, designated SEQ ID:15815, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91080] Another function of VGAM2718 is therefore inhibition of Protocadherin 17 (PCDH17, Accession NM_014459). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH17. Syntaxin 6 (STX6, Accession NM_005819) is another VGAM2718 host target gene. STX6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STX6,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STX6 BINDING SITE, designated SEQ ID:12421, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91081] Another function of VGAM2718 is therefore inhibition of Syntaxin 6 (STX6, Accession NM_005819). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX6. LOC145624 (Accession XM_096824) is another VGAM2718 host target gene. LOC145624 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145624, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145624 BINDING SITE, designated SEQ ID:40550, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91082] Another function of VGAM2718 is therefore inhibition of LOC145624 (Accession XM_096824). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145624. LOC146909 (Accession XM_085634) is another VGAM2718 host target gene. LOC146909 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146909, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE, designated SEQ ID:38274, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91083] Another function of VGAM2718 is therefore inhibition of LOC146909 (Accession XM_085634). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909. LOC152742 (Accession XM_098259) is another VGAM2718 host target gene. LOC152742 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152742, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152742 BINDING SITE, designated SEQ ID:41546, to

the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91084] Another function of VGAM2718 is therefore inhibition of LOC152742 (Accession XM_098259). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152742. LOC158435 (Accession NM_138497) is another VGAM2718 host target gene. LOC158435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158435 BINDING SITE, designated SEQ ID:28847, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91085] Another function of VGAM2718 is therefore inhibition of LOC158435 (Accession NM_138497). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158435. LOC219649 (Accession XM_167562) is another VGAM2718 host target gene. LOC219649 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC219649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219649 BINDING SITE, designated SEQ ID:44670, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91086] Another function of VGAM2718 is therefore inhibition of LOC219649 (Accession XM_167562). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219649. LOC219940 (Accession XM_167791) is another VGAM2718 host target gene. LOC219940 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219940 BINDING SITE, designated SEQ ID:44831, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91087] Another function of VGAM2718 is therefore inhibition of LOC219940 (Accession XM_167791). Accordingly, utilities

of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219940. LOC93613 (Accession XM_052568) is another VGAM2718 host target gene. LOC93613 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93613, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93613 BINDING SITE, designated SEQ ID:35998, to the nucleotide sequence of VGAM2718 RNA, herein designated VGAM RNA, also designated SEQ ID:5429.

[91088] Another function of VGAM2718 is therefore inhibition of LOC93613 (Accession XM_052568). Accordingly, utilities of VGAM2718 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93613. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2719 (VGAM2719) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91089] VGAM2719 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2719 was detected is described hereinabove with reference to Figs. 1-8.

[91090] VGAM2719 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2719 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91091] VGAM2719 gene encodes a VGAM2719 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2719 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2719 precursor RNA is designated SEQ ID:2705, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2705 is located at position 5960 relative to the genome of Aphid Lethal Paralysis Virus.

[91092] VGAM2719 precursor RNA folds onto itself, forming VGAM2719 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91093] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2719 folded precursor RNA into VGAM2719 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2719 RNA is designated SEQ ID:5430, and is provided hereinbelow with reference to the sequence listing part.

[91094] VGAM2719 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2719 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[91095] VGAM2719 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2719 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2719 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91096] The complementary binding of VGAM2719 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2719 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2719 host target RNA into VGAM2719 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91097] It is appreciated that VGAM2719 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2719 host target genes. The mRNA of each one of this plurality of VGAM2719 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2719 RNA, herein designated VGAM RNA, and which when bound by VGAM2719 RNA causes inhibition of translation of respective one or more VGAM2719 host target proteins.

[91098] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2719 gene, herein designated VGAM GENE, on one or more VGAM2719 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91099] It is yet further appreciated that a function of VGAM2719 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2719 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2719 correlate with, and may be deduced from, the identity of the host target genes which VGAM2719 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91100] Nucleotide sequences of the VGAM2719 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2719 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2719 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2719 are further described hereinbelow with reference to Table 1.

[91101] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2719 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2719 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91102] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2719 gene, herein designated VGAM is inhibition of expression of VGAM2719 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2719 correlate with, and may be deduced from, the identity of the target genes which VGAM2719 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91103] Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155)

is a VGAM2719 host target gene. SERPINB9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINB9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE, designated SEQ ID:10358, to the nucleotide sequence of VGAM2719 RNA, herein designated VGAM RNA, also designated SEQ ID:5430.

[91104] A function of VGAM2719 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of VGAM2719 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB9. The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM60.T-complex-associated-testis-expressed 1-like (TCTE1L, Accession XM_048205) is another VGAM2719 host target gene. TCTE1L BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by TCTE1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCTE1L BINDING SITE, designated SEQ ID:35141, to the nucleotide sequence of VGAM2719 RNA, herein designated VGAM RNA, also designated SEQ ID:5430.

[91105] Another function of VGAM2719 is therefore inhibition of T-complex-associated-testis-expressed 1-like (TCTE1L, Accession XM_048205). Accordingly, utilities of VGAM2719 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCTE1L. KIAA0318 (Accession XM_044334) is another VGAM2719 host target gene. KIAA0318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0318 BINDING SITE, designated SEQ ID:34182, to the nucleotide sequence of VGAM2719 RNA, herein designated VGAM RNA, also designated SEQ ID:5430.

[91106] Another function of VGAM2719 is therefore inhibition of KIAA0318 (Accession XM_044334). Accordingly, utilities of VGAM2719 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0318. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2720 (VGAM2720) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91107] VGAM2720 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2720 was detected is described hereinabove with reference to Figs. 1-8.

[91108] VGAM2720 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2720 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91109] VGAM2720 gene encodes a VGAM2720 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2720 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2720 precursor RNA is designated SEQ ID:2706, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2706 is located at position 4386 relative to the genome of Aphid Lethal Paralysis Virus.

[91110] VGAM2720 precursor RNA folds onto itself, forming VGAM2720 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91111] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2720 folded precursor RNA into VGAM2720 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2720 RNA is designated SEQ ID:5431, and is provided hereinbelow with reference to the sequence listing part.

[91112] VGAM2720 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2720 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91113] VGAM2720 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2720 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2720 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91114] The complementary binding of VGAM2720 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2720 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2720 host target RNA into VGAM2720 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91115] It is appreciated that VGAM2720 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2720 host target genes. The mRNA of each one of this plurality of VGAM2720 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2720 RNA, herein designated VGAM RNA, and which when bound by VGAM2720 RNA causes inhibition of translation of respective one or more VGAM2720 host target proteins.

[91116] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2720 gene, herein designated VGAM GENE, on one or more VGAM2720 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91117] It is yet further appreciated that a function of VGAM2720 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2720 correlate with, and may be deduced from, the identity of the host target genes which VGAM2720 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91118] Nucleotide sequences of the VGAM2720 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2720 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2720 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2720 are further described hereinbelow with reference to Table 1.

[91119] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2720 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2720 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[91120] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2720 gene, herein designated VGAM is inhibition of expression of VGAM2720 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2720 correlate with, and may be deduced from, the identity of the target genes which VGAM2720 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91121] Fukuyama Type Congenital Muscular Dystrophy (fukutin) (FCMD, Accession NM_006731) is a VGAM2720 host target gene. FCMD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FCMD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCMD BINDING SITE, designated SEQ ID:13576, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91122] A function of VGAM2720 is therefore inhibition of Fukuyama Type Congenital Muscular Dystrophy (fukutin) (FCMD, Accession NM_006731). Accordingly, utilities of

VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCMD. TEM8 (Accession NM_032208) is another VGAM2720 host target gene. TEM8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEM8 BINDING SITE, designated SEQ ID:25921, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91123] Another function of VGAM2720 is therefore inhibition of TEM8 (Accession NM_032208), a gene which is a tumor-specific endothelial marker. Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEM8. The function of TEM8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1489.Thrombomodulin (THBD, Accession NM_000361) is another VGAM2720 host target gene. THBD BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by THBD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of THBD BINDING SITE, designated SEQ ID:5922, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91124] Another function of VGAM2720 is therefore inhibition of Thrombomodulin (THBD, Accession NM_000361). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THBD. VAMP (vesicle-associated membrane protein)-associated Protein B and C (VAPB, Accession NM_004738) is another VGAM2720 host target gene. VAPB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VAPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VAPB BINDING SITE, designated SEQ ID:11134, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91125] Another function of VGAM2720 is therefore inhibition of

VAMP (vesicle-associated membrane protein)-associated Protein B and C (VAPB, Accession NM_004738). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VAPB. Tryptophanyl-tRNA Synthetase (WARS, Accession XM_041014) is another VGAM2720 host target gene. WARS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WARS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WARS BINDING SITE, designated SEQ ID:33414, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91126] Another function of VGAM2720 is therefore inhibition of Tryptophanyl-tRNA Synthetase (WARS, Accession XM_041014), a gene which is a tryptophanyl-tRNA synthetase. Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WARS. The function of WARS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM68.FLJ20802

(Accession NM_017959) is another VGAM2720 host target gene. FLJ20802 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20802, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20802 BINDING SITE, designated SEQ ID:19676, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91127] Another function of VGAM2720 is therefore inhibition of FLJ20802 (Accession NM_017959). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20802. FLJ22087 (Accession NM_022070) is another VGAM2720 host target gene. FLJ22087 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22087, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22087 BINDING SITE, designated SEQ ID:22614, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM

RNA, also designated SEQ ID:5431.

[91128] Another function of VGAM2720 is therefore inhibition of FLJ22087 (Accession NM_022070). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22087. KIAA1497 (Accession XM_041431) is another VGAM2720 host target gene. KIAA1497 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1497, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1497 BINDING SITE, designated SEQ ID:33531, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91129] Another function of VGAM2720 is therefore inhibition of KIAA1497 (Accession XM_041431). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1497. P66 (Accession NM_020699) is another VGAM2720 host target gene. P66 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P66, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P66 BINDING SITE, designated SEQ ID:21849, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91130] Another function of VGAM2720 is therefore inhibition of P66 (Accession NM_020699). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P66. LOC152274 (Accession XM_087418) is another VGAM2720 host target gene. LOC152274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152274 BINDING SITE, designated SEQ ID:39232, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91131] Another function of VGAM2720 is therefore inhibition of LOC152274 (Accession XM_087418). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC152274. LOC157247 (Accession XM_088275) is another VGAM2720 host target gene. LOC157247 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157247 BINDING SITE, designated SEQ ID:39577, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91132] Another function of VGAM2720 is therefore inhibition of LOC157247 (Accession XM_088275). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157247. LOC199986 (Accession XM_117168) is another VGAM2720 host target gene. LOC199986 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199986, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199986 BINDING SITE, designated SEQ ID:43274, to

the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91133] Another function of VGAM2720 is therefore inhibition of LOC199986 (Accession XM_117168). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199986. LOC90750 (Accession XM_033868) is another VGAM2720 host target gene. LOC90750 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90750, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90750 BINDING SITE, designated SEQ ID:31971, to the nucleotide sequence of VGAM2720 RNA, herein designated VGAM RNA, also designated SEQ ID:5431.

[91134] Another function of VGAM2720 is therefore inhibition of LOC90750 (Accession XM_033868). Accordingly, utilities of VGAM2720 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90750. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2721 (VGAM2721) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91135] VGAM2721 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2721 was detected is described hereinabove with reference to Figs. 1-8.

[91136] VGAM2721 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2721 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91137] VGAM2721 gene encodes a VGAM2721 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2721 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2721 precursor RNA is designated SEQ ID:2707, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2707 is located at position 3755 relative to the genome of Aphid Lethal Paralysis Virus.

[91138] VGAM2721 precursor RNA folds onto itself, forming VGAM2721 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91139] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2721 folded precursor RNA into VGAM2721 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2721 RNA is designated SEQ ID:5432, and is provided hereinbelow with reference to the sequence listing part.

[91140] VGAM2721 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2721 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2721 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91141] VGAM2721 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2721 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2721 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91142] The complementary binding of VGAM2721 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2721 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2721 host target RNA into VGAM2721 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91143] It is appreciated that VGAM2721 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2721 host target genes. The mRNA of each one of this plurality of VGAM2721 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2721 RNA, herein designated VGAM RNA, and which when bound by VGAM2721 RNA causes inhibition of translation of respective one or more VGAM2721 host target proteins.

[91144] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2721 gene, herein designated VGAM GENE, on one or more VGAM2721 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91145] It is yet further appreciated that a function of VGAM2721 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2721 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2721 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2721 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91146] Nucleotide sequences of the VGAM2721 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2721 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2721 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2721 are further described hereinbelow with reference to Table 1.

[91147] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2721 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2721 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91148] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2721 gene, herein designated VGAM is inhibition of expression of VGAM2721 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2721 correlate with, and may be deduced from, the identity of the target genes which VGAM2721

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91149] Filamin B, Beta (actin binding protein 278) (FLNB, Accession XM_030806) is a VGAM2721 host target gene. FLNB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLNB BINDING SITE, designated SEQ ID:31142, to the nucleotide sequence of VGAM2721 RNA, herein designated VGAM RNA, also designated SEQ ID:5432.

[91150] A function of VGAM2721 is therefore inhibition of Filamin B, Beta (actin binding protein 278) (FLNB, Accession XM_030806), a gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. Accordingly, utilities of VGAM2721 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLNB. The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM416.Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession

NM_003615) is another VGAM2721 host target gene. SLC4A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC4A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC4A7 BINDING SITE, designated SEQ ID:9671, to the nucleotide sequence of VGAM2721 RNA, herein designated VGAM RNA, also designated SEQ ID:5432.

[91151] Another function of VGAM2721 is therefore inhibition of Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615), a gene which mediates the coupled movement of sodium and bicarbonate ions across the plasma membrane. Accordingly, utilities of VGAM2721 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A7. The function of SLC4A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM66.FLJ10704 (Accession NM_018185) is another VGAM2721 host target gene. FLJ10704 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by FLJ10704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10704 BINDING SITE, designated SEQ ID:20031, to the nucleotide sequence of VGAM2721 RNA, herein designated VGAM RNA, also designated SEQ ID:5432.

[91152] Another function of VGAM2721 is therefore inhibition of FLJ10704 (Accession NM_018185). Accordingly, utilities of VGAM2721 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10704. KIAA0229 (Accession XM_166478) is another VGAM2721 host target gene. KIAA0229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0229 BINDING SITE, designated SEQ ID:44398, to the nucleotide sequence of VGAM2721 RNA, herein designated VGAM RNA, also designated SEQ ID:5432.

[91153] Another function of VGAM2721 is therefore inhibition of

KIAA0229 (Accession XM_166478). Accordingly, utilities of VGAM2721 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0229. Synaptosomal-associated Protein, 29kDa (SNAP29, Accession NM_004782) is another VGAM2721 host target gene. SNAP29 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNAP29, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNAP29 BINDING SITE, designated SEQ ID:11185, to the nucleotide sequence of VGAM2721 RNA, herein designated VGAM RNA, also designated SEQ ID:5432.

[91154] Another function of VGAM2721 is therefore inhibition of Synaptosomal-associated Protein, 29kDa (SNAP29, Accession NM_004782). Accordingly, utilities of VGAM2721 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP29. LOC89932 (Accession XM_027341) is another VGAM2721 host target gene. LOC89932 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC89932, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89932 BINDING SITE, designated SEQ ID:30490, to the nucleotide sequence of VGAM2721 RNA, herein designated VGAM RNA, also designated SEQ ID:5432.

[91155] Another function of VGAM2721 is therefore inhibition of LOC89932 (Accession XM_027341). Accordingly, utilities of VGAM2721 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC89932. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2722 (VGAM2722) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91156] VGAM2722 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2722 was detected is described hereinabove with reference to Figs. 1-8.

[91157] VGAM2722 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis

Virus. VGAM2722 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91158] VGAM2722 gene encodes a VGAM2722 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2722 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2722 precursor RNA is designated SEQ ID:2708, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2708 is located at position 5202 relative to the genome of Aphid Lethal Paralysis Virus.

[91159] VGAM2722 precursor RNA folds onto itself, forming VGAM2722 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91160] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2722 folded precursor RNA into VGAM2722 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2722 RNA is designated SEQ ID:5433, and is provided hereinbelow with reference to the sequence listing part.

[91161] VGAM2722 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2722 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91162] VGAM2722 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2722 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2722 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91163] The complementary binding of VGAM2722 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2722 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2722 host target RNA into VGAM2722 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91164] It is appreciated that VGAM2722 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2722 host target genes. The mRNA of each one of this plurality of VGAM2722 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2722 RNA, herein designated VGAM RNA, and which when bound by VGAM2722 RNA causes inhibition of translation of respective one or more VGAM2722 host target proteins.

[91165] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2722 gene, herein designated VGAM GENE, on one or more VGAM2722 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91166] It is yet further appreciated that a function of VGAM2722 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2722 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2722 correlate with, and may be deduced from, the identity of the host target genes which VGAM2722 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91167] Nucleotide sequences of the VGAM2722 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2722 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2722 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2722 are further described hereinbelow with reference to Table 1.

[91168] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2722 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2722 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91169] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2722 gene, herein designated VGAM is inhibition of expression of VGAM2722 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2722 correlate with, and may be deduced from, the identity of the target genes which VGAM2722 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91170] Alpha Thalassemia/mental Retardation Syndrome X-linked (RAD54 homolog, S. cerevisiae) (ATRX, Accession NM_000489) is a VGAM2722 host target gene. ATRX BINDING SITE1 and ATRX BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ATRX, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of ATRX BINDING SITE1 and ATRX BINDING SITE2, designated SEQ ID:6097 and SEQ ID:28686 respectively, to the nucleotide sequence of VGAM2722 RNA, herein designated VGAM RNA, also designated SEQ ID:5433.

[91171] A function of VGAM2722 is therefore inhibition of Alpha Thalassemia/mental Retardation Syndrome X-linked (RAD54 homolog, S. cerevisiae) (ATRX, Accession NM_000489). Accordingly, utilities of VGAM2722 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATRX. DKFZp761H2121 (Accession NM_138339) is another VGAM2722 host target gene. DKFZp761H2121 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp761H2121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761H2121 BINDING SITE, designated SEQ ID:28739, to the nucleotide sequence of VGAM2722 RNA, herein designated VGAM RNA, also designated SEQ ID:5433.

[91172] Another function of VGAM2722 is therefore inhibition of DKFZp761H2121 (Accession NM_138339). Accordingly,

utilities of VGAM2722 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H2121. MGC2452 (Accession NM_032644) is another VGAM2722 host target gene. MGC2452 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC2452, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2452 BINDING SITE, designated SEQ ID:26366, to the nucleotide sequence of VGAM2722 RNA, herein designated VGAM RNA, also designated SEQ ID:5433.

[91173] Another function of VGAM2722 is therefore inhibition of MGC2452 (Accession NM_032644). Accordingly, utilities of VGAM2722 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2452. Transcription Factor-like 5 (basic helix-loop-helix) (TCFL5, Accession NM_006602) is another VGAM2722 host target gene. TCFL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCFL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of TCFL5 BINDING SITE, designated SEQ ID:13383, to the nucleotide sequence of VGAM2722 RNA, herein designated VGAM RNA, also designated SEQ ID:5433.

[91174] Another function of VGAM2722 is therefore inhibition of Transcription Factor-like 5 (basic helix-loop-helix) (TCFL5, Accession NM_006602). Accordingly, utilities of VGAM2722 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCFL5. LOC152313 (Accession XM_098190) is another VGAM2722 host target gene. LOC152313 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152313, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152313 BINDING SITE, designated SEQ ID:41477, to the nucleotide sequence of VGAM2722 RNA, herein designated VGAM RNA, also designated SEQ ID:5433.

[91175] Another function of VGAM2722 is therefore inhibition of LOC152313 (Accession XM_098190). Accordingly, utilities of VGAM2722 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC152313. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2723 (VGAM2723) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91176] VGAM2723 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2723 was detected is described hereinabove with reference to Figs. 1-8.

[91177] VGAM2723 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2723 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91178] VGAM2723 gene encodes a VGAM2723 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2723 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2723 precursor RNA is designated SEQ ID:2709, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2709 is located at position 3973 relative to the genome of Aphid Lethal Paralysis Virus.

[91179] VGAM2723 precursor RNA folds onto itself, forming VGAM2723 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91180] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2723 folded precursor RNA into VGAM2723 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2723 RNA is designated SEQ ID:5434, and is provided hereinbelow with reference to the sequence listing part.

[91181] VGAM2723 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2723 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91182] VGAM2723 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2723 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2723 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91183] The complementary binding of VGAM2723 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2723 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2723 host target RNA into VGAM2723 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91184] It is appreciated that VGAM2723 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2723 host target genes. The mRNA of each one of this plurality of VGAM2723 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2723 RNA, herein designated VGAM RNA, and which when bound by VGAM2723 RNA causes

inhibition of translation of respective one or more VGAM2723 host target proteins.

[91185] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2723 gene, herein designated VGAM GENE, on one or more VGAM2723 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91186] It is yet further appreciated that a function of VGAM2723 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2723 include diagnosis, prevention and

treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2723 correlate with, and may be deduced from, the identity of the host target genes which VGAM2723 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91187] Nucleotide sequences of the VGAM2723 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2723 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2723 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2723 are further described hereinbelow with reference to Table 1.

[91188] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2723 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2723 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91189] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2723 gene, herein designated VGAM is inhibition of expression of VGAM2723 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2723 correlate with, and may be deduced from, the identity of the target genes which VGAM2723 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91190] GA Binding Protein Transcription Factor, Beta Subunit 1, 53kDa (GABPB1, Accession NM_005254) is a VGAM2723 host target gene. GABPB1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GABPB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABPB1 BINDING SITE, designated SEQ ID:11759, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91191] A function of VGAM2723 is therefore inhibition of GA Binding Protein Transcription Factor, Beta Subunit 1, 53kDa (GABPB1, Accession NM_005254), a gene which activates adenovirus E4 gene transcription. Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABPB1. The function of GABPB1 and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.Regulator of G-protein Signalling 5 (RGS5, Accession NM_003617) is another VGAM2723 host target gene. RGS5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RGS5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGS5 BINDING SITE, designated SEQ ID:9678, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91192] Another function of VGAM2723 is therefore inhibition of Regulator of G-protein Signalling 5 (RGS5, Accession NM_003617). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS5. F-box Only Protein 24 (FBXO24, Accession NM_012172) is another VGAM2723 host target gene. FBXO24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXO24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXO24 BINDING SITE, designated SEQ ID:14464, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91193] Another function of VGAM2723 is therefore inhibition of F-box Only Protein 24 (FBXO24, Accession NM_012172). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO24. FLJ13852 (Accession NM_023078) is another VGAM2723 host target gene. FLJ13852 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13852, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13852 BINDING SITE, designated SEQ ID:23342, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91194] Another function of VGAM2723 is therefore inhibition of FLJ13852 (Accession NM_023078). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13852. FLJ20202 (Accession NM_017709) is another VGAM2723 host target gene. FLJ20202 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20202 BINDING SITE, designated SEQ ID:19289, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91195] Another function of VGAM2723 is therefore inhibition of FLJ20202 (Accession NM_017709). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20202. FLJ23519 (Accession NM_032240) is another VGAM2723 host target gene. FLJ23519 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23519 BINDING SITE, designated SEQ ID:25972, to the nucleotide

sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91196] Another function of VGAM2723 is therefore inhibition of FLJ23519 (Accession NM_032240). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23519. GA Binding Protein Transcription Factor, Beta Subunit 2, 47kDa (GABPB2, Accession NM_002041) is another VGAM2723 host target gene. GABPB2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GABPB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABPB2 BINDING SITE, designated SEQ ID:7794, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91197] Another function of VGAM2723 is therefore inhibition of GA Binding Protein Transcription Factor, Beta Subunit 2, 47kDa (GABPB2, Accession NM_002041). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABPB2. GFR (Accession NM_012294) is another

VGAM2723 host target gene. GFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GFR BINDING SITE, designated SEQ ID:14640, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91198] Another function of VGAM2723 is therefore inhibition of GFR (Accession NM_012294). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFR. SEC15B (Accession XM_039570) is another VGAM2723 host target gene. SEC15B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC15B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC15B BINDING SITE, designated SEQ ID:33127, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91199] Another function of VGAM2723 is therefore inhibition of SEC15B (Accession XM_039570). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC15B. LOC253782 (Accession XM_171023) is another VGAM2723 host target gene. LOC253782 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253782, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253782 BINDING SITE, designated SEQ ID:45799, to the nucleotide sequence of VGAM2723 RNA, herein designated VGAM RNA, also designated SEQ ID:5434.

[91200] Another function of VGAM2723 is therefore inhibition of LOC253782 (Accession XM_171023). Accordingly, utilities of VGAM2723 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253782. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2724 (VGAM2724) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[91201] VGAM2724 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2724 was detected is described hereinabove with reference to Figs. 1-8.

[91202] VGAM2724 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2724 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91203] VGAM2724 gene encodes a VGAM2724 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2724 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2724 precursor RNA is designated SEQ ID:2710, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2710 is located at position 1635 relative to the genome of Aphid Lethal Paralysis Virus.

[91204] VGAM2724 precursor RNA folds onto itself, forming VGAM2724 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91205] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2724 folded precursor RNA into VGAM2724 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2724 RNA is designated SEQ ID:5435, and is provided hereinbelow with reference to the sequence listing part.

[91206] VGAM2724 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2724 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91207] VGAM2724 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2724 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2724 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91208] The complementary binding of VGAM2724 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2724 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2724 host target RNA into VGAM2724 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91209] It is appreciated that VGAM2724 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2724 host target genes. The mRNA of each one of this plurality of VGAM2724 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2724 RNA, herein designated VGAM RNA, and which when bound by VGAM2724 RNA causes inhibition of translation of respective one or more VGAM2724 host target proteins.

[91210] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2724 gene, herein designated VGAM GENE, on one or more VGAM2724 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91211] It is yet further appreciated that a function of VGAM2724 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2724 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2724 correlate with, and may be deduced from, the identity of the host target genes which VGAM2724 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[91212] Nucleotide sequences of the VGAM2724 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2724 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2724 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2724 are further described hereinbelow with reference to Table 1.

[91213] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2724 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2724 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91214] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2724 gene, herein designated VGAM is inhibition of expression of VGAM2724 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2724 correlate with, and may be deduced from, the identity of the target genes which VGAM2724 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91215] Numb Homolog (Drosophila) (NUMB, Accession NM_003744) is a VGAM2724 host target gene. NUMB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUMB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUMB BINDING SITE, designated SEQ ID:9833, to the nucleotide sequence of VGAM2724 RNA, herein designated VGAM RNA, also designated SEQ ID:5435.

[91216] A function of VGAM2724 is therefore inhibition of Numb Homolog (Drosophila) (NUMB, Accession NM_003744), a gene which may act in generating asymmetric cell division during neurogenesisand is strongly similar to murine Numb. Accordingly, utilities of VGAM2724 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUMB. The function of NUMB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2322.DKFZp434E1822 (Accession XM_043624) is another VGAM2724 host target gene. DKFZp434E1822 BINDING SITE is HOST TARGET binding site found in the

5` untranslated region of mRNA encoded by DKFZp434E1822, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434E1822 BINDING SITE, designated SEQ ID:33984, to the nucleotide sequence of VGAM2724 RNA, herein designated VGAM RNA, also designated SEQ ID:5435.

[91217] Another function of VGAM2724 is therefore inhibition of DKFZp434E1822 (Accession XM_043624). Accordingly, utilities of VGAM2724 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E1822. E74-like Factor 4 (ets domain transcription factor) (ELF4, Accession NM_001421) is another VGAM2724 host target gene. ELF4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELF4 BINDING SITE, designated SEQ ID:7123, to the nucleotide sequence of VGAM2724 RNA, herein designated VGAM RNA, also designated SEQ ID:5435.

[91218] Another function of VGAM2724 is therefore inhibition of E74-like Factor 4 (ets domain transcription factor) (ELF4, Accession NM_001421). Accordingly, utilities of VGAM2724 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELF4. FLJ10656 (Accession NM_018170) is another VGAM2724 host target gene. FLJ10656 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10656, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10656 BINDING SITE, designated SEQ ID:19991, to the nucleotide sequence of VGAM2724 RNA, herein designated VGAM RNA, also designated SEQ ID:5435.

[91219] Another function of VGAM2724 is therefore inhibition of FLJ10656 (Accession NM_018170). Accordingly, utilities of VGAM2724 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10656. KIAA1728 (Accession XM_043492) is another VGAM2724 host target gene. KIAA1728 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1728, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1728 BINDING SITE, designated SEQ ID:33950, to the nucleotide sequence of VGAM2724 RNA, herein designated VGAM RNA, also designated SEQ ID:5435.

[91220] Another function of VGAM2724 is therefore inhibition of KIAA1728 (Accession XM_043492). Accordingly, utilities of VGAM2724 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1728. LOC154877 (Accession XM_098626) is another VGAM2724 host target gene. LOC154877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE, designated SEQ ID:41744, to the nucleotide sequence of VGAM2724 RNA, herein designated VGAM RNA, also designated SEQ ID:5435.

[91221] Another function of VGAM2724 is therefore inhibition of LOC154877 (Accession XM_098626). Accordingly, utilities of VGAM2724 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC154877. LOC54103 (Accession XM_168508) is another VGAM2724 host target gene. LOC54103 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC54103, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC54103 BINDING SITE, designated SEQ ID:45210, to the nucleotide sequence of VGAM2724 RNA, herein designated VGAM RNA, also designated SEQ ID:5435.

[91222] Another function of VGAM2724 is therefore inhibition of LOC54103 (Accession XM_168508). Accordingly, utilities of VGAM2724 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC54103. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2725 (VGAM2725) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91223] VGAM2725 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2725 was detected is described hereinabove with reference to Figs. 1-8.

[91224] VGAM2725 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2725 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91225] VGAM2725 gene encodes a VGAM2725 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2725 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2725 precursor RNA is designated SEQ ID:2711, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2711 is located at position 4120 relative to the genome of Aphid Lethal Paralysis Virus.

[91226] VGAM2725 precursor RNA folds onto itself, forming VGAM2725 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91227] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2725 folded precursor RNA into VGAM2725 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2725 RNA is designated SEQ ID:5436, and is provided hereinbelow with reference to the sequence listing part.

[91228] VGAM2725 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2725 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91229] VGAM2725 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2725 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2725 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91230] The complementary binding of VGAM2725 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2725 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2725 host target RNA into VGAM2725 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91231] It is appreciated that VGAM2725 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2725 host target genes. The mRNA of each one of this plurality of VGAM2725 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2725 RNA, herein designated VGAM RNA, and which when bound by VGAM2725 RNA causes inhibition of translation of respective one or more VGAM2725 host target proteins.

[91232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2725 gene, herein designated VGAM GENE, on one or more VGAM2725 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91233] It is yet further appreciated that a function of VGAM2725 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2725 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2725 correlate with, and may be deduced from, the identity of the host target genes which VGAM2725 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91234] Nucleotide sequences of the VGAM2725 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2725 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2725 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2725 are further described hereinbelow with reference to Table 1.

[91235] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2725 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2725 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91236] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2725 gene, herein designated VGAM is inhibition of expression of VGAM2725 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2725 correlate with, and may be deduced from, the identity of the target genes which VGAM2725 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91237] Fibroblast Growth Factor 5 (FGF5, Accession NM_004464) is a VGAM2725 host target gene. FGF5 BINDING SITE1 and FGF5 BINDING SITE2 are HOST TARGET binding sites found

in untranslated regions of mRNA encoded by FGF5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE1 and FGF5 BINDING SITE2, designated SEQ ID:10770 and SEQ ID:26997 respectively, to the nucleotide sequence of VGAM2725 RNA, herein designated VGAM RNA, also designated SEQ ID:5436.

[91238] A function of VGAM2725 is therefore inhibition of Fibroblast Growth Factor 5 (FGF5, Accession NM_004464), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of VGAM2725 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5. The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM276.KIAA1870 (Accession NM_032888) is another VGAM2725 host target gene. KIAA1870 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1870, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1870 BINDING SITE, designated SEQ ID:26711, to the nucleotide sequence of VGAM2725 RNA, herein designated VGAM RNA, also designated SEQ ID:5436.

[91239] Another function of VGAM2725 is therefore inhibition of KIAA1870 (Accession NM_032888). Accordingly, utilities of VGAM2725 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1870. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2726 (VGAM2726) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91240] VGAM2726 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2726 was detected is described hereinabove with reference to Figs. 1-8.

[91241] VGAM2726 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2726 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[91242] VGAM2726 gene encodes a VGAM2726 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2726 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2726 precursor RNA is designated SEQ ID:2712, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2712 is located at position 3591 relative to the genome of Aphid Lethal Paralysis Virus.

[91243] VGAM2726 precursor RNA folds onto itself, forming VGAM2726 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91244] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2726 folded precursor RNA into VGAM2726 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2726 RNA is designated SEQ ID:5437, and is provided hereinbelow with reference to the sequence listing part.

[91245] VGAM2726 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2726 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91246] VGAM2726 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2726 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2726 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91247] The complementary binding of VGAM2726 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2726 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2726 host target RNA into VGAM2726 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91248] It is appreciated that VGAM2726 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2726 host target genes. The mRNA of each one of this plurality of VGAM2726 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2726 RNA, herein designated VGAM RNA, and which when bound by VGAM2726 RNA causes inhibition of translation of respective one or more VGAM2726 host target proteins.

[91249] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2726 gene, herein designated VGAM GENE, on one or more VGAM2726 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91250] It is yet further appreciated that a function of VGAM2726 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2726 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2726 correlate with, and may be deduced from, the identity of the host target genes which VGAM2726 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91251] Nucleotide sequences of the VGAM2726 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2726 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2726 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2726 are further described hereinbelow with reference to Table 1.

[91252] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2726 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2726 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91253] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2726 gene, herein designated VGAM is inhibition of expression of VGAM2726 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2726 correlate with, and may be deduced from, the identity of the target genes which VGAM2726 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91254] DKFZp761B0514 (Accession NM_032289) is a VGAM2726 host target gene. DKFZp761B0514 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761B0514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761B0514 BINDING SITE, designated SEQ ID:26048, to the nucleotide sequence of VGAM2726 RNA, herein designated VGAM RNA, also designated SEQ ID:5437.

[91255] A function of VGAM2726 is therefore inhibition of DKFZp761B0514 (Accession NM_032289). Accordingly, utilities of VGAM2726 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B0514. KIAA1028 (Accession XM_166324) is another VGAM2726 host target gene. KIAA1028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1028 BINDING SITE, designated SEQ ID:44162, to the nucleotide sequence of VGAM2726 RNA, herein designated VGAM RNA, also designated SEQ ID:5437.

[91256] Another function of VGAM2726 is therefore inhibition of KIAA1028 (Accession XM_166324). Accordingly, utilities of VGAM2726 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1028. PRO2831 (Accession NM_018540) is another VGAM2726 host target gene. PRO2831 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2831, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2831 BINDING SITE, designated SEQ ID:20612, to the nucleotide sequence of VGAM2726 RNA, herein designated VGAM RNA, also designated SEQ ID:5437.

[91257] Another function of VGAM2726 is therefore inhibition of PRO2831 (Accession NM_018540). Accordingly, utilities of VGAM2726 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2831. LOC200734 (Accession XM_114286) is another VGAM2726 host target gene. LOC200734 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200734, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200734 BINDING SITE, designated SEQ ID:42841, to the nucleotide sequence of VGAM2726 RNA, herein designated VGAM RNA, also designated SEQ ID:5437.

[91258] Another function of VGAM2726 is therefore inhibition of LOC200734 (Accession XM_114286). Accordingly, utilities of VGAM2726 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC200734. LOC219940 (Accession XM_167791) is another VGAM2726 host target gene. LOC219940 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219940 BINDING SITE, designated SEQ ID:44833, to the nucleotide sequence of VGAM2726 RNA, herein designated VGAM RNA, also designated SEQ ID:5437.

[91259] Another function of VGAM2726 is therefore inhibition of LOC219940 (Accession XM_167791). Accordingly, utilities of VGAM2726 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219940. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2727 (VGAM2727) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91260] VGAM2727 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2727 was detected is described hereinabove with reference to Figs. 1-8.

[91261] VGAM2727 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2727 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91262] VGAM2727 gene encodes a VGAM2727 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2727 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2727 precursor RNA is designated SEQ ID:2713, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2713 is located at position 4727 relative to the genome of Aphid Lethal Paralysis Virus.

[91263] VGAM2727 precursor RNA folds onto itself, forming VGAM2727 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91264] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2727 folded precursor RNA into VGAM2727 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2727 RNA is designated SEQ ID:5438, and is provided hereinbelow with reference to the sequence listing part.

[91265] VGAM2727 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2727 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91266] VGAM2727 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2727 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2727 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91267] The complementary binding of VGAM2727 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2727 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2727 host target RNA into VGAM2727 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91268] It is appreciated that VGAM2727 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2727 host target genes. The mRNA of each one of this plurality of VGAM2727 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2727 RNA, herein designated VGAM RNA, and which when bound by VGAM2727 RNA causes inhibition of translation of respective one or more VGAM2727 host target proteins.

[91269] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2727 gene, herein designated VGAM GENE, on one or more VGAM2727 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91270] It is yet further appreciated that a function of VGAM2727 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2727 correlate with, and may be deduced from, the identity of the host target genes which VGAM2727 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91271] Nucleotide sequences of the VGAM2727 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2727 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2727 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2727 are further described hereinbelow with reference to Table 1.

[91272] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2727 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2727 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91273] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2727 gene, herein designated VGAM is inhibition of expression of VGAM2727 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2727 correlate with, and may be deduced from, the identity of the target genes which VGAM2727 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91274] C-terminal Binding Protein 2 (CTBP2, Accession NM_001329) is a VGAM2727 host target gene. CTBP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CTBP2, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTBP2 BINDING SITE, designated SEQ ID:7010, to the nucleotide sequence of VGAM2727 RNA, herein designated VGAM RNA, also designated SEQ ID:5438.

[91275] A function of VGAM2727 is therefore inhibition of C-terminal Binding Protein 2 (CTBP2, Accession NM_001329), a gene which binds to cellular and viral transcriptional repressors regulated by NAD+ and NADH. Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTBP2. The function of CTBP2 has been established by previous studies. In Drosophila and in vertebrates, the Polycomb (Pc) group (PcG) genes have been identified as being part of a cellular memory system that is responsible for the stable and heritable repression of gene expression. PC2 (OMIM Ref. No. 603079), a human Pc homolog, CBX2 (OMIM Ref. No. 602770), HPH1 (OMIM Ref. No. 602978), HPH2 (OMIM Ref. No. 602979), BMI1 (OMIM Ref. No. 164831), and RING1 (OMIM Ref. No. 602045) form a complex that localizes in large nuclear domains termed PcG domains. Using a yeast 2-hybrid as-

say, Sewalt et al. (1999) found that CTBP2 interacts with PC2 and that Xenopus Ctbp1 interacts with Xenopus Pc. The CTBP2 and PC2 interaction also exists in vivo, since the proteins coimmunoprecipitate with each other and partially colocalize in large PcG domains in interphase nuclei. CTBP1 showed the same localization pattern. As with PC2, chimeric LexA-CTBP2 and LexA-CTBP1 proteins repressed gene activity when targeted to a reporter gene. Sewalt et al. (1999) suggested that the CTBP proteins target PC2, and thereby the PcG complex, to particular loci in chromatin that contain binding sites for specific repressors of gene activity, thereby forming a complex between the repressors and the PcG complex, with CTBP as a bridging protein. They speculated that the interference of the adenoviral E1A protein with the transcription machinery of the infected cell may involve interference with PcG-mediated repression through disruption of the CTBP-PcG interaction Zhang et al. (2002) demonstrated that CTBP binding to cellular and viral transcriptional repressors is regulated by NAD+ and NADH, with NADH being 2 to 3 orders of magnitude more effective. Levels of free nuclear nicotinamide adenine dinucleotides, determined using 2-photon microscopy, corresponded to the levels required

for half-maximal CTBP binding and were considerably lower than those previously reported. Agents capable of increasing NADH levels stimulated CTBP binding to its partners in vivo and potentiated CTBP-mediated repression. Zhang et al. (2002) proposed that this ability to detect changes in nuclear NAD+/NADH ratio allows CTBP to serve as a redox sensor for transcription

[91276] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[91277] Sewalt, R. G. A. B.; Gunster, M. J.; van der Vlag, J.; Satijn, D. P. E.; Otte, A. P. : C-terminal binding protein is a transcriptional repressor that interacts with a specific class of vertebrate polycomb proteins. Molec. Cell. Biol. 19: 777-787, 1999. ; and

[91278] Zhang, Q.; Piston, D. W.; Goodman, R. H. : Regulation of corepressor function by nuclear NADH. Science 295: 1895-1897, 2002.

[91279] Further studies establishing the function and utilities of CTBP2 are found in John Hopkins OMIM database record ID 602619, and in sited publications numbered 8464-846 and 8553-8468 listed in the bibliography section herein-below, which are also hereby incorporated by refer-

ence.DKFZP434O125 (Accession XM_036284) is another VGAM2727 host target gene. DKFZP434O125 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434O125, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434O125 BINDING SITE, designated SEQ ID:32405, to the nucleotide sequence of VGAM2727 RNA, herein designated VGAM RNA, also designated SEQ ID:5438.

[91280] Another function of VGAM2727 is therefore inhibition of DKFZP434O125 (Accession XM_036284). Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434O125. KIAA0546 (Accession XM_049055) is another VGAM2727 host target gene. KIAA0546 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0546, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0546 BINDING SITE, designated SEQ ID:35329, to the

nucleotide sequence of VGAM2727 RNA, herein designated VGAM RNA, also designated SEQ ID:5438.

[91281] Another function of VGAM2727 is therefore inhibition of KIAA0546 (Accession XM_049055). Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0546. Leucine-rich Repeat Protein, Neuronal 3 (LRRN3, Accession XM_045261) is another VGAM2727 host target gene. LRRN3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LRRN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRRN3 BINDING SITE, designated SEQ ID:34402, to the nucleotide sequence of VGAM2727 RNA, herein designated VGAM RNA, also designated SEQ ID:5438.

[91282] Another function of VGAM2727 is therefore inhibition of Leucine-rich Repeat Protein, Neuronal 3 (LRRN3, Accession XM_045261). Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRRN3. Rpo1-2 (Accession NM_019014) is another VGAM2727 host target

gene. Rpo1-2 BINDING SITE1 and Rpo1-2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by Rpo1-2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rpo1-2 BINDING SITE1 and Rpo1-2 BINDING SITE2, designated SEQ ID:21106 and SEQ ID:25936 respectively, to the nucleotide sequence of VGAM2727 RNA, herein designated VGAM RNA, also designated SEQ ID:5438.

[91283] Another function of VGAM2727 is therefore inhibition of Rpo1-2 (Accession NM_019014). Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rpo1-2. LOC157695 (Accession XM_098811) is another VGAM2727 host target gene. LOC157695 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157695, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157695 BINDING SITE, designated SEQ ID:41833, to the nucleotide sequence of VGAM2727 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5438.

[91284] Another function of VGAM2727 is therefore inhibition of LOC157695 (Accession XM_098811). Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157695. LOC221042 (Accession XM_167669) is another VGAM2727 host target gene. LOC221042 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221042 BINDING SITE, designated SEQ ID:44758, to the nucleotide sequence of VGAM2727 RNA, herein designated VGAM RNA, also designated SEQ ID:5438.

[91285] Another function of VGAM2727 is therefore inhibition of LOC221042 (Accession XM_167669). Accordingly, utilities of VGAM2727 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221042. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2728 (VGAM2728) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91286] VGAM2728 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2728 was detected is described hereinabove with reference to Figs. 1-8.

[91287] VGAM2728 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2728 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91288] VGAM2728 gene encodes a VGAM2728 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2728 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2728 precursor RNA is designated SEQ ID:2714, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2714 is located at position 7888 relative to the genome of Aphid Lethal Paralysis Virus.

[91289] VGAM2728 precursor RNA folds onto itself, forming

VGAM2728 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91290] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2728 folded precursor RNA into VGAM2728 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2728 RNA is designated SEQ ID:5439, and is provided hereinbelow with reference to the sequence listing part.

[91291] VGAM2728 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2728 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91292] VGAM2728 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2728 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2728 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91293] The complementary binding of VGAM2728 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2728 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2728 host target RNA into VGAM2728 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91294] It is appreciated that VGAM2728 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2728 host target genes. The mRNA of each one of this plurality of VGAM2728 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2728 RNA, herein designated VGAM RNA, and which when bound by VGAM2728 RNA causes inhibition of translation of respective one or more VGAM2728 host target proteins.

[91295] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2728 gene, herein designated VGAM GENE, on one or more VGAM2728 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91296] It is yet further appreciated that a function of VGAM2728 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2728 correlate with, and may be deduced from, the identity of the host target genes which VGAM2728 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[91297] Nucleotide sequences of the VGAM2728 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2728 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2728 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2728 are further described hereinbelow with reference to Table 1.

[91298] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2728 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2728 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91299] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2728 gene, herein designated VGAM is inhibition of expression of VGAM2728 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2728 correlate with, and may be deduced from, the identity of the target genes which VGAM2728 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[91300] Hepatoma-derived Growth Factor (high-mobility group protein 1-like) (HDGF, Accession NM_004494) is a VGAM2728 host target gene. HDGF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HDGF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HDGF BINDING SITE, designated SEQ ID:10831, to the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91301] A function of VGAM2728 is therefore inhibition of Hepatoma-derived Growth Factor (high-mobility group protein 1-like) (HDGF, Accession NM_004494), a gene which is a heparin-binding protein, with mitogenic activity for fibroblasts. Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HDGF. The function of HDGF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Insulin-like Growth Factor Binding Protein 4

(IGFBP4, Accession NM_001552) is another VGAM2728 host target gene. IGFBP4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IGFBP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IGFBP4 BINDING SITE, designated SEQ ID:7274, to the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91302] Another function of VGAM2728 is therefore inhibition of Insulin-like Growth Factor Binding Protein 4 (IGFBP4, Accession NM_001552), a gene which prolongs the half-life of the igfs and inhibit or stimulate their growth promoting effects on cell culture. Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IGFBP4. The function of IGFBP4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2537.Phospholamban (PLN, Accession NM_002667) is another VGAM2728 host target gene. PLN BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by PLN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLN BINDING SITE, designated SEQ ID:8537, to the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91303] Another function of VGAM2728 is therefore inhibition of Phospholamban (PLN, Accession NM_002667), a gene which regulates the activity of the calcium pump of cardiac sarcoplasmic reticulum. Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLN. The function of PLN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM119.Protein Phosphatase 1, Catalytic Subunit, Beta Isoform (PPP1CB, Accession NM_002709) is another VGAM2728 host target gene. PPP1CB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1CB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PPP1CB BINDING SITE, designated SEQ ID:8557, to the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91304] Another function of VGAM2728 is therefore inhibition of Protein Phosphatase 1, Catalytic Subunit, Beta Isoform (PPP1CB, Accession NM_002709), a gene which is the catalytic subunit of protein phosphatase 1. Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1CB. The function of PPP1CB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM46.Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977) is another VGAM2728 host target gene. SLC22A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC22A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A3 BINDING SITE, designated SEQ ID:22502, to the nucleotide sequence of

VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91305] Another function of VGAM2728 is therefore inhibition of Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977), a gene which is a sodium-ion dependent, high affinity carnitine transporter. also transports organic cations without the involvement of sodium. involved in the active cellular uptake of carnitine. Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC22A3. The function of SLC22A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2147.DKFZP434H132 (Accession NM_015492) is another VGAM2728 host target gene. DKFZP434H132 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434H132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434H132 BINDING SITE, designated SEQ ID:17763, to the nucleotide sequence of

VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91306] Another function of VGAM2728 is therefore inhibition of DKFZP434H132 (Accession NM_015492). Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H132. FLJ22833 (Accession NM_022837) is another VGAM2728 host target gene. FLJ22833 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22833, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22833 BINDING SITE, designated SEQ ID:23120, to the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91307] Another function of VGAM2728 is therefore inhibition of FLJ22833 (Accession NM_022837). Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22833. KIAA1821 (Accession XM_050101) is another VGAM2728 host target gene. KIAA1821 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1821, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1821 BINDING SITE, designated SEQ ID:35552, to the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91308] Another function of VGAM2728 is therefore inhibition of KIAA1821 (Accession XM_050101). Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1821. MGC22014 (Accession XM_035307) is another VGAM2728 host target gene. MGC22014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC22014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC22014 BINDING SITE, designated SEQ ID:32225, to the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91309] Another function of VGAM2728 is therefore inhibition of MGC22014 (Accession XM_035307). Accordingly, utilities

of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC22014. LOC90829 (Accession XM_034325) is another VGAM2728 host target gene. LOC90829 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90829 BINDING SITE, designated SEQ ID:32054, to the nucleotide sequence of VGAM2728 RNA, herein designated VGAM RNA, also designated SEQ ID:5439.

[91310] Another function of VGAM2728 is therefore inhibition of LOC90829 (Accession XM_034325). Accordingly, utilities of VGAM2728 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90829. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2729 (VGAM2729) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91311] VGAM2729 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2729 was detected is described hereinabove with reference to Figs. 1-8.

[91312] VGAM2729 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Aphid Lethal Paralysis Virus. VGAM2729 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91313] VGAM2729 gene encodes a VGAM2729 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2729 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2729 precursor RNA is designated SEQ ID:2715, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2715 is located at position 7811 relative to the genome of Aphid Lethal Paralysis Virus.

[91314] VGAM2729 precursor RNA folds onto itself, forming VGAM2729 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91315] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2729 folded precursor RNA into VGAM2729 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2729 RNA is designated SEQ ID:5440, and is provided hereinbelow with reference to the sequence listing part.

[91316] VGAM2729 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2729 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[91317] VGAM2729 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2729 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2729 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91318] The complementary binding of VGAM2729 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2729 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2729 host target RNA into VGAM2729 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91319] It is appreciated that VGAM2729 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2729 host target genes. The mRNA of each one of this plurality of VGAM2729 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2729 RNA, herein designated VGAM RNA, and which when bound by VGAM2729 RNA causes inhibition of translation of respective one or more VGAM2729 host target proteins.

[91320] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2729 gene, herein designated VGAM GENE, on one or more VGAM2729 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91321] It is yet further appreciated that a function of VGAM2729 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2729 include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGAM2729 correlate with, and may be deduced from, the identity of the host target genes which VGAM2729 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91322] Nucleotide sequences of the VGAM2729 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2729 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2729 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2729 are further described hereinbelow with reference to Table 1.

[91323] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2729 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2729 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91324] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2729 gene, herein designated VGAM is inhibition of expression of VGAM2729 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2729 correlate with, and may be deduced from, the identity of the target genes which VGAM2729 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91325] Fukuyama Type Congenital Muscular Dystrophy (fukutin) (FCMD, Accession NM_006731) is a VGAM2729 host tar-

get gene. FCMD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FCMD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCMD BINDING SITE, designated SEQ ID:13573, to the nucleotide sequence of VGAM2729 RNA, herein designated VGAM RNA, also designated SEQ ID:5440.

[91326] A function of VGAM2729 is therefore inhibition of Fukuyama Type Congenital Muscular Dystrophy (fukutin) (FCMD, Accession NM_006731). Accordingly, utilities of VGAM2729 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCMD. Keratocan (KERA, Accession NM_007035) is another VGAM2729 host target gene. KERA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KERA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KERA BINDING SITE, designated SEQ ID:13908, to the nucleotide sequence of VGAM2729 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5440.

[91327] Another function of VGAM2729 is therefore inhibition of Keratocan (KERA, Accession NM_007035), a gene which may be important in developing and maintaining corneal transparency and for the structure of the stromal matrix. Accordingly, utilities of VGAM2729 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KERA. The function of KERA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM723.Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695) is another VGAM2729 host target gene. VANGL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VANGL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VANGL2 BINDING SITE, designated SEQ ID:35485, to the nucleotide sequence of VGAM2729 RNA, herein designated VGAM RNA, also designated SEQ ID:5440.

[91328] Another function of VGAM2729 is therefore inhibition of Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession

XM_049695), a gene which may take part in defining the lateral boundary of floorplate differentiation. Accordingly, utilities of VGAM2729 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VANGL2. The function of VANGL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2730 (VGAM2730) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91329] VGAM2730 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2730 was detected is described hereinabove with reference to Figs. 1-8.

[91330] VGAM2730 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine Herpesvirus 3. VGAM2730 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91331] VGAM2730 gene encodes a VGAM2730 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2730 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2730 precursor RNA is designated SEQ ID:2716, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2716 is located at position 95914 relative to the genome of Callitrichine Herpesvirus 3.

[91332] VGAM2730 precursor RNA folds onto itself, forming VGAM2730 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91333] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2730 folded precursor RNA into VGAM2730 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2730 RNA is designated SEQ ID:5441, and is provided hereinbelow with reference to the sequence listing part.

[91334] VGAM2730 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2730 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91335] VGAM2730 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2730 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2730 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91336] The complementary binding of VGAM2730 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2730 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2730 host target RNA into VGAM2730 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91337] It is appreciated that VGAM2730 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2730 host target genes. The mRNA of each one of this plurality of VGAM2730 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2730 RNA, herein designated VGAM RNA, and which when bound by VGAM2730 RNA causes inhibition of translation of respective one or more VGAM2730 host target proteins.

[91338] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2730 gene, herein designated VGAM GENE, on one or more VGAM2730 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91339] It is yet further appreciated that a function of VGAM2730 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2730 include diagnosis, prevention and treatment of viral infection by Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2730 correlate with, and may be deduced from, the identity of the host target genes which VGAM2730 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91340] Nucleotide sequences of the VGAM2730 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2730 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2730 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2730 are further described hereinbelow with reference to Table 1.

[91341] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2730 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2730 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91342] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2730 gene, herein designated VGAM is inhibition of expression of VGAM2730 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2730 correlate with, and may be deduced from, the identity of the target genes which VGAM2730 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91343] Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006) is a VGAM2730 host target gene. FGF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF2 BINDING SITE, designated SEQ ID:7740, to the nucleotide sequence of VGAM2730 RNA, herein designated VGAM RNA, also designated SEQ ID:5441.

[91344] A function of VGAM2730 is therefore inhibition of Fibrob-

last Growth Factor 2 (basic) (FGF2, Accession NM_002006), a gene which probably involved in nervous system development and function. Accordingly, utilities of VGAM2730 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF2. The function of FGF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM51.Sex Comb On Midleg-like 1 (Drosophila) (SCML1, Accession NM_006746) is another VGAM2730 host target gene. SCML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCML1 BINDING SITE, designated SEQ ID:13593, to the nucleotide sequence of VGAM2730 RNA, herein designated VGAM RNA, also designated SEQ ID:5441.

[91345] Another function of VGAM2730 is therefore inhibition of Sex Comb On Midleg-like 1 (Drosophila) (SCML1, Accession NM_006746). Accordingly, utilities of VGAM2730 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with SCML1. Titin (TTN, Accession NM_133378) is another VGAM2730 host target gene. TTN BINDING SITE1 through TTN BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TTN, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTN BINDING SITE1 through TTN BINDING SITE3, designated SEQ ID:28504, SEQ ID:28509 and SEQ ID:28519 respectively, to the nucleotide sequence of VGAM2730 RNA, herein designated VGAM RNA, also designated SEQ ID:5441.

[91346] Another function of VGAM2730 is therefore inhibition of Titin (TTN, Accession NM_133378). Accordingly, utilities of VGAM2730 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTN. KIAA1116 (Accession NM_014892) is another VGAM2730 host target gene. KIAA1116 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1116, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1116 BINDING SITE, designated SEQ ID:17041, to the nucleotide sequence of VGAM2730 RNA, herein designated VGAM RNA, also designated SEQ ID:5441.

[91347] Another function of VGAM2730 is therefore inhibition of KIAA1116 (Accession NM_014892). Accordingly, utilities of VGAM2730 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1116. Rpo1-2 (Accession NM_019014) is another VGAM2730 host target gene. Rpo1-2 BINDING SITE1 and Rpo1-2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by Rpo1-2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rpo1-2 BINDING SITE1 and Rpo1-2 BINDING SITE2, designated SEQ ID:21104 and SEQ ID:25934 respectively, to the nucleotide sequence of VGAM2730 RNA, herein designated VGAM RNA, also designated SEQ ID:5441.

[91348] Another function of VGAM2730 is therefore inhibition of Rpo1-2 (Accession NM_019014). Accordingly, utilities of VGAM2730 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

Rpo1-2. LOC93613 (Accession XM_052568) is another VGAM2730 host target gene. LOC93613 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93613, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93613 BINDING SITE, designated SEQ ID:35995, to the nucleotide sequence of VGAM2730 RNA, herein designated VGAM RNA, also designated SEQ ID:5441.

[91349] Another function of VGAM2730 is therefore inhibition of LOC93613 (Accession XM_052568). Accordingly, utilities of VGAM2730 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93613. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2731 (VGAM2731) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91350] VGAM2731 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2731 was detected is described hereinabove with reference to Figs. 1-8.

[91351] VGAM2731 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine Herpesvirus 3. VGAM2731 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91352] VGAM2731 gene encodes a VGAM2731 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2731 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2731 precursor RNA is designated SEQ ID:2717, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2717 is located at position 96552 relative to the genome of Callitrichine Herpesvirus 3.

[91353] VGAM2731 precursor RNA folds onto itself, forming VGAM2731 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91354] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2731 folded precursor RNA into VGAM2731 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2731 RNA is designated SEQ ID:5442, and is provided hereinbelow with reference to the sequence listing part.

[91355] VGAM2731 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2731 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91356] VGAM2731 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2731 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2731 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91357] The complementary binding of VGAM2731 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2731 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2731 host target RNA into VGAM2731 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91358] It is appreciated that VGAM2731 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2731 host target genes. The mRNA of each one of this plurality of VGAM2731 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2731 RNA, herein designated VGAM RNA, and which when bound by VGAM2731 RNA causes inhibition of translation of respective one or more VGAM2731 host target proteins.

[91359] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2731 gene, herein designated VGAM GENE, on one or more VGAM2731 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91360] It is yet further appreciated that a function of VGAM2731 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2731 include diagnosis, prevention and treatment of viral infection by Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2731 correlate with, and may be deduced from, the identity of the host target genes which VGAM2731 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91361] Nucleotide sequences of the VGAM2731 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2731 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2731 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2731 are further described hereinbelow with reference to Table 1.

[91362] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2731 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2731 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91363] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2731 gene, herein designated VGAM is inhibition of expression of VGAM2731 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2731 correlate with, and may be deduced from, the identity of the target genes which VGAM2731 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91364] LOC152328 (Accession XM_087420) is a VGAM2731 host target gene. LOC152328 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152328, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152328 BINDING SITE, designated SEQ ID:39242, to the nucleotide sequence of VGAM2731 RNA, herein designated VGAM RNA, also designated SEQ ID:5442.

[91365] A function of VGAM2731 is therefore inhibition of LOC152328 (Accession XM_087420). Accordingly, utilities of VGAM2731 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152328. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2732 (VGAM2732) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91366] VGAM2732 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2732 was detected is described hereinabove with reference to Figs. 1-8.

[91367] VGAM2732 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Callitrichine Herpesvirus

3. VGAM2732 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91368] VGAM2732 gene encodes a VGAM2732 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2732 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2732 precursor RNA is designated SEQ ID:2718, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2718 is located at position 136708 relative to the genome of Callitrichine Herpesvirus 3.

[91369] VGAM2732 precursor RNA folds onto itself, forming VGAM2732 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91370] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2732 folded precursor RNA into VGAM2732 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2732 RNA is designated SEQ ID:5443, and is provided hereinbelow with reference to the sequence listing part.

[91371] VGAM2732 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2732 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91372] VGAM2732 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2732 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2732 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91373] The complementary binding of VGAM2732 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2732 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2732 host target RNA into VGAM2732 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91374] It is appreciated that VGAM2732 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2732 host target genes. The mRNA of each one of this plurality of VGAM2732 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2732 RNA, herein designated VGAM RNA, and which when bound by VGAM2732 RNA causes inhibition of translation of respective one or more VGAM2732 host target proteins.

[91375] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2732 gene, herein designated VGAM GENE, on one or more VGAM2732 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91376] It is yet further appreciated that a function of VGAM2732 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2732 include diagnosis, prevention and treatment of viral infection by Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2732 correlate with, and may be deduced from, the identity of the host target genes which VGAM2732 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91377] Nucleotide sequences of the VGAM2732 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2732 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2732 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2732 are further described hereinbelow with reference to Table 1.

[91378] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2732 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2732 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91379] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2732 gene, herein designated VGAM is inhibition of expression of VGAM2732 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2732 correlate with, and may be deduced from, the identity of the target genes which VGAM2732 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91380] FLJ20701 (Accession NM_017933) is a VGAM2732 host target gene. FLJ20701 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20701, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20701 BINDING SITE, designated SEQ ID:19621, to the nucleotide sequence of

VGAM2732 RNA, herein designated VGAM RNA, also designated SEQ ID:5443.

[91381] A function of VGAM2732 is therefore inhibition of FLJ20701 (Accession NM_017933). Accordingly, utilities of VGAM2732 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20701. P5-1 (Accession NM_006674) is another VGAM2732 host target gene. P5-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P5-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P5-1 BINDING SITE, designated SEQ ID:13495, to the nucleotide sequence of VGAM2732 RNA, herein designated VGAM RNA, also designated SEQ ID:5443.

[91382] Another function of VGAM2732 is therefore inhibition of P5-1 (Accession NM_006674). Accordingly, utilities of VGAM2732 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P5-1. LOC149705 (Accession XM_097711) is another VGAM2732 host target gene. LOC149705 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC149705, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149705 BINDING SITE, designated SEQ ID:41051, to the nucleotide sequence of VGAM2732 RNA, herein designated VGAM RNA, also designated SEQ ID:5443.

[91383] Another function of VGAM2732 is therefore inhibition of LOC149705 (Accession XM_097711). Accordingly, utilities of VGAM2732 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149705. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2733 (VGAM2733) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91384] VGAM2733 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2733 was detected is described hereinabove with reference to Figs. 1-8.

[91385] VGAM2733 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Broad Bean Necrosis Virus. VGAM2733 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91386] VGAM2733 gene encodes a VGAM2733 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2733 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2733 precursor RNA is designated SEQ ID:2719, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2719 is located at position 1316 relative to the genome of Broad Bean Necrosis Virus.

[91387] VGAM2733 precursor RNA folds onto itself, forming VGAM2733 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91388] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2733 folded precursor RNA into VGAM2733 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2733 RNA is designated SEQ ID:5444, and is provided hereinbelow with reference to the sequence listing part.

[91389] VGAM2733 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2733 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91390] VGAM2733 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2733 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2733 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91391] The complementary binding of VGAM2733 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2733 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2733

host target RNA into VGAM2733 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91392] It is appreciated that VGAM2733 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2733 host target genes. The mRNA of each one of this plurality of VGAM2733 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2733 RNA, herein designated VGAM RNA, and which when bound by VGAM2733 RNA causes inhibition of translation of respective one or more VGAM2733 host target proteins.

[91393] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2733 gene, herein designated VGAM GENE, on one or more VGAM2733 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91394] It is yet further appreciated that a function of VGAM2733 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2733 correlate with, and may be deduced from, the identity of the host target genes which VGAM2733 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91395] Nucleotide sequences of the VGAM2733 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2733 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2733 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2733 are further

described hereinbelow with reference to Table 1.

[91396] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2733 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2733 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91397] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2733 gene, herein designated VGAM is inhibition of expression of VGAM2733 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2733 correlate with, and may be deduced from, the identity of the target genes which VGAM2733 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91398] B-cell CLL/lymphoma 7A (BCL7A, Accession NM_020993) is a VGAM2733 host target gene. BCL7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL7A BIND-

ING SITE, designated SEQ ID:21996, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91399] A function of VGAM2733 is therefore inhibition of B-cell CLL/lymphoma 7A (BCL7A, Accession NM_020993). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL7A. BRF1 Homolog, Subunit of RNA Polymerase III Transcription Initiation Factor IIIB (S. cerevisiae) (BRF1, Accession NM_001519) is another VGAM2733 host target gene. BRF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRF1 BINDING SITE, designated SEQ ID:7257, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91400] Another function of VGAM2733 is therefore inhibition of BRF1 Homolog, Subunit of RNA Polymerase III Transcription Initiation Factor IIIB (S. cerevisiae) (BRF1, Accession NM_001519), a gene which is a general activator of RNA

polymerase III. Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRF1. The function of BRF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM232.Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116) is another VGAM2733 host target gene. CAPZA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAPZA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPZA1 BINDING SITE, designated SEQ ID:35948, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91401] Another function of VGAM2733 is therefore inhibition of Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116), a gene which is alpha 1 subunit of actin filament capping protein; binds actin, has roles in cell motility and actin assembly. Accordingly, utilities of VGAM2733 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with CAPZA1. The function of CAPZA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM547.Fibroblast Growth Factor 23 (FGF23, Accession NM_020638) is another VGAM2733 host target gene. FGF23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGF23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF23 BINDING SITE, designated SEQ ID:21795, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91402] Another function of VGAM2733 is therefore inhibition of Fibroblast Growth Factor 23 (FGF23, Accession NM_020638), a gene which a member of the fibroblast growth factor family . Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF23. The function of FGF23 and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to VGAM24.Oculocerebrorenal Syndrome of Lowe (OCRL, Accession NM_000276) is another VGAM2733 host target gene. OCRL BINDING SITE1 and OCRL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OCRL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OCRL BINDING SITE1 and OCRL BINDING SITE2, designated SEQ ID:5820 and SEQ ID:7307 respectively, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91403] Another function of VGAM2733 is therefore inhibition of Oculocerebrorenal Syndrome of Lowe (OCRL, Accession NM_000276). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OCRL. SMP1 (Accession NM_014313) is another VGAM2733 host target gene. SMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of SMP1 BINDING SITE, designated SEQ ID:15612, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91404] Another function of VGAM2733 is therefore inhibition of SMP1 (Accession NM_014313), a gene which is a potential integral membrane protein. Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMP1. The function of SMP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM127.SORCS3 (Accession NM_014978) is another VGAM2733 host target gene. SORCS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SORCS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SORCS3 BINDING SITE, designated SEQ ID:17365, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91405] Another function of VGAM2733 is therefore inhibition of

SORCS3 (Accession NM_014978). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SORCS3. Tumor Necrosis Factor Receptor Superfamily, Member 10b (TNFRSF10B, Accession NM_003842) is another VGAM2733 host target gene. TNFRSF10B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF10B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE, designated SEQ ID:9937, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91406] Another function of VGAM2733 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 10b (TNFRSF10B, Accession NM_003842), a gene which forms complex that induces apoptosis. Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF10B. The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM400.BRAG (Accession NM_014863) is another VGAM2733 host target gene. BRAG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRAG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRAG BINDING SITE, designated SEQ ID:16943, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91407] Another function of VGAM2733 is therefore inhibition of BRAG (Accession NM_014863). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRAG. DNA Cross-link Repair 1A (PSO2 homolog, S. cerevisiae) (DCLRE1A, Accession XM_044815) is another VGAM2733 host target gene. DCLRE1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCLRE1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCLRE1A BINDING SITE, designated SEQ ID:34282, to the nucleotide sequence of

VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91408] Another function of VGAM2733 is therefore inhibition of DNA Cross-link Repair 1A (PSO2 homolog, S. cerevisiae) (DCLRE1A, Accession XM_044815). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCLRE1A. DKFZP434P0111 (Accession XM_041116) is another VGAM2733 host target gene. DKFZP434P0111 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P0111, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434P0111 BINDING SITE, designated SEQ ID:33459, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91409] Another function of VGAM2733 is therefore inhibition of DKFZP434P0111 (Accession XM_041116). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P0111. FLJ22944 (Accession NM_025145)

is another VGAM2733 host target gene. FLJ22944 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22944, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22944 BINDING SITE, designated SEQ ID:24783, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91410] Another function of VGAM2733 is therefore inhibition of FLJ22944 (Accession NM_025145). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22944. FLJ23022 (Accession NM_025051) is another VGAM2733 host target gene. FLJ23022 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23022, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23022 BINDING SITE, designated SEQ ID:24648, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91411] Another function of VGAM2733 is therefore inhibition of FLJ23022 (Accession NM_025051). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23022. Junctional Adhesion Molecule 1 (JAM1, Accession NM_144502) is another VGAM2733 host target gene. JAM1 BINDING SITE1 through JAM1 BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by JAM1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAM1 BINDING SITE1 through JAM1 BINDING SITE5, designated SEQ ID:29330, SEQ ID:29341, SEQ ID:18863, SEQ ID:29322 and SEQ ID:29351 respectively, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91412] Another function of VGAM2733 is therefore inhibition of Junctional Adhesion Molecule 1 (JAM1, Accession NM_144502). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAM1. MYLE (Accession NM_014015) is another VGAM2733 host target gene.

MYLE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYLE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYLE BINDING SITE, designated SEQ ID:15235, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91413] Another function of VGAM2733 is therefore inhibition of MYLE (Accession NM_014015). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLE. LOC118738 (Accession XM_061125) is another VGAM2733 host target gene. LOC118738 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC118738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118738 BINDING SITE, designated SEQ ID:37195, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91414] Another function of VGAM2733 is therefore inhibition of

LOC118738 (Accession XM_061125). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118738. LOC142913 (Accession XM_084378) is another VGAM2733 host target gene. LOC142913 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC142913, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142913 BINDING SITE, designated SEQ ID:37564, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91415] Another function of VGAM2733 is therefore inhibition of LOC142913 (Accession XM_084378). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142913. LOC144519 (Accession XM_084890) is another VGAM2733 host target gene. LOC144519 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC144519 BINDING SITE, designated SEQ ID:37761, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91416] Another function of VGAM2733 is therefore inhibition of LOC144519 (Accession XM_084890). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144519. LOC145501 (Accession XM_085157) is another VGAM2733 host target gene. LOC145501 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145501, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145501 BINDING SITE, designated SEQ ID:37884, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91417] Another function of VGAM2733 is therefore inhibition of LOC145501 (Accession XM_085157). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145501. LOC148930 (Accession XM_086369) is an-

other VGAM2733 host target gene. LOC148930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148930 BINDING SITE, designated SEQ ID:38621, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91418] Another function of VGAM2733 is therefore inhibition of LOC148930 (Accession XM_086369). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148930. LOC166206 (Accession XM_093743) is another VGAM2733 host target gene. LOC166206 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC166206, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC166206 BINDING SITE, designated SEQ ID:40209, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91419] Another function of VGAM2733 is therefore inhibition of LOC166206 (Accession XM_093743). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC166206. LOC200227 (Accession XM_114162) is another VGAM2733 host target gene. LOC200227 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200227, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200227 BINDING SITE, designated SEQ ID:42746, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91420] Another function of VGAM2733 is therefore inhibition of LOC200227 (Accession XM_114162). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200227. LOC221466 (Accession XM_168087) is another VGAM2733 host target gene. LOC221466 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221466, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221466 BINDING SITE, designated SEQ ID:44999, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91421] Another function of VGAM2733 is therefore inhibition of LOC221466 (Accession XM_168087). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221466. LOC254531 (Accession XM_170773) is another VGAM2733 host target gene. LOC254531 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254531, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254531 BINDING SITE, designated SEQ ID:45539, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91422] Another function of VGAM2733 is therefore inhibition of LOC254531 (Accession XM_170773). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC254531. LOC91097 (Accession XM_035977) is another VGAM2733 host target gene. LOC91097 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91097, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91097 BINDING SITE, designated SEQ ID:32371, to the nucleotide sequence of VGAM2733 RNA, herein designated VGAM RNA, also designated SEQ ID:5444.

[91423] Another function of VGAM2733 is therefore inhibition of LOC91097 (Accession XM_035977). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91097. LOC91689 (Accession NM_033318) is another VGAM2733 host target gene. LOC91689 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91689, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91689 BINDING SITE, designated SEQ ID:27156, to the nucleotide sequence of VGAM2733 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5444.

[91424] Another function of VGAM2733 is therefore inhibition of LOC91689 (Accession NM_033318). Accordingly, utilities of VGAM2733 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91689. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2734 (VGAM2734) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91425] VGAM2734 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2734 was detected is described hereinabove with reference to Figs. 1-8.

[91426] VGAM2734 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad Bean Necrosis Virus. VGAM2734 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91427] VGAM2734 gene encodes a VGAM2734 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2734 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2734 precursor RNA is designated SEQ ID:2720, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2720 is located at position 3664 relative to the genome of Broad Bean Necrosis Virus.

[91428] VGAM2734 precursor RNA folds onto itself, forming VGAM2734 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91429] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2734 folded precursor RNA into VGAM2734 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of VGAM2734 RNA is designated SEQ ID:5445, and is provided hereinbelow with reference to the sequence listing part.

[91430] VGAM2734 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2734 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91431] VGAM2734 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2734 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2734 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91432] The complementary binding of VGAM2734 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2734 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2734 host target RNA into VGAM2734 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91433] It is appreciated that VGAM2734 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2734 host target genes. The mRNA of

each one of this plurality of VGAM2734 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2734 RNA, herein designated VGAM RNA, and which when bound by VGAM2734 RNA causes inhibition of translation of respective one or more VGAM2734 host target proteins.

[91434] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2734 gene, herein designated VGAM GENE, on one or more VGAM2734 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[91435] It is yet further appreciated that a function of VGAM2734 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2734 correlate with, and may be deduced from, the identity of the host target genes which VGAM2734 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91436] Nucleotide sequences of the VGAM2734 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2734 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2734 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2734 are further described hereinbelow with reference to Table 1.

[91437] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2734 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2734 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91438] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2734 gene, herein designated VGAM is inhibition of expression of VGAM2734 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2734 correlate with, and may be deduced from, the identity of the target genes which VGAM2734 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91439] UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 1 (B4GALT1, Accession NM_001497) is a VGAM2734 host target gene. B4GALT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B4GALT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B4GALT1 BINDING SITE, designated SEQ ID:7243, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91440] A function of VGAM2734 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypep-

tide 1 (B4GALT1, Accession NM_001497). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT1. Corticotropin Releasing Hormone Receptor 1 (CRHR1, Accession NM_004382) is another VGAM2734 host target gene. CRHR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRHR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRHR1 BINDING SITE, designated SEQ ID:10605, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91441] Another function of VGAM2734 is therefore inhibition of Corticotropin Releasing Hormone Receptor 1 (CRHR1, Accession NM_004382), a gene which likely mediates physiological and behavioral response to stress. Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRHR1. The function of CRHR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM435.Von Hippel-Lindau Syndrome (VHL, Accession NM_000551) is another VGAM2734 host target gene. VHL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VHL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VHL BINDING SITE, designated SEQ ID:6155, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91442] Another function of VGAM2734 is therefore inhibition of Von Hippel-Lindau Syndrome (VHL, Accession NM_000551), a gene which may control rna stability through the selective degradation of rna-bound proteins. Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VHL. The function of VHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM197.Cyclin-dependent Kinase-like 2 (CDC2-related kinase) (CDKL2, Accession NM_003948) is another VGAM2734 host target gene. CDKL2 BINDING SITE is HOST TARGET binding site found

in the 5` untranslated region of mRNA encoded by CDKL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDKL2 BINDING SITE, designated SEQ ID:10069, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91443] Another function of VGAM2734 is therefore inhibition of Cyclin-dependent Kinase-like 2 (CDC2-related kinase) (CDKL2, Accession NM_003948). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKL2. FLJ11117 (Accession NM_018329) is another VGAM2734 host target gene. FLJ11117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11117 BINDING SITE, designated SEQ ID:20325, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91444] Another function of VGAM2734 is therefore inhibition of FLJ11117 (Accession NM_018329). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11117. FLJ12649 (Accession NM_024597) is another VGAM2734 host target gene. FLJ12649 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12649 BINDING SITE, designated SEQ ID:23832, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91445] Another function of VGAM2734 is therefore inhibition of FLJ12649 (Accession NM_024597). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12649. FLJ13081 (Accession NM_024834) is another VGAM2734 host target gene. FLJ13081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13081 BINDING SITE, designated SEQ ID:24236, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91446] Another function of VGAM2734 is therefore inhibition of FLJ13081 (Accession NM_024834). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13081. FLJ22794 (Accession XM_166220) is another VGAM2734 host target gene. FLJ22794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:44021, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91447] Another function of VGAM2734 is therefore inhibition of FLJ22794 (Accession XM_166220). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ22794. KIAA0084 (Accession XM_042841) is another VGAM2734 host target gene. KIAA0084 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0084, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0084 BINDING SITE, designated SEQ ID:33803, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91448] Another function of VGAM2734 is therefore inhibition of KIAA0084 (Accession XM_042841). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0084. LOC155179 (Accession XM_088169) is another VGAM2734 host target gene. LOC155179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155179 BINDING SITE, designated SEQ ID:39550, to the nucleotide sequence of VGAM2734 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5445.

[91449] Another function of VGAM2734 is therefore inhibition of LOC155179 (Accession XM_088169). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155179. LOC90092 (Accession XM_028862) is another VGAM2734 host target gene. LOC90092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90092 BINDING SITE, designated SEQ ID:30780, to the nucleotide sequence of VGAM2734 RNA, herein designated VGAM RNA, also designated SEQ ID:5445.

[91450] Another function of VGAM2734 is therefore inhibition of LOC90092 (Accession XM_028862). Accordingly, utilities of VGAM2734 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90092. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2735 (VGAM2735) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91451] VGAM2735 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2735 was detected is described hereinabove with reference to Figs. 1-8.

[91452] VGAM2735 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad Bean Necrosis Virus. VGAM2735 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91453] VGAM2735 gene encodes a VGAM2735 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2735 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2735 precursor RNA is designated SEQ ID:2721, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2721 is located at position 2997 relative to the genome of Broad Bean Necrosis Virus.

[91454] VGAM2735 precursor RNA folds onto itself, forming

VGAM2735 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91455] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2735 folded precursor RNA into VGAM2735 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2735 RNA is designated SEQ ID:5446, and is provided hereinbelow with reference to the sequence listing part.

[91456] VGAM2735 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2735 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91457] VGAM2735 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2735 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2735 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91458] The complementary binding of VGAM2735 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2735 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2735 host target RNA into VGAM2735 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91459] It is appreciated that VGAM2735 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2735 host target genes. The mRNA of each one of this plurality of VGAM2735 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2735 RNA, herein designated VGAM RNA, and which when bound by VGAM2735 RNA causes inhibition of translation of respective one or more VGAM2735 host target proteins.

[91460] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2735 gene, herein designated VGAM GENE, on one or more VGAM2735 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91461] It is yet further appreciated that a function of VGAM2735 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2735 include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2735 correlate with, and may be deduced from, the identity of the host target genes which VGAM2735 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[91462] Nucleotide sequences of the VGAM2735 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2735 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2735 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2735 are further described hereinbelow with reference to Table 1.

[91463] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2735 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2735 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91464] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2735 gene, herein designated VGAM is inhibition of expression of VGAM2735 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2735 correlate with, and may be deduced from, the identity of the target genes which VGAM2735 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[91465] Prodynorphin (PDYN, Accession NM_024411) is a VGAM2735 host target gene. PDYN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDYN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDYN BINDING SITE, designated SEQ ID:23654, to the nucleotide sequence of VGAM2735 RNA, herein designated VGAM RNA, also designated SEQ ID:5446.

[91466] A function of VGAM2735 is therefore inhibition of Prodynorphin (PDYN, Accession NM_024411), a gene which is an opioid peptide acting on the kappa-receptor . Accordingly, utilities of VGAM2735 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDYN. The function of PDYN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM444.BHC80 (Accession NM_016621) is another VGAM2735 host target gene. BHC80 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

BHC80, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BHC80 BINDING SITE, designated SEQ ID:18730, to the nucleotide sequence of VGAM2735 RNA, herein designated VGAM RNA, also designated SEQ ID:5446.

[91467] Another function of VGAM2735 is therefore inhibition of BHC80 (Accession NM_016621). Accordingly, utilities of VGAM2735 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHC80. Chromosome 20 Open Reading Frame 50 (C20orf50, Accession XM_046437) is another VGAM2735 host target gene. C20orf50 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf50, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf50 BINDING SITE, designated SEQ ID:34719, to the nucleotide sequence of VGAM2735 RNA, herein designated VGAM RNA, also designated SEQ ID:5446.

[91468] Another function of VGAM2735 is therefore inhibition of

Chromosome 20 Open Reading Frame 50 (C20orf50, Accession XM_046437). Accordingly, utilities of VGAM2735 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf50. LOC151760 (Accession XM_098117) is another VGAM2735 host target gene. LOC151760 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151760, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151760 BINDING SITE, designated SEQ ID:41389, to the nucleotide sequence of VGAM2735 RNA, herein designated VGAM RNA, also designated SEQ ID:5446.

[91469] Another function of VGAM2735 is therefore inhibition of LOC151760 (Accession XM_098117). Accordingly, utilities of VGAM2735 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151760. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2736 (VGAM2736) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[91470] VGAM2736 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2736 was detected is described hereinabove with reference to Figs. 1-8.

[91471] VGAM2736 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad Bean Necrosis Virus. VGAM2736 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91472] VGAM2736 gene encodes a VGAM2736 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2736 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2736 precursor RNA is designated SEQ ID:2722, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2722 is located at position 2155 relative to the genome of Broad Bean Necrosis Virus.

[91473] VGAM2736 precursor RNA folds onto itself, forming VGAM2736 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91474] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2736 folded precursor RNA into VGAM2736 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2736 RNA is designated SEQ ID:5447, and is provided hereinbelow with reference to the sequence listing part.

[91475] VGAM2736 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2736 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91476] VGAM2736 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2736 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2736 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91477] The complementary binding of VGAM2736 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2736 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2736 host target RNA into VGAM2736 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91478] It is appreciated that VGAM2736 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2736 host target genes. The mRNA of each one of this plurality of VGAM2736 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2736 RNA, herein designated VGAM RNA, and which when bound by VGAM2736 RNA causes inhibition of translation of respective one or more VGAM2736 host target proteins.

[91479] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2736 gene, herein designated VGAM GENE, on one or more VGAM2736 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91480] It is yet further appreciated that a function of VGAM2736 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2736 include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2736 correlate with, and may be deduced from, the identity of the host target genes which VGAM2736 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[91481] Nucleotide sequences of the VGAM2736 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2736 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2736 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2736 are further described hereinbelow with reference to Table 1.

[91482] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2736 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2736 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91483] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2736 gene, herein designated VGAM is inhibition of expression of VGAM2736 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2736 correlate with, and may be deduced from, the identity of the target genes which VGAM2736 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91484] TEM8 (Accession NM_032208) is a VGAM2736 host target gene. TEM8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEM8 BINDING SITE, designated SEQ ID:25919, to the nucleotide sequence of VGAM2736 RNA, herein designated VGAM RNA, also designated SEQ ID:5447.

[91485] A function of VGAM2736 is therefore inhibition of TEM8 (Accession NM_032208), a gene which is a tumor-specific endothelial marker. Accordingly, utilities of VGAM2736 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEM8. The function of TEM8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1489.FLJ13612 (Accession NM_025202) is another VGAM2736 host target gene. FLJ13612 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13612, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ13612 BINDING SITE, designated SEQ ID:24860, to the nucleotide sequence of VGAM2736 RNA, herein designated VGAM RNA, also designated SEQ ID:5447.

[91486] Another function of VGAM2736 is therefore inhibition of FLJ13612 (Accession NM_025202). Accordingly, utilities of VGAM2736 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13612. KIAA0534 (Accession XM_049349) is another VGAM2736 host target gene. KIAA0534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0534 BINDING SITE, designated SEQ ID:35386, to the nucleotide sequence of VGAM2736 RNA, herein designated VGAM RNA, also designated SEQ ID:5447.

[91487] Another function of VGAM2736 is therefore inhibition of KIAA0534 (Accession XM_049349). Accordingly, utilities of VGAM2736 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0534. PRO2214 (Accession NM_018517) is another

VGAM2736 host target gene. PRO2214 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2214, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2214 BINDING SITE, designated SEQ ID:20589, to the nucleotide sequence of VGAM2736 RNA, herein designated VGAM RNA, also designated SEQ ID:5447.

[91488] Another function of VGAM2736 is therefore inhibition of PRO2214 (Accession NM_018517). Accordingly, utilities of VGAM2736 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2214. LOC149721 (Accession XM_086649) is another VGAM2736 host target gene. LOC149721 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149721 BINDING SITE, designated SEQ ID:38813, to the nucleotide sequence of VGAM2736 RNA, herein designated VGAM RNA, also designated SEQ ID:5447.

[91489] Another function of VGAM2736 is therefore inhibition of LOC149721 (Accession XM_086649). Accordingly, utilities of VGAM2736 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149721. LOC153883 (Accession XM_087798) is another VGAM2736 host target gene. LOC153883 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153883, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153883 BINDING SITE, designated SEQ ID:39430, to the nucleotide sequence of VGAM2736 RNA, herein designated VGAM RNA, also designated SEQ ID:5447.

[91490] Another function of VGAM2736 is therefore inhibition of LOC153883 (Accession XM_087798). Accordingly, utilities of VGAM2736 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153883. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2737 (VGAM2737) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[91491] VGAM2737 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2737 was detected is described hereinabove with reference to Figs. 1-8.

[91492] VGAM2737 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad Bean Necrosis Virus. VGAM2737 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91493] VGAM2737 gene encodes a VGAM2737 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2737 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2737 precursor RNA is designated SEQ ID:2723, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2723 is located at position 4765 relative to the genome of Broad Bean Necrosis Virus.

[91494] VGAM2737 precursor RNA folds onto itself, forming VGAM2737 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91495] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2737 folded precursor RNA into VGAM2737 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2737 RNA is designated SEQ ID:5448, and is provided hereinbelow with reference to the sequence listing part.

[91496] VGAM2737 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2737 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91497] VGAM2737 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2737 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2737 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91498] The complementary binding of VGAM2737 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2737 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2737 host target RNA into VGAM2737 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91499] It is appreciated that VGAM2737 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2737 host target genes. The mRNA of each one of this plurality of VGAM2737 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2737 RNA, herein designated VGAM RNA, and which when bound by VGAM2737 RNA causes inhibition of translation of respective one or more VGAM2737 host target proteins.

[91500] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2737 gene, herein designated VGAM GENE, on one or more VGAM2737 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91501] It is yet further appreciated that a function of VGAM2737 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2737 include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2737 correlate with, and may be deduced from, the identity of the host target genes which VGAM2737 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[91502] Nucleotide sequences of the VGAM2737 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2737 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2737 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2737 are further described hereinbelow with reference to Table 1.

[91503] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2737 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2737 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91504] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2737 gene, herein designated VGAM is inhibition of expression of VGAM2737 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2737 correlate with, and may be deduced from, the identity of the target genes which VGAM2737 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91505] RIG (Accession NM_006394) is a VGAM2737 host target gene. RIG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RIG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RIG BINDING SITE, designated SEQ ID:13107, to the nucleotide sequence of VGAM2737 RNA, herein designated VGAM RNA, also designated SEQ ID:5448.

[91506] A function of VGAM2737 is therefore inhibition of RIG (Accession NM_006394), a gene which is ribosomal protein S15. Accordingly, utilities of VGAM2737 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIG. The function of RIG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.LOC85479 (Accession NM_033105) is another VGAM2737 host target gene. LOC85479 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC85479, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC85479 BINDING SITE, designated SEQ ID:26957, to the nucleotide sequence of VGAM2737 RNA, herein designated VGAM RNA, also designated SEQ ID:5448.

[91507] Another function of VGAM2737 is therefore inhibition of LOC85479 (Accession NM_033105). Accordingly, utilities of VGAM2737 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC85479. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2738 (VGAM2738) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91508] VGAM2738 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2738 was detected is described hereinabove with reference to Figs. 1-8.

[91509] VGAM2738 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad Bean Necrosis Virus. VGAM2738 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[91510] VGAM2738 gene encodes a VGAM2738 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2738 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2738 precursor RNA is designated SEQ ID:2724, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2724 is located at position 4423 relative to the genome of Broad Bean Necrosis Virus.

[91511] VGAM2738 precursor RNA folds onto itself, forming VGAM2738 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91512] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2738 folded precursor RNA into VGAM2738 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2738 RNA is designated SEQ ID:5449, and is provided hereinbelow with reference to the sequence listing part.

[91513] VGAM2738 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2738 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91514] VGAM2738 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2738 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2738 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91515] The complementary binding of VGAM2738 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2738 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2738 host target RNA into VGAM2738 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91516] It is appreciated that VGAM2738 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2738 host target genes. The mRNA of each one of this plurality of VGAM2738 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2738 RNA, herein designated VGAM RNA, and which when bound by VGAM2738 RNA causes inhibition of translation of respective one or more VGAM2738 host target proteins.

[91517] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2738 gene, herein designated VGAM GENE, on one or more VGAM2738 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91518] It is yet further appreciated that a function of VGAM2738 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2738 include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2738 correlate with, and may be deduced from, the identity of the host target genes which VGAM2738 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91519] Nucleotide sequences of the VGAM2738 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2738 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2738 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2738 are further described hereinbelow with reference to Table 1.

[91520] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2738 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2738 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91521] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2738 gene, herein designated VGAM is inhibition of expression of VGAM2738 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2738 correlate with, and may be deduced from, the identity of the target genes which VGAM2738 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91522] SMT3 Suppressor of Mif Two 3 Homolog 1 (yeast) (SMT3H1, Accession XM_009805) is a VGAM2738 host target gene. SMT3H1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMT3H1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMT3H1 BINDING SITE, designated SEQ ID:30127, to the nucleotide sequence of VGAM2738 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5449.

[91523] A function of VGAM2738 is therefore inhibition of SMT3 Suppressor of Mif Two 3 Homolog 1 (yeast) (SMT3H1, Accession XM_009805), a gene which is involved in the function and/or structure of the eukaryotic kinetochore. Accordingly, utilities of VGAM2738 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMT3H1. The function of SMT3H1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM119.FLJ23071 (Accession NM_025192) is another VGAM2738 host target gene. FLJ23071 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23071, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23071 BINDING SITE, designated SEQ ID:24844, to the nucleotide sequence of VGAM2738 RNA, herein designated VGAM RNA, also designated SEQ ID:5449.

[91524] Another function of VGAM2738 is therefore inhibition of FLJ23071 (Accession NM_025192). Accordingly, utilities of

VGAM2738 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23071. KIAA0332 (Accession XM_031553) is another VGAM2738 host target gene. KIAA0332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0332 BINDING SITE, designated SEQ ID:31423, to the nucleotide sequence of VGAM2738 RNA, herein designated VGAM RNA, also designated SEQ ID:5449.

[91525] Another function of VGAM2738 is therefore inhibition of KIAA0332 (Accession XM_031553). Accordingly, utilities of VGAM2738 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0332. PRSC (Accession NM_006587) is another VGAM2738 host target gene. PRSC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRSC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRSC BINDING SITE,

designated SEQ ID:13350, to the nucleotide sequence of VGAM2738 RNA, herein designated VGAM RNA, also designated SEQ ID:5449.

[91526] Another function of VGAM2738 is therefore inhibition of PRSC (Accession NM_006587). Accordingly, utilities of VGAM2738 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRSC. LOC256158 (Accession XM_175125) is another VGAM2738 host target gene. LOC256158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256158 BINDING SITE, designated SEQ ID:46631, to the nucleotide sequence of VGAM2738 RNA, herein designated VGAM RNA, also designated SEQ ID:5449.

[91527] Another function of VGAM2738 is therefore inhibition of LOC256158 (Accession XM_175125). Accordingly, utilities of VGAM2738 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256158. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2739 (VGAM2739) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[91528] VGAM2739 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2739 was detected is described hereinabove with reference to Figs. 1-8.

[91529] VGAM2739 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Broad Bean Necrosis Virus. VGAM2739 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[91530] VGAM2739 gene encodes a VGAM2739 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2739 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2739 precursor RNA is designated SEQ ID:2725, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2725 is located at position 2143 relative to the

genome of Broad Bean Necrosis Virus.

[91531] VGAM2739 precursor RNA folds onto itself, forming VGAM2739 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[91532] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2739 folded precursor RNA into VGAM2739 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2739 RNA is designated SEQ ID:5450, and is provided hereinbelow with reference to the sequence listing part.

[91533] VGAM2739 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2739 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[91534] VGAM2739 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2739 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2739 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[91535] The complementary binding of VGAM2739 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2739 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2739 host target RNA into VGAM2739 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[91536] It is appreciated that VGAM2739 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2739 host target genes. The mRNA of each one of this plurality of VGAM2739 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2739 RNA, herein designated VGAM RNA, and which when bound by VGAM2739 RNA causes inhibition of translation of respective one or more VGAM2739 host target proteins.

[91537] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2739 gene, herein designated VGAM GENE, on one or more VGAM2739 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[91538] It is yet further appreciated that a function of VGAM2739 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2739 include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2739

correlate with, and may be deduced from, the identity of the host target genes which VGAM2739 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[91539] Nucleotide sequences of the VGAM2739 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2739 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2739 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2739 are further described hereinbelow with reference to Table 1.

[91540] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2739 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2739 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[91541] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2739 gene, herein designated VGAM is inhibition of expression of VGAM2739 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2739 correlate with, and may be deduced

from, the identity of the target genes which VGAM2739 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[91542] TEM8 (Accession NM_032208) is a VGAM2739 host target gene. TEM8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEM8 BINDING SITE, designated SEQ ID:25919, to the nucleotide sequence of VGAM2739 RNA, herein designated VGAM RNA, also designated SEQ ID:5450.

[91543] A function of VGAM2739 is therefore inhibition of TEM8 (Accession NM_032208), a gene which is a tumor-specific endothelial marker. Accordingly, utilities of VGAM2739 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEM8. The function of TEM8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1489.FLJ13612 (Accession NM_025202) is another VGAM2739 host target gene. FLJ13612 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ13612, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13612 BINDING SITE, designated SEQ ID:24860, to the nucleotide sequence of VGAM2739 RNA, herein designated VGAM RNA, also designated SEQ ID:5450.

[91544] Another function of VGAM2739 is therefore inhibition of FLJ13612 (Accession NM_025202). Accordingly, utilities of VGAM2739 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13612. KIAA0534 (Accession XM_049349) is another VGAM2739 host target gene. KIAA0534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0534 BINDING SITE, designated SEQ ID:35386, to the nucleotide sequence of VGAM2739 RNA, herein designated VGAM RNA, also designated SEQ ID:5450.

[91545] Another function of VGAM2739 is therefore inhibition of KIAA0534 (Accession XM_049349). Accordingly, utilities

of VGAM2739 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0534. PRO2214 (Accession NM_018517) is another VGAM2739 host target gene. PRO2214 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2214, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2214 BINDING SITE, designated SEQ ID:20589, to the nucleotide sequence of VGAM2739 RNA, herein designated VGAM RNA, also designated SEQ ID:5450.

[91546] Another function of VGAM2739 is therefore inhibition of PRO2214 (Accession NM_018517). Accordingly, utilities of VGAM2739 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2214. LOC149721 (Accession XM_086649) is another VGAM2739 host target gene. LOC149721 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC149721 BINDING SITE, designated SEQ ID:38813, to the nucleotide sequence of VGAM2739 RNA, herein designated VGAM RNA, also designated SEQ ID:5450.

[91547] Another function of VGAM2739 is therefore inhibition of LOC149721 (Accession XM_086649). Accordingly, utilities of VGAM2739 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149721. LOC153883 (Accession XM_087798) is another VGAM2739 host target gene. LOC153883 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153883, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153883 BINDING SITE, designated SEQ ID:39430, to the nucleotide sequence of VGAM2739 RNA, herein designated VGAM RNA, also designated SEQ ID:5450.

[91548] Another function of VGAM2739 is therefore inhibition of LOC153883 (Accession XM_087798). Accordingly, utilities of VGAM2739 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153883. Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral

gene, referred to here as Viral Genomic Record 2740(VGR2740) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91549] VGR2740 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2740 gene was detected is described hereinabove with reference to Figs. 1-9.

[91550] VGR2740 gene encodes VGR2740 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91551] VGR2740 precursor RNA folds spatially, forming VGR2740 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2740 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2740 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[91552] VGR2740 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM15 precursor RNA and VGAM16 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91553] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM15 RNA and VGAM16 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91554] VGAM15 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM15 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM15 host target RNA into VGAM15 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91555] VGAM16 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM16 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM16 host target RNA into VGAM16 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91556] It is appreciated that a function of VGR2740 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2740 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 7. Specific functions, and accordingly

utilities, of VGR2740 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2740 gene: VGAM15 host target protein and VGAM16 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM15 and VGAM16.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2741(VGR2741) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91557] VGR2741 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2741 gene was detected is described hereinabove with reference to Figs. 1-9.

[91558] VGR2741 gene encodes VGR2741 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[91559] VGR2741 precursor RNA folds spatially, forming VGR2741 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2741 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2741 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91560] VGR2741 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM18 precursor RNA, VGAM19 precursor RNA, VGAM20 precursor RNA, VGAM21 precursor RNA, VGAM22 precursor RNA, VGAM23 precursor RNA, VGAM24 precursor RNA and VGAM25 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91561] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM18 RNA, VGAM19 RNA, VGAM20 RNA, VGAM21 RNA, VGAM22 RNA, VGAM23 RNA, VGAM24 RNA and VGAM25 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91562] VGAM18 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM18 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM18 host target RNA into VGAM18 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91563] VGAM19 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM19 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM19 host target RNA into VGAM19 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91564] VGAM20 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM20 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM20 host target RNA into VGAM20 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91565] VGAM21 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM21 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM21 host target RNA into VGAM21 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91566] VGAM22 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM22 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM22 host target RNA into VGAM22 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91567] VGAM23 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM23 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM23 host target RNA into VGAM23 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91568] VGAM24 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM24 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM24 host target RNA into VGAM24 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91569] VGAM25 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM25 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM25 host target RNA into VGAM25 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91570] It is appreciated that a function of VGR2741 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2741 gene include diagnosis, prevention and treatment of viral infection by Invertebrate Iridescent Virus 6. Specific functions, and accordingly utilities, of VGR2741 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2741 gene: VGAM18 host target protein, VGAM19 host target protein, VGAM20 host

target protein, VGAM21 host target protein, VGAM22 host target protein, VGAM23 host target protein, VGAM24 host target protein and VGAM25 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM18, VGAM19, VGAM20, VGAM21, VGAM22, VGAM23, VGAM24 and VGAM25.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2742(VGR2742) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91571] VGR2742 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2742 gene was detected is described hereinabove with reference to Figs. 1-9.

[91572] VGR2742 gene encodes VGR2742 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91573] VGR2742 precursor RNA folds spatially, forming VGR2742 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2742 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2742 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91574] VGR2742 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM26 precursor RNA, VGAM27 precursor RNA, VGAM28 precursor RNA, VGAM29 precursor RNA, VGAM30 precursor RNA, VGAM31 precursor RNA, VGAM32 precursor RNA and VGAM33 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91575] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM26 RNA, VGAM27 RNA, VGAM28 RNA, VGAM29 RNA, VGAM30 RNA, VGAM31 RNA, VGAM32 RNA and VGAM33 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91576] VGAM26 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM26 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM26 host target RNA into VGAM26 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91577] VGAM27 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM27 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM27 host target RNA into VGAM27 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91578] VGAM28 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM28 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM28 host target RNA into VGAM28 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91579] VGAM29 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM29 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM29 host target RNA into VGAM29 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91580] VGAM30 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM30 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM30 host target RNA into VGAM30 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91581] VGAM31 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM31 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM31 host target RNA into VGAM31 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91582] VGAM32 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM32 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM32 host target RNA into VGAM32 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91583] VGAM33 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM33 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM33 host target RNA into VGAM33 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91584] It is appreciated that a function of VGR2742 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2742 gene include diagnosis, prevention and treatment of viral infection by Invertebrate Iridescent Virus 6. Specific functions, and accordingly utilities, of VGR2742 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2742 gene: VGAM26 host target protein, VGAM27 host target protein, VGAM28 host target protein, VGAM29 host target protein, VGAM30 host

target protein, VGAM31 host target protein, VGAM32 host target protein and VGAM33 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM26, VGAM27, VGAM28, VGAM29, VGAM30, VGAM31, VGAM32 and VGAM33.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2743(VGR2743) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91585] VGR2743 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2743 gene was detected is described hereinabove with reference to Figs. 1-9.

[91586] VGR2743 gene encodes VGR2743 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91587] VGR2743 precursor RNA folds spatially, forming VGR2743

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2743 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2743 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91588] VGR2743 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM34 precursor RNA, VGAM35 precursor RNA, VGAM36 precursor RNA, VGAM37 precursor RNA, VGAM38 precursor RNA, VGAM39 precursor RNA, VGAM40 precursor RNA and VGAM41 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91589] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM34 RNA, VGAM35 RNA, VGAM36 RNA, VGAM37 RNA, VGAM38 RNA, VGAM39 RNA, VGAM40 RNA and VGAM41 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91590] VGAM34 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM34 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM34 host target RNA into VGAM34 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91591] VGAM35 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM35 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM35 host target RNA into VGAM35 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91592] VGAM36 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM36 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM36 host target RNA into VGAM36 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91593] VGAM37 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM37 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM37 host target RNA into VGAM37 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91594] VGAM38 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM38 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM38 host target RNA into VGAM38 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91595] VGAM39 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM39 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM39 host target RNA into VGAM39 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91596] VGAM40 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM40 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM40 host target RNA into VGAM40 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91597] VGAM41 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM41 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM41 host target RNA into VGAM41 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91598] It is appreciated that a function of VGR2743 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2743 gene include diagnosis, prevention and treatment of viral infection by Invertebrate Iridescent Virus 6. Specific functions, and accordingly utilities, of VGR2743 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2743 gene: VGAM34 host target protein, VGAM35 host target protein, VGAM36 host target protein, VGAM37 host target protein, VGAM38 host target protein, VGAM39 host target protein, VGAM40 host

target protein and VGAM41 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM34, VGAM35, VGAM36, VGAM37, VGAM38, VGAM39, VGAM40 and VGAM41.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2744(VGR2744) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91599] VGR2744 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2744 gene was detected is described hereinabove with reference to Figs. 1-9.

[91600] VGR2744 gene encodes VGR2744 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91601] VGR2744 precursor RNA folds spatially, forming VGR2744 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2744 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2744 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91602] VGR2744 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM42 precursor RNA, VGAM43 precursor RNA, VGAM44 precursor RNA, VGAM45 precursor RNA, VGAM46 precursor RNA, VGAM47 precursor RNA, VGAM48 precursor RNA and VGAM49 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91603] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM42

RNA, VGAM43 RNA, VGAM44 RNA, VGAM45 RNA, VGAM46 RNA, VGAM47 RNA, VGAM48 RNA and VGAM49 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91604] VGAM42 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM42 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM42 host target RNA into VGAM42 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91605] VGAM43 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM43 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM43 host target RNA into VGAM43 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91606] VGAM44 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM44 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM44 host target RNA into VGAM44 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91607] VGAM45 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM45 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM45 host target RNA into VGAM45 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91608] VGAM46 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM46 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM46 host target RNA into VGAM46 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91609] VGAM47 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM47 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM47 host target RNA into VGAM47 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91610] VGAM48 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM48 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM48 host target RNA into VGAM48 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91611] VGAM49 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM49 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM49 host target RNA into VGAM49 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91612] It is appreciated that a function of VGR2744 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2744 gene include diagnosis, prevention and treatment of viral infection by Invertebrate Iridescent Virus 6. Specific functions, and accordingly utilities, of VGR2744 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2744 gene: VGAM42 host target protein, VGAM43 host target protein, VGAM44 host target protein, VGAM45 host target protein, VGAM46 host target protein, VGAM47 host target protein, VGAM48 host target protein and VGAM49 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM42, VGAM43, VGAM44, VGAM45, VGAM46, VGAM47, VGAM48 and VGAM49.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2745(VGR2745) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91613] VGR2745 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2745 gene was detected is described hereinabove with reference to Figs. 1-9.

[91614] VGR2745 gene encodes VGR2745 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91615] VGR2745 precursor RNA folds spatially, forming VGR2745 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2745 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2745 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91616] VGR2745 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM50 precursor RNA, VGAM51 precursor RNA, VGAM52 precursor RNA, VGAM53 precursor RNA, VGAM54 precursor RNA, VGAM55 precursor RNA, VGAM56 precursor RNA and VGAM57 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91617] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM50 RNA, VGAM51 RNA, VGAM52 RNA, VGAM53 RNA, VGAM54

RNA, VGAM55 RNA, VGAM56 RNA and VGAM57 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91618] VGAM50 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM50 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM50 host target RNA into VGAM50 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91619] VGAM51 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM51 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM51 host target RNA into VGAM51 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91620] VGAM52 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM52 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM52 host target RNA into VGAM52 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91621] VGAM53 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM53 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM53 host target RNA into VGAM53 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91622] VGAM54 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM54 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM54 host target RNA into VGAM54 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91623] VGAM55 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM55 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM55 host target RNA into VGAM55 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91624] VGAM56 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM56 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM56 host target RNA into VGAM56 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91625] VGAM57 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM57 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM57 host target RNA into VGAM57 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91626] It is appreciated that a function of VGR2745 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2745 gene include diagnosis, prevention and treatment of viral infection by Invertebrate Iridescent Virus 6. Specific functions, and accordingly utilities, of VGR2745 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2745 gene: VGAM50 host target protein, VGAM51 host target protein, VGAM52 host target protein, VGAM53 host target protein, VGAM54 host target protein, VGAM55 host target protein, VGAM56 host target protein and VGAM57 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM50, VGAM51, VGAM52, VGAM53, VGAM54, VGAM55, VGAM56 and VGAM57.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2746(VGR2746) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91627] VGR2746 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2746 gene was detected is described hereinabove with reference to Figs. 1-9.

[91628] VGR2746 gene encodes VGR2746 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91629] VGR2746 precursor RNA folds spatially, forming VGR2746 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2746 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2746 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91630] VGR2746 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM58 precursor RNA, VGAM59 precursor RNA, VGAM60 precursor RNA, VGAM61 precursor RNA, VGAM62 precursor RNA, VGAM63 precursor RNA, VGAM64 precursor RNA and VGAM65 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91631] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM58 RNA, VGAM59 RNA, VGAM60 RNA, VGAM61 RNA, VGAM62 RNA, VGAM63 RNA, VGAM64 RNA and VGAM65 RNA,

herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91632] VGAM58 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM58 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM58 host target RNA into VGAM58 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91633] VGAM59 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM59 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM59 host target RNA into VGAM59 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91634] VGAM60 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM60 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM60 host target RNA into VGAM60 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91635] VGAM61 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM61 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM61 host target RNA into VGAM61 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91636] VGAM62 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM62 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM62 host target RNA into VGAM62 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91637] VGAM63 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM63 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM63 host target RNA into VGAM63 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91638] VGAM64 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM64 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM64 host target RNA into VGAM64 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91639] VGAM65 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM65 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM65 host target RNA into VGAM65 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91640] It is appreciated that a function of VGR2746 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2746 gene include diagnosis, prevention and treatment of viral infection by Invertebrate Iridescent Virus 6. Specific functions, and accordingly utilities, of VGR2746 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2746 gene: VGAM58 host target protein, VGAM59 host target protein, VGAM60 host target protein, VGAM61 host target protein, VGAM62 host target protein, VGAM63 host target protein, VGAM64 host target protein and VGAM65 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The func-

tion of these host target genes is elaborated hereinabove with reference to VGAM58, VGAM59, VGAM60, VGAM61, VGAM62, VGAM63, VGAM64 and VGAM65.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2747(VGR2747) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91641] VGR2747 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2747 gene was detected is described hereinabove with reference to Figs. 1-9.

[91642] VGR2747 gene encodes VGR2747 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91643] VGR2747 precursor RNA folds spatially, forming VGR2747 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2747 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2747 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91644] VGR2747 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM66 precursor RNA, VGAM67 precursor RNA, VGAM68 precursor RNA, VGAM69 precursor RNA, VGAM70 precursor RNA, VGAM71 precursor RNA, VGAM72 precursor RNA and VGAM73 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91645] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM66 RNA, VGAM67 RNA, VGAM68 RNA, VGAM69 RNA, VGAM70 RNA, VGAM71 RNA, VGAM72 RNA and VGAM73 RNA, herein schematically represented by VGAM1 RNA through

VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91646] VGAM66 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM66 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM66 host target RNA into VGAM66 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91647] VGAM67 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM67 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM67 host target RNA into

VGAM67 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91648] VGAM68 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM68 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM68 host target RNA into VGAM68 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91649] VGAM69 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM69 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM69 host target RNA into VGAM69 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91650] VGAM70 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM70 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM70 host target RNA into VGAM70 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91651] VGAM71 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM71 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM71 host target RNA into VGAM71 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91652] VGAM72 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM72 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM72 host target RNA into VGAM72 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91653] VGAM73 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM73 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM73 host target RNA into VGAM73 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91654] It is appreciated that a function of VGR2747 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2747 gene include diagnosis, prevention and treatment of viral infection by Invertebrate Iridescent Virus 6. Specific functions, and accordingly utilities, of VGR2747 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2747 gene: VGAM66 host target protein, VGAM67 host target protein, VGAM68 host target protein, VGAM69 host target protein, VGAM70 host target protein, VGAM71 host target protein, VGAM72 host target protein and VGAM73 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove

with reference to VGAM66, VGAM67, VGAM68, VGAM69, VGAM70, VGAM71, VGAM72 and VGAM73.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2748(VGR2748) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91655] VGR2748 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2748 gene was detected is described hereinabove with reference to Figs. 1-9.

[91656] VGR2748 gene encodes VGR2748 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91657] VGR2748 precursor RNA folds spatially, forming VGR2748 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2748 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2748 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91658] VGR2748 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM76 precursor RNA and VGAM77 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91659] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM76 RNA and VGAM77 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91660] VGAM76 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM76 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM76 host target RNA into VGAM76 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91661] VGAM77 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM77 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM77 host target RNA into VGAM77 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91662] It is appreciated that a function of VGR2748 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2748 gene include diagnosis, prevention and treatment of viral infection by Murine Adenovirus A. Specific functions, and accordingly utilities, of VGR2748 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2748 gene: VGAM76 host target protein and VGAM77 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM76 and VGAM77.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2749(VGR2749) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91663] VGR2749 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2749 gene was detected is described hereinabove with reference to Figs.

1-9.

[91664] VGR2749 gene encodes VGR2749 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91665] VGR2749 precursor RNA folds spatially, forming VGR2749 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2749 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2749 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91666] VGR2749 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM78 precursor RNA, VGAM79 precursor RNA, VGAM80 precursor RNA, VGAM81 precursor RNA, VGAM82 precursor RNA, VGAM83 precursor RNA, VGAM84 precursor RNA and VGAM85 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91667] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM78 RNA, VGAM79 RNA, VGAM80 RNA, VGAM81 RNA, VGAM82 RNA, VGAM83 RNA, VGAM84 RNA and VGAM85 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91668] VGAM78 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM78 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM78 host target RNA into VGAM78 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91669] VGAM79 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM79 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM79 host target RNA into VGAM79 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91670] VGAM80 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM80 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM80 host target RNA into VGAM80 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91671] VGAM81 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM81 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM81 host target RNA into VGAM81 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91672] VGAM82 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM82 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM82 host target RNA into VGAM82 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91673] VGAM83 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM83 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM83 host target RNA into VGAM83 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91674] VGAM84 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM84 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM84 host target RNA into

VGAM84 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91675] VGAM85 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM85 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM85 host target RNA into VGAM85 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91676] It is appreciated that a function of VGR2749 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2749 gene include diagnosis, prevention and treatment of viral infection by Plutella Xylostella Granulovirus. Specific functions, and accordingly utilities, of VGR2749 gene correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2749 gene: VGAM78 host target protein, VGAM79 host target protein, VGAM80 host target protein, VGAM81 host target protein, VGAM82 host target protein, VGAM83 host target protein, VGAM84 host target protein and VGAM85 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM78, VGAM79, VGAM80, VGAM81, VGAM82, VGAM83, VGAM84 and VGAM85.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2750(VGR2750) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91677] VGR2750 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2750 gene was detected is described hereinabove with reference to Figs. 1-9.

[91678] VGR2750 gene encodes VGR2750 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91679] VGR2750 precursor RNA folds spatially, forming VGR2750 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2750 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2750 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91680] VGR2750 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM86 precursor RNA, VGAM87 precursor RNA, VGAM88 precursor RNA, VGAM89 precursor RNA, VGAM90 precursor RNA, VGAM91 precursor RNA, VGAM92 precursor RNA and VGAM93 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91681] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM86 RNA, VGAM87 RNA, VGAM88 RNA, VGAM89 RNA, VGAM90 RNA, VGAM91 RNA, VGAM92 RNA and VGAM93 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91682] VGAM86 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM86 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM86 host target RNA into VGAM86 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91683] VGAM87 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM87 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM87 host target RNA into VGAM87 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91684] VGAM88 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM88 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM88 host target RNA into VGAM88 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91685] VGAM89 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM89 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM89 host target RNA into VGAM89 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91686] VGAM90 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM90 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM90 host target RNA into VGAM90 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91687] VGAM91 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM91 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM91 host target RNA into VGAM91 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91688] VGAM92 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM92 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM92 host target RNA into VGAM92 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91689] VGAM93 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM93 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM93 host target RNA into VGAM93 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91690] It is appreciated that a function of VGR2750 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2750 gene include diagnosis, prevention and treatment of viral infection by Plutella Xylostella Granulovirus. Specific functions, and accordingly utilities, of VGR2750 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR2750 gene: VGAM86 host target protein, VGAM87 host target protein, VGAM88 host target protein, VGAM89 host target protein, VGAM90 host target protein, VGAM91 host target protein, VGAM92 host target protein and VGAM93 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM86, VGAM87, VGAM88, VGAM89, VGAM90, VGAM91, VGAM92 and VGAM93.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2751(VGR2751) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91691] VGR2751 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2751 gene was detected is described hereinabove with reference to Figs. 1-9.

[91692] VGR2751 gene encodes VGR2751 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91693] VGR2751 precursor RNA folds spatially, forming VGR2751 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2751 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2751 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91694] VGR2751 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM94 precursor RNA, VGAM95 precursor RNA, VGAM96 precursor RNA, VGAM97 precursor RNA, VGAM98 precursor RNA, VGAM99 precursor RNA, VGAM100 precursor RNA and VGAM101 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR

RNA of Fig. 1.

[91695] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM94 RNA, VGAM95 RNA, VGAM96 RNA, VGAM97 RNA, VGAM98 RNA, VGAM99 RNA, VGAM100 RNA and VGAM101 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91696] VGAM94 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM94 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM94 host target RNA into VGAM94 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91697] VGAM95 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM95 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM95 host target RNA into VGAM95 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91698] VGAM96 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM96 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM96 host target RNA into VGAM96 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91699] VGAM97 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM97 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM97 host target RNA into VGAM97 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91700] VGAM98 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM98 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM98 host target RNA into VGAM98 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91701] VGAM99 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM99 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM99 host target RNA into VGAM99 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91702] VGAM100 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM100 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM100 host target RNA into VGAM100 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91703] VGAM101 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM101 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM101 host target RNA into VGAM101 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91704] It is appreciated that a function of VGR2751 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2751 gene include diagnosis, prevention and treatment of viral infection by Plutella Xylostella Granulovirus. Specific functions, and accordingly utilities, of VGR2751 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2751 gene: VGAM94 host

target protein, VGAM95 host target protein, VGAM96 host target protein, VGAM97 host target protein, VGAM98 host target protein, VGAM99 host target protein, VGAM100 host target protein and VGAM101 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM94, VGAM95, VGAM96, VGAM97, VGAM98, VGAM99, VGAM100 and VGAM101.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2752(VGR2752) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91705] VGR2752 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2752 gene was detected is described hereinabove with reference to Figs. 1-9.

[91706] VGR2752 gene encodes VGR2752 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91707] VGR2752 precursor RNA folds spatially, forming VGR2752 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2752 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2752 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91708] VGR2752 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM102 precursor RNA, VGAM103 precursor RNA, VGAM104 precursor RNA and VGAM105 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91709] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM102 RNA, VGAM103 RNA, VGAM104 RNA and VGAM105 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91710] VGAM102 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM102 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM102 host target RNA into VGAM102 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91711] VGAM103 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM103 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM103 host target RNA into VGAM103 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91712] VGAM104 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM104 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM104 host target RNA into VGAM104 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91713] VGAM105 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM105 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM105 host target RNA into VGAM105 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91714] It is appreciated that a function of VGR2752 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2752 gene include diagnosis, prevention and treatment of viral infection by Plutella Xylostella Granulovirus. Specific functions, and accordingly utilities, of VGR2752 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2752 gene: VGAM102 host target protein, VGAM103 host target protein, VGAM104 host target protein and VGAM105 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated

hereinabove with reference to VGAM102, VGAM103, VGAM104 and VGAM105.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2753(VGR2753) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91715] VGR2753 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2753 gene was detected is described hereinabove with reference to Figs. 1-9.

[91716] VGR2753 gene encodes VGR2753 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91717] VGR2753 precursor RNA folds spatially, forming VGR2753 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2753 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2753 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91718] VGR2753 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM106 precursor RNA, VGAM107 precursor RNA, VGAM108 precursor RNA and VGAM109 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91719] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM106 RNA, VGAM107 RNA, VGAM108 RNA and VGAM109 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91720] VGAM106 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM106 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM106 host target RNA into VGAM106 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91721] VGAM107 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM107 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM107 host target RNA into VGAM107 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91722] VGAM108 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM108 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM108 host target RNA into VGAM108 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91723] VGAM109 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM109 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM109 host target RNA into VGAM109 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91724] It is appreciated that a function of VGR2753 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2753 gene include diagnosis, prevention and treatment of viral infection by Saimiriine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2753 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2753 gene: VGAM106 host target protein, VGAM107 host target protein, VGAM108 host target protein and VGAM109 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM106, VGAM107, VGAM108 and VGAM109.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2754(VGR2754) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[91725] VGR2754 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2754 gene was detected is described hereinabove with reference to Figs. 1-9.

[91726] VGR2754 gene encodes VGR2754 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91727] VGR2754 precursor RNA folds spatially, forming VGR2754 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2754 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2754 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91728] VGR2754 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM110 precursor RNA, VGAM111 precursor RNA, VGAM112 precursor RNA, VGAM113 precursor RNA, VGAM114 precursor RNA, VGAM115 precursor RNA, VGAM116 precursor RNA and VGAM117 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91729] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM110 RNA, VGAM111 RNA, VGAM112 RNA, VGAM113 RNA, VGAM114 RNA, VGAM115 RNA, VGAM116 RNA and VGAM117 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91730] VGAM110 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM110 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM110 host target RNA into VGAM110 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91731] VGAM111 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM111 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM111 host target RNA into VGAM111 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91732] VGAM112 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM112 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM112 host target RNA into VGAM112 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91733] VGAM113 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM113 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM113 host target RNA into VGAM113 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91734] VGAM114 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM114 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM114 host target RNA into VGAM114 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91735] VGAM115 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM115 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM115 host target RNA into VGAM115 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91736] VGAM116 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM116 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM116 host target RNA into VGAM116 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91737] VGAM117 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM117 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM117 host target RNA into VGAM117 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91738] It is appreciated that a function of VGR2754 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2754 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2754 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited

by VGAM RNAs comprised in the `operon-like` cluster of VGR2754 gene: VGAM110 host target protein, VGAM111 host target protein, VGAM112 host target protein, VGAM113 host target protein, VGAM114 host target protein, VGAM115 host target protein, VGAM116 host target protein and VGAM117 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM110, VGAM111, VGAM112, VGAM113, VGAM114, VGAM115, VGAM116 and VGAM117.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2755(VGR2755) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91739] VGR2755 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2755 gene was detected is described hereinabove with reference to Figs.

1-9.

[91740] VGR2755 gene encodes VGR2755 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91741] VGR2755 precursor RNA folds spatially, forming VGR2755 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2755 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2755 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91742] VGR2755 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM118 precursor RNA, VGAM119 precursor RNA, VGAM120 precursor RNA, VGAM121 precursor RNA, VGAM122 precursor RNA, VGAM123 precursor RNA, VGAM124 precursor RNA and VGAM125 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of

which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91743] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM118 RNA, VGAM119 RNA, VGAM120 RNA, VGAM121 RNA, VGAM122 RNA, VGAM123 RNA, VGAM124 RNA and VGAM125 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91744] VGAM118 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM118 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM118 host target RNA into VGAM118 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91745] VGAM119 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM119 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM119 host target RNA into VGAM119 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91746] VGAM120 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM120 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM120 host target RNA into VGAM120 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91747] VGAM121 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM121 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM121 host target RNA into VGAM121 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91748] VGAM122 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM122 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM122 host target RNA into VGAM122 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91749] VGAM123 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM123 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM123 host target RNA into VGAM123 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91750] VGAM124 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM124 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM124 host target RNA into

VGAM124 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91751] VGAM125 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM125 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM125 host target RNA into VGAM125 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91752] It is appreciated that a function of VGR2755 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2755 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2755 gene correlate with, and may be deduced from,

the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2755 gene: VGAM118 host target protein, VGAM119 host target protein, VGAM120 host target protein, VGAM121 host target protein, VGAM122 host target protein, VGAM123 host target protein, VGAM124 host target protein and VGAM125 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM118, VGAM119, VGAM120, VGAM121, VGAM122, VGAM123, VGAM124 and VGAM125.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2756(VGR2756) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91753] VGR2756 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2756 gene was

detected is described hereinabove with reference to Figs. 1-9.

[91754] VGR2756 gene encodes VGR2756 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91755] VGR2756 precursor RNA folds spatially, forming VGR2756 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2756 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2756 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91756] VGR2756 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM126 precursor RNA, VGAM127 precursor RNA, VGAM128 precursor RNA, VGAM129 precursor RNA, VGAM130 precursor RNA, VGAM131 precursor RNA, VGAM132 precursor RNA and VGAM133 precursor RNA, herein schematically represented by VGAM1 FOLDED

PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91757] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM126 RNA, VGAM127 RNA, VGAM128 RNA, VGAM129 RNA, VGAM130 RNA, VGAM131 RNA, VGAM132 RNA and VGAM133 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91758] VGAM126 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM126 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM126 host target RNA into VGAM126 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91759] VGAM127 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM127 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM127 host target RNA into VGAM127 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91760] VGAM128 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM128 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM128 host target RNA into VGAM128 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91761] VGAM129 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM129 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM129 host target RNA into VGAM129 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91762] VGAM130 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM130 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM130 host target RNA into

VGAM130 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91763] VGAM131 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM131 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM131 host target RNA into VGAM131 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91764] VGAM132 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM132 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM132 host target RNA into VGAM132 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91765] VGAM133 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM133 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM133 host target RNA into VGAM133 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91766] It is appreciated that a function of VGR2756 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2756 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of

VGR2756 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2756 gene: VGAM126 host target protein, VGAM127 host target protein, VGAM128 host target protein, VGAM129 host target protein, VGAM130 host target protein, VGAM131 host target protein, VGAM132 host target protein and VGAM133 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM126, VGAM127, VGAM128, VGAM129, VGAM130, VGAM131, VGAM132 and VGAM133.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2757(VGR2757) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91767] VGR2757 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2757 gene was detected is described hereinabove with reference to Figs. 1-9.

[91768] VGR2757 gene encodes VGR2757 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91769] VGR2757 precursor RNA folds spatially, forming VGR2757 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2757 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2757 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91770] VGR2757 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM134 precursor RNA, VGAM135 precursor RNA, VGAM136 precursor RNA, VGAM137 precursor RNA, VGAM138 precursor RNA, VGAM139 precursor RNA, VGAM140 precursor RNA and VGAM141 precursor

RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91771] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM134 RNA, VGAM135 RNA, VGAM136 RNA, VGAM137 RNA, VGAM138 RNA, VGAM139 RNA, VGAM140 RNA and VGAM141 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91772] VGAM134 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM134 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM134 host target RNA into VGAM134 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91773] VGAM135 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM135 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM135 host target RNA into VGAM135 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91774] VGAM136 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM136 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM136 host target RNA into

VGAM136 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91775] VGAM137 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM137 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM137 host target RNA into VGAM137 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91776] VGAM138 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM138 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM138 host target RNA into VGAM138 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91777] VGAM139 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM139 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM139 host target RNA into VGAM139 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91778] VGAM140 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM140 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM140 host target RNA into VGAM140 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91779] VGAM141 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM141 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM141 host target RNA into VGAM141 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91780] It is appreciated that a function of VGR2757 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2757 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform

virus). Specific functions, and accordingly utilities, of VGR2757 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2757 gene: VGAM134 host target protein, VGAM135 host target protein, VGAM136 host target protein, VGAM137 host target protein, VGAM138 host target protein, VGAM139 host target protein, VGAM140 host target protein and VGAM141 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM134, VGAM135, VGAM136, VGAM137, VGAM138, VGAM139, VGAM140 and VGAM141.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2758(VGR2758) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91781] VGR2758 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2758 gene was detected is described hereinabove with reference to Figs. 1-9.

[91782] VGR2758 gene encodes VGR2758 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91783] VGR2758 precursor RNA folds spatially, forming VGR2758 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2758 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2758 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91784] VGR2758 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM142 precursor RNA, VGAM143 precursor RNA, VGAM144 precursor RNA, VGAM145 precursor RNA, VGAM146 precursor RNA, VGAM147 precursor

RNA, VGAM148 precursor RNA and VGAM149 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91785] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM142 RNA, VGAM143 RNA, VGAM144 RNA, VGAM145 RNA, VGAM146 RNA, VGAM147 RNA, VGAM148 RNA and VGAM149 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91786] VGAM142 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM142 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM142 host target RNA into

VGAM142 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91787] VGAM143 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM143 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM143 host target RNA into VGAM143 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91788] VGAM144 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM144 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM144 host target RNA into VGAM144 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91789] VGAM145 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM145 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM145 host target RNA into VGAM145 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91790] VGAM146 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM146 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM146 host target RNA into VGAM146 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91791] VGAM147 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM147 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM147 host target RNA into VGAM147 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91792] VGAM148 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM148 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM148 host target RNA into VGAM148 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91793] VGAM149 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM149 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM149 host target RNA into VGAM149 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91794] It is appreciated that a function of VGR2758 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2758 gene include diagnosis, prevention and treatment of viral infection by

Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2758 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2758 gene: VGAM142 host target protein, VGAM143 host target protein, VGAM144 host target protein, VGAM145 host target protein, VGAM146 host target protein, VGAM147 host target protein, VGAM148 host target protein and VGAM149 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM142, VGAM143, VGAM144, VGAM145, VGAM146, VGAM147, VGAM148 and VGAM149.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2759(VGR2759) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91795] VGR2759 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2759 gene was detected is described hereinabove with reference to Figs. 1-9.

[91796] VGR2759 gene encodes VGR2759 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91797] VGR2759 precursor RNA folds spatially, forming VGR2759 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2759 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2759 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91798] VGR2759 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM150 precursor RNA, VGAM151 precursor RNA, VGAM152 precursor RNA, VGAM153 precur-

sor RNA, VGAM154 precursor RNA, VGAM155 precursor RNA, VGAM156 precursor RNA and VGAM157 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91799] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM150 RNA, VGAM151 RNA, VGAM152 RNA, VGAM153 RNA, VGAM154 RNA, VGAM155 RNA, VGAM156 RNA and VGAM157 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91800] VGAM150 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM150 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM150 host target RNA into VGAM150 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91801] VGAM151 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM151 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM151 host target RNA into VGAM151 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91802] VGAM152 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM152 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM152 host target RNA into VGAM152 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91803] VGAM153 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM153 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM153 host target RNA into VGAM153 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91804] VGAM154 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM154 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM154 host target RNA into VGAM154 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91805] VGAM155 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM155 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM155 host target RNA into VGAM155 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91806] VGAM156 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM156 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM156 host target RNA into VGAM156 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91807] VGAM157 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM157 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM157 host target RNA into VGAM157 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91808] It is appreciated that a function of VGR2759 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2759 gene include

diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2759 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2759 gene: VGAM150 host target protein, VGAM151 host target protein, VGAM152 host target protein, VGAM153 host target protein, VGAM154 host target protein, VGAM155 host target protein, VGAM156 host target protein and VGAM157 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM150, VGAM151, VGAM152, VGAM153, VGAM154, VGAM155, VGAM156 and VGAM157.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2760(VGR2760) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene

is known in the art.

[91809] VGR2760 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2760 gene was detected is described hereinabove with reference to Figs. 1-9.

[91810] VGR2760 gene encodes VGR2760 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91811] VGR2760 precursor RNA folds spatially, forming VGR2760 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2760 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2760 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91812] VGR2760 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM158 precursor RNA, VGAM159 pre-

cursor RNA, VGAM160 precursor RNA, VGAM161 precursor RNA, VGAM162 precursor RNA, VGAM163 precursor RNA, VGAM164 precursor RNA and VGAM165 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91813] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM158 RNA, VGAM159 RNA, VGAM160 RNA, VGAM161 RNA, VGAM162 RNA, VGAM163 RNA, VGAM164 RNA and VGAM165 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91814] VGAM158 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM158 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM158 host target RNA into VGAM158 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91815] VGAM159 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM159 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM159 host target RNA into VGAM159 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91816] VGAM160 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM160 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM160 host target RNA into VGAM160 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91817] VGAM161 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM161 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM161 host target RNA into VGAM161 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91818] VGAM162 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM162 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM162 host target RNA into VGAM162 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91819] VGAM163 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM163 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM163 host target RNA into VGAM163 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91820] VGAM164 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM164 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM164 host target RNA into VGAM164 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91821] VGAM165 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM165 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM165 host target RNA into VGAM165 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91822] It is appreciated that a function of VGR2760 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2760 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2760 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2760 gene: VGAM158 host target protein, VGAM159 host target protein, VGAM160 host target protein, VGAM161 host target protein, VGAM162 host target protein, VGAM163 host target protein, VGAM164 host target protein and VGAM165 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM158, VGAM159, VGAM160, VGAM161, VGAM162, VGAM163, VGAM164 and VGAM165.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2761(VGR2761) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the

function and utility of which at least one host target gene is known in the art.

[91823] VGR2761 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2761 gene was detected is described hereinabove with reference to Figs. 1-9.

[91824] VGR2761 gene encodes VGR2761 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91825] VGR2761 precursor RNA folds spatially, forming VGR2761 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2761 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2761 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91826] VGR2761 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM

precursor RNAs, VGAM166 precursor RNA, VGAM167 precursor RNA, VGAM168 precursor RNA, VGAM169 precursor RNA, VGAM170 precursor RNA, VGAM171 precursor RNA, VGAM172 precursor RNA and VGAM173 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91827] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM166 RNA, VGAM167 RNA, VGAM168 RNA, VGAM169 RNA, VGAM170 RNA, VGAM171 RNA, VGAM172 RNA and VGAM173 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91828] VGAM166 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM166 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM166 host target RNA into VGAM166 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91829] VGAM167 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM167 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM167 host target RNA into VGAM167 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91830] VGAM168 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM168 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM168 host target RNA into VGAM168 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91831] VGAM169 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM169 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM169 host target RNA into VGAM169 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91832] VGAM170 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM170 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM170 host target RNA into VGAM170 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91833] VGAM171 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM171 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM171 host target RNA into VGAM171 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91834] VGAM172 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM172 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM172 host target RNA into VGAM172 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91835] VGAM173 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM173 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM173 host target RNA into VGAM173 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91836] It is appreciated that a function of VGR2761 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2761 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2761 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2761 gene: VGAM166 host target protein, VGAM167 host target protein, VGAM168 host target protein, VGAM169 host target protein, VGAM170 host target protein, VGAM171 host target protein, VGAM172 host target protein and VGAM173 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM166, VGAM167, VGAM168, VGAM169, VGAM170, VGAM171, VGAM172 and VGAM173.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2762(VGR2762) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn

modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91837] VGR2762 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2762 gene was detected is described hereinabove with reference to Figs. 1-9.

[91838] VGR2762 gene encodes VGR2762 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91839] VGR2762 precursor RNA folds spatially, forming VGR2762 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2762 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2762 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91840] VGR2762 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM174 precursor RNA, VGAM175 precursor RNA, VGAM176 precursor RNA, VGAM177 precursor RNA, VGAM178 precursor RNA, VGAM179 precursor RNA, VGAM180 precursor RNA and VGAM181 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91841] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM174 RNA, VGAM175 RNA, VGAM176 RNA, VGAM177 RNA, VGAM178 RNA, VGAM179 RNA, VGAM180 RNA and VGAM181 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91842] VGAM174 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM174 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM174 host target RNA into VGAM174 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91843] VGAM175 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM175 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM175 host target RNA into VGAM175 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91844] VGAM176 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM176 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM176 host target RNA into VGAM176 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91845] VGAM177 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM177 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM177 host target RNA into VGAM177 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91846] VGAM178 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM178 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM178 host target RNA into VGAM178 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91847] VGAM179 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM179 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM179 host target RNA into VGAM179 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91848] VGAM180 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM180 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM180 host target RNA into VGAM180 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91849] VGAM181 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM181 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM181 host target RNA into VGAM181 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91850] It is appreciated that a function of VGR2762 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2762 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2762 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2762 gene: VGAM174 host target protein, VGAM175 host target protein, VGAM176 host target protein, VGAM177 host target protein, VGAM178 host target protein, VGAM179 host target protein, VGAM180 host target protein and VGAM181 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM174, VGAM175, VGAM176, VGAM177, VGAM178, VGAM179, VGAM180 and VGAM181.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2763(VGR2763) viral gene, which encodes an `operon-like` cluster of

novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91851] VGR2763 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2763 gene was detected is described hereinabove with reference to Figs. 1-9.

[91852] VGR2763 gene encodes VGR2763 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91853] VGR2763 precursor RNA folds spatially, forming VGR2763 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2763 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2763 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91854] VGR2763 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM182 precursor RNA, VGAM183 precursor RNA, VGAM184 precursor RNA, VGAM185 precursor RNA, VGAM186 precursor RNA, VGAM187 precursor RNA, VGAM188 precursor RNA and VGAM189 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91855] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM182 RNA, VGAM183 RNA, VGAM184 RNA, VGAM185 RNA, VGAM186 RNA, VGAM187 RNA, VGAM188 RNA and VGAM189 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91856] VGAM182 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM182 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM182 host target RNA into VGAM182 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91857] VGAM183 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM183 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM183 host target RNA into VGAM183 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91858] VGAM184 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM184 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM184 host target RNA into VGAM184 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91859] VGAM185 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM185 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM185 host target RNA into VGAM185 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91860] VGAM186 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM186 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM186 host target RNA into VGAM186 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91861] VGAM187 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM187 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM187 host target RNA into VGAM187 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91862] VGAM188 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM188 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM188 host target RNA into VGAM188 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91863] VGAM189 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM189 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM189 host target RNA into VGAM189 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91864] It is appreciated that a function of VGR2763 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2763 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2763 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2763 gene: VGAM182 host target protein, VGAM183 host target protein, VGAM184 host target protein, VGAM185 host target protein, VGAM186 host target protein, VGAM187 host target protein, VGAM188 host target protein and VGAM189 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM182, VGAM183, VGAM184, VGAM185, VGAM186, VGAM187, VGAM188 and VGAM189.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2764(VGR2764)

viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91865] VGR2764 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2764 gene was detected is described hereinabove with reference to Figs. 1-9.

[91866] VGR2764 gene encodes VGR2764 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91867] VGR2764 precursor RNA folds spatially, forming VGR2764 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2764 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2764 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[91868] VGR2764 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM190 precursor RNA, VGAM191 precursor RNA, VGAM192 precursor RNA, VGAM193 precursor RNA, VGAM194 precursor RNA, VGAM195 precursor RNA, VGAM196 precursor RNA and VGAM197 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91869] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM190 RNA, VGAM191 RNA, VGAM192 RNA, VGAM193 RNA, VGAM194 RNA, VGAM195 RNA, VGAM196 RNA and VGAM197 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91870] VGAM190 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM190 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM190 host target RNA into VGAM190 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91871] VGAM191 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM191 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM191 host target RNA into VGAM191 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91872] VGAM192 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM192 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM192 host target RNA into VGAM192 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91873] VGAM193 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM193 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM193 host target RNA into VGAM193 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91874] VGAM194 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM194 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM194 host target RNA into VGAM194 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91875] VGAM195 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM195 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM195 host target RNA into VGAM195 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91876] VGAM196 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM196 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM196 host target RNA into VGAM196 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91877] VGAM197 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM197 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM197 host target RNA into VGAM197 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91878] It is appreciated that a function of VGR2764 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2764 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2764 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2764 gene: VGAM190 host target protein, VGAM191 host target protein, VGAM192 host target protein, VGAM193 host target protein, VGAM194 host target protein, VGAM195 host target protein, VGAM196 host target protein and VGAM197 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM190, VGAM191, VGAM192, VGAM193, VGAM194, VGAM195, VGAM196 and VGAM197.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene,

referred to here as Viral Genomic Record 2765(VGR2765) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91879] VGR2765 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2765 gene was detected is described hereinabove with reference to Figs. 1-9.

[91880] VGR2765 gene encodes VGR2765 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91881] VGR2765 precursor RNA folds spatially, forming VGR2765 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2765 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2765 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[91882] VGR2765 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM198 precursor RNA, VGAM199 precursor RNA, VGAM200 precursor RNA, VGAM201 precursor RNA, VGAM202 precursor RNA, VGAM203 precursor RNA, VGAM204 precursor RNA and VGAM205 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91883] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM198 RNA, VGAM199 RNA, VGAM200 RNA, VGAM201 RNA, VGAM202 RNA, VGAM203 RNA, VGAM204 RNA and VGAM205 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91884] VGAM198 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM198 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM198 host target RNA into VGAM198 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91885] VGAM199 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM199 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM199 host target RNA into VGAM199 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91886] VGAM200 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM200 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM200 host target RNA into VGAM200 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91887] VGAM201 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM201 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM201 host target RNA into VGAM201 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91888] VGAM202 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM202 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM202 host target RNA into VGAM202 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91889] VGAM203 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM203 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM203 host target RNA into VGAM203 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91890] VGAM204 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM204 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM204 host target RNA into VGAM204 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91891] VGAM205 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM205 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM205 host target RNA into VGAM205 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91892] It is appreciated that a function of VGR2765 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2765 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2765 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2765 gene: VGAM198 host target protein, VGAM199 host target protein, VGAM200 host target protein, VGAM201 host target protein, VGAM202 host target protein, VGAM203 host target protein, VGAM204 host target protein and VGAM205 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM198, VGAM199, VGAM200, VGAM201, VGAM202, VGAM203, VGAM204 and VGAM205.Fig. 9 further provides a conceptual description

of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2766(VGR2766) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91893] VGR2766 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2766 gene was detected is described hereinabove with reference to Figs. 1-9.

[91894] VGR2766 gene encodes VGR2766 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91895] VGR2766 precursor RNA folds spatially, forming VGR2766 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2766 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2766 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91896] VGR2766 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM206 precursor RNA, VGAM207 precursor RNA, VGAM208 precursor RNA, VGAM209 precursor RNA and VGAM210 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91897] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM206 RNA, VGAM207 RNA, VGAM208 RNA, VGAM209 RNA and VGAM210 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91898] VGAM206 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM206 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM206 host target RNA into VGAM206 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91899] VGAM207 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM207 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM207 host target RNA into VGAM207 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91900] VGAM208 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM208 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM208 host target RNA into VGAM208 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91901] VGAM209 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM209 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM209 host target RNA into VGAM209 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91902] VGAM210 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM210 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM210 host target RNA into VGAM210 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91903] It is appreciated that a function of VGR2766 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2766 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2766 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2766 gene: VGAM206 host target protein, VGAM207 host target protein, VGAM208 host target protein, VGAM209 host target protein and VGAM210 host target

protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM206, VGAM207, VGAM208, VGAM209 and VGAM210.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2767(VGR2767) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91904] VGR2767 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2767 gene was detected is described hereinabove with reference to Figs. 1-9.

[91905] VGR2767 gene encodes VGR2767 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91906] VGR2767 precursor RNA folds spatially, forming VGR2767 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2767 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2767 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91907] VGR2767 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM211 precursor RNA, VGAM212 precursor RNA and VGAM213 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91908] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM211 RNA, VGAM212 RNA and VGAM213 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 1.

[91909] VGAM211 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM211 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM211 host target RNA into VGAM211 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91910] VGAM212 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM212 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM212 host target RNA into VGAM212 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91911] VGAM213 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM213 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM213 host target RNA into VGAM213 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91912] It is appreciated that a function of VGR2767 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2767 gene include diagnosis, prevention and treatment of viral infection by Simian Virus 40. Specific functions, and accordingly utilities, of VGR2767 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR2767 gene: VGAM211 host target protein, VGAM212 host target protein and VGAM213 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM211, VGAM212 and VGAM213.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2768(VGR2768) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91913] VGR2768 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2768 gene was detected is described hereinabove with reference to Figs. 1-9.

[91914] VGR2768 gene encodes VGR2768 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91915] VGR2768 precursor RNA folds spatially, forming VGR2768

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2768 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2768 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91916] VGR2768 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM214 precursor RNA and VGAM215 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91917] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM214 RNA and VGAM215 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[91918] VGAM214 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM214 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM214 host target RNA into VGAM214 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91919] VGAM215 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM215 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM215 host target RNA into VGAM215 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91920] It is appreciated that a function of VGR2768 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2768 gene include diagnosis, prevention and treatment of viral infection by Autographa Californica Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2768 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2768 gene: VGAM214 host target protein and VGAM215 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM214 and VGAM215.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2769(VGR2769) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the

function and utility of which at least one host target gene is known in the art.

[91921] VGR2769 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2769 gene was detected is described hereinabove with reference to Figs. 1-9.

[91922] VGR2769 gene encodes VGR2769 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91923] VGR2769 precursor RNA folds spatially, forming VGR2769 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2769 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2769 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91924] VGR2769 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM216 precursor RNA and VGAM217 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91925] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM216 RNA and VGAM217 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91926] VGAM216 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM216 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM216 host target RNA into VGAM216 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[91927] VGAM217 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM217 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM217 host target RNA into VGAM217 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91928] It is appreciated that a function of VGR2769 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2769 gene include diagnosis, prevention and treatment of viral infection by Avian Leukosis Virus. Specific functions, and accordingly utilities, of VGR2769 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2769 gene: VGAM216 host

target protein and VGAM217 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM216 and VGAM217.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2770(VGR2770) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91929] VGR2770 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2770 gene was detected is described hereinabove with reference to Figs. 1-9.

[91930] VGR2770 gene encodes VGR2770 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91931] VGR2770 precursor RNA folds spatially, forming VGR2770 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2770 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2770 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91932] VGR2770 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM218 precursor RNA and VGAM219 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91933] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM218 RNA and VGAM219 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91934] VGAM218 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM218 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM218 host target RNA into VGAM218 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91935] VGAM219 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM219 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM219 host target RNA into VGAM219 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91936] It is appreciated that a function of VGR2770 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2770 gene include diagnosis, prevention and treatment of viral infection by Bovine Leukemia Virus. Specific functions, and accordingly utilities, of VGR2770 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2770 gene: VGAM218 host target protein and VGAM219 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM218 and VGAM219.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2771(VGR2771) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91937] VGR2771 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2771 gene was detected is described hereinabove with reference to Figs. 1-9.

[91938] VGR2771 gene encodes VGR2771 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91939] VGR2771 precursor RNA folds spatially, forming VGR2771 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2771 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2771 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91940] VGR2771 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM220 precursor RNA, VGAM221 precursor RNA, VGAM222 precursor RNA, VGAM223 precursor RNA, VGAM224 precursor RNA, VGAM225 precursor

RNA, VGAM226 precursor RNA and VGAM227 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91941] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM220 RNA, VGAM221 RNA, VGAM222 RNA, VGAM223 RNA, VGAM224 RNA, VGAM225 RNA, VGAM226 RNA and VGAM227 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91942] VGAM220 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM220 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM220 host target RNA into

VGAM220 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91943] VGAM221 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM221 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM221 host target RNA into VGAM221 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91944] VGAM222 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM222 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM222 host target RNA into VGAM222 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91945] VGAM223 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM223 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM223 host target RNA into VGAM223 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91946] VGAM224 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM224 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM224 host target RNA into VGAM224 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91947] VGAM225 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM225 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM225 host target RNA into VGAM225 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91948] VGAM226 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM226 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM226 host target RNA into VGAM226 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91949] VGAM227 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM227 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM227 host target RNA into VGAM227 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91950] It is appreciated that a function of VGR2771 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2771 gene include diagnosis, prevention and treatment of viral infection by

Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2771 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2771 gene: VGAM220 host target protein, VGAM221 host target protein, VGAM222 host target protein, VGAM223 host target protein, VGAM224 host target protein, VGAM225 host target protein, VGAM226 host target protein and VGAM227 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM220, VGAM221, VGAM222, VGAM223, VGAM224, VGAM225, VGAM226 and VGAM227.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2772(VGR2772) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91951] VGR2772 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2772 gene was detected is described hereinabove with reference to Figs. 1-9.

[91952] VGR2772 gene encodes VGR2772 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91953] VGR2772 precursor RNA folds spatially, forming VGR2772 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2772 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2772 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91954] VGR2772 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM228 precursor RNA, VGAM229 precursor RNA, VGAM230 precursor RNA, VGAM231 precursor RNA, VGAM232 precursor RNA, VGAM233 precursor

RNA, VGAM234 precursor RNA and VGAM235 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91955] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM228 RNA, VGAM229 RNA, VGAM230 RNA, VGAM231 RNA, VGAM232 RNA, VGAM233 RNA, VGAM234 RNA and VGAM235 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91956] VGAM228 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM228 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM228 host target RNA into

VGAM228 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91957] VGAM229 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM229 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM229 host target RNA into VGAM229 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91958] VGAM230 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM230 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM230 host target RNA into VGAM230 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91959] VGAM231 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM231 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM231 host target RNA into VGAM231 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91960] VGAM232 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM232 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM232 host target RNA into VGAM232 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91961] VGAM233 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM233 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM233 host target RNA into VGAM233 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91962] VGAM234 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM234 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM234 host target RNA into VGAM234 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91963] VGAM235 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM235 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM235 host target RNA into VGAM235 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91964] It is appreciated that a function of VGR2772 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2772 gene include diagnosis, prevention and treatment of viral infection by

Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2772 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2772 gene: VGAM228 host target protein, VGAM229 host target protein, VGAM230 host target protein, VGAM231 host target protein, VGAM232 host target protein, VGAM233 host target protein, VGAM234 host target protein and VGAM235 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM228, VGAM229, VGAM230, VGAM231, VGAM232, VGAM233, VGAM234 and VGAM235.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2773(VGR2773) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91965] VGR2773 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2773 gene was detected is described hereinabove with reference to Figs. 1-9.

[91966] VGR2773 gene encodes VGR2773 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91967] VGR2773 precursor RNA folds spatially, forming VGR2773 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2773 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2773 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91968] VGR2773 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM236 precursor RNA, VGAM237 precursor RNA, VGAM238 precursor RNA, VGAM239 precursor RNA, VGAM240 precursor RNA, VGAM241 precursor

RNA, VGAM242 precursor RNA and VGAM243 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91969] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM236 RNA, VGAM237 RNA, VGAM238 RNA, VGAM239 RNA, VGAM240 RNA, VGAM241 RNA, VGAM242 RNA and VGAM243 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91970] VGAM236 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM236 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM236 host target RNA into

VGAM236 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91971] VGAM237 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM237 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM237 host target RNA into VGAM237 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91972] VGAM238 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM238 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM238 host target RNA into VGAM238 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91973] VGAM239 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM239 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM239 host target RNA into VGAM239 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91974] VGAM240 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM240 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM240 host target RNA into VGAM240 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91975] VGAM241 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM241 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM241 host target RNA into VGAM241 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91976] VGAM242 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM242 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM242 host target RNA into VGAM242 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91977] VGAM243 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM243 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM243 host target RNA into VGAM243 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91978] It is appreciated that a function of VGR2773 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2773 gene include diagnosis, prevention and treatment of viral infection by

Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2773 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2773 gene: VGAM236 host target protein, VGAM237 host target protein, VGAM238 host target protein, VGAM239 host target protein, VGAM240 host target protein, VGAM241 host target protein, VGAM242 host target protein and VGAM243 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM236, VGAM237, VGAM238, VGAM239, VGAM240, VGAM241, VGAM242 and VGAM243.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2774(VGR2774) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91979] VGR2774 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2774 gene was detected is described hereinabove with reference to Figs. 1-9.

[91980] VGR2774 gene encodes VGR2774 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91981] VGR2774 precursor RNA folds spatially, forming VGR2774 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2774 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2774 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91982] VGR2774 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM244 precursor RNA, VGAM245 precursor RNA, VGAM246 precursor RNA, VGAM247 precursor RNA, VGAM248 precursor RNA, VGAM249 precursor

RNA, VGAM250 precursor RNA and VGAM251 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91983] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM244 RNA, VGAM245 RNA, VGAM246 RNA, VGAM247 RNA, VGAM248 RNA, VGAM249 RNA, VGAM250 RNA and VGAM251 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91984] VGAM244 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM244 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM244 host target RNA into

VGAM244 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91985] VGAM245 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM245 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM245 host target RNA into VGAM245 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91986] VGAM246 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM246 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM246 host target RNA into VGAM246 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91987] VGAM247 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM247 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM247 host target RNA into VGAM247 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91988] VGAM248 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM248 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM248 host target RNA into VGAM248 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91989] VGAM249 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM249 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM249 host target RNA into VGAM249 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91990] VGAM250 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM250 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM250 host target RNA into VGAM250 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91991] VGAM251 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM251 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM251 host target RNA into VGAM251 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91992] It is appreciated that a function of VGR2774 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2774 gene include diagnosis, prevention and treatment of viral infection by

Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2774 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2774 gene: VGAM244 host target protein, VGAM245 host target protein, VGAM246 host target protein, VGAM247 host target protein, VGAM248 host target protein, VGAM249 host target protein, VGAM250 host target protein and VGAM251 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM244, VGAM245, VGAM246, VGAM247, VGAM248, VGAM249, VGAM250 and VGAM251.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2775(VGR2775) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[91993] VGR2775 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2775 gene was detected is described hereinabove with reference to Figs. 1-9.

[91994] VGR2775 gene encodes VGR2775 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[91995] VGR2775 precursor RNA folds spatially, forming VGR2775 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2775 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2775 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[91996] VGR2775 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM252 precursor RNA, VGAM253 precursor RNA, VGAM254 precursor RNA, VGAM255 precursor RNA, VGAM256 precursor RNA, VGAM257 precursor

RNA, VGAM258 precursor RNA and VGAM259 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[91997] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM252 RNA, VGAM253 RNA, VGAM254 RNA, VGAM255 RNA, VGAM256 RNA, VGAM257 RNA, VGAM258 RNA and VGAM259 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[91998] VGAM252 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM252 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM252 host target RNA into

VGAM252 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[91999] VGAM253 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM253 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM253 host target RNA into VGAM253 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92000] VGAM254 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM254 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM254 host target RNA into VGAM254 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92001] VGAM255 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM255 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM255 host target RNA into VGAM255 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92002] VGAM256 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM256 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM256 host target RNA into VGAM256 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92003] VGAM257 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM257 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM257 host target RNA into VGAM257 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92004] VGAM258 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM258 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM258 host target RNA into VGAM258 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92005] VGAM259 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM259 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM259 host target RNA into VGAM259 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92006] It is appreciated that a function of VGR2775 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2775 gene include diagnosis, prevention and treatment of viral infection by

Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2775 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2775 gene: VGAM252 host target protein, VGAM253 host target protein, VGAM254 host target protein, VGAM255 host target protein, VGAM256 host target protein, VGAM257 host target protein, VGAM258 host target protein and VGAM259 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM252, VGAM253, VGAM254, VGAM255, VGAM256, VGAM257, VGAM258 and VGAM259.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2776(VGR2776) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92007] VGR2776 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2776 gene was detected is described hereinabove with reference to Figs. 1-9.

[92008] VGR2776 gene encodes VGR2776 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92009] VGR2776 precursor RNA folds spatially, forming VGR2776 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2776 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2776 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92010] VGR2776 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM260 precursor RNA, VGAM261 precursor RNA, VGAM262 precursor RNA, VGAM263 precursor RNA, VGAM264 precursor RNA and VGAM265 precur-

sor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92011] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM260 RNA, VGAM261 RNA, VGAM262 RNA, VGAM263 RNA, VGAM264 RNA and VGAM265 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92012] VGAM260 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM260 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM260 host target RNA into VGAM260 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92013] VGAM261 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM261 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM261 host target RNA into VGAM261 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92014] VGAM262 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM262 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM262 host target RNA into VGAM262 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92015] VGAM263 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM263 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM263 host target RNA into VGAM263 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92016] VGAM264 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM264 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM264 host target RNA into

VGAM264 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92017] VGAM265 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM265 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM265 host target RNA into VGAM265 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92018] It is appreciated that a function of VGR2776 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2776 gene include diagnosis, prevention and treatment of viral infection by Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2776 gene correlate with, and may be deduced from, the identity of the host target genes,

which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2776 gene: VGAM260 host target protein, VGAM261 host target protein, VGAM262 host target protein, VGAM263 host target protein, VGAM264 host target protein and VGAM265 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM260, VGAM261, VGAM262, VGAM263, VGAM264 and VGAM265.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2777(VGR2777) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92019] VGR2777 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2777 gene was detected is described hereinabove with reference to Figs. 1-9.

[92020] VGR2777 gene encodes VGR2777 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92021] VGR2777 precursor RNA folds spatially, forming VGR2777 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2777 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2777 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92022] VGR2777 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM266 precursor RNA, VGAM267 precursor RNA, VGAM268 precursor RNA, VGAM269 precursor RNA, VGAM270 precursor RNA, VGAM271 precursor RNA, VGAM272 precursor RNA and VGAM273 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92023] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM266 RNA, VGAM267 RNA, VGAM268 RNA, VGAM269 RNA, VGAM270 RNA, VGAM271 RNA, VGAM272 RNA and VGAM273 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92024] VGAM266 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM266 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM266 host target RNA into VGAM266 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92025] VGAM267 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM267 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM267 host target RNA into VGAM267 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92026] VGAM268 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM268 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM268 host target RNA into VGAM268 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92027] VGAM269 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM269 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM269 host target RNA into VGAM269 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92028] VGAM270 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM270 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM270 host target RNA into VGAM270 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92029] VGAM271 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM271 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM271 host target RNA into VGAM271 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92030] VGAM272 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM272 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM272 host target RNA into VGAM272 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92031] VGAM273 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM273 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM273 host target RNA into VGAM273 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92032] It is appreciated that a function of VGR2777 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2777 gene include diagnosis, prevention and treatment of viral infection by Epiphyas Postvittana Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2777 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs com-

prised in the `operon-like` cluster of VGR2777 gene: VGAM266 host target protein, VGAM267 host target protein, VGAM268 host target protein, VGAM269 host target protein, VGAM270 host target protein, VGAM271 host target protein, VGAM272 host target protein and VGAM273 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM266, VGAM267, VGAM268, VGAM269, VGAM270, VGAM271, VGAM272 and VGAM273.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2778(VGR2778) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92033] VGR2778 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2778 gene was detected is described hereinabove with reference to Figs. 1-9.

[92034] VGR2778 gene encodes VGR2778 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92035] VGR2778 precursor RNA folds spatially, forming VGR2778 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2778 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2778 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92036] VGR2778 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM274 precursor RNA, VGAM275 precursor RNA, VGAM276 precursor RNA, VGAM277 precursor RNA, VGAM278 precursor RNA, VGAM279 precursor RNA, VGAM280 precursor RNA and VGAM281 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92037] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM274 RNA, VGAM275 RNA, VGAM276 RNA, VGAM277 RNA, VGAM278 RNA, VGAM279 RNA, VGAM280 RNA and VGAM281 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92038] VGAM274 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM274 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM274 host target RNA into VGAM274 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92039] VGAM275 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM275 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM275 host target RNA into VGAM275 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92040] VGAM276 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM276 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM276 host target RNA into VGAM276 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92041] VGAM277 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM277 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM277 host target RNA into VGAM277 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92042] VGAM278 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM278 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM278 host target RNA into VGAM278 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92043] VGAM279 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM279 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM279 host target RNA into VGAM279 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92044] VGAM280 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM280 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM280 host target RNA into VGAM280 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92045] VGAM281 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM281 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM281 host target RNA into VGAM281 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92046] It is appreciated that a function of VGR2778 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2778 gene include diagnosis, prevention and treatment of viral infection by Epiphyas Postvittana Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2778 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs com-

prised in the `operon-like` cluster of VGR2778 gene: VGAM274 host target protein, VGAM275 host target protein, VGAM276 host target protein, VGAM277 host target protein, VGAM278 host target protein, VGAM279 host target protein, VGAM280 host target protein and VGAM281 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM274, VGAM275, VGAM276, VGAM277, VGAM278, VGAM279, VGAM280 and VGAM281.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2779(VGR2779) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92047] VGR2779 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2779 gene was detected is described hereinabove with reference to Figs. 1-9.

[92048] VGR2779 gene encodes VGR2779 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92049] VGR2779 precursor RNA folds spatially, forming VGR2779 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2779 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2779 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92050] VGR2779 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM282 precursor RNA, VGAM283 precursor RNA, VGAM284 precursor RNA, VGAM285 precursor RNA, VGAM286 precursor RNA, VGAM287 precursor RNA, VGAM288 precursor RNA and VGAM289 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92051] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM282 RNA, VGAM283 RNA, VGAM284 RNA, VGAM285 RNA, VGAM286 RNA, VGAM287 RNA, VGAM288 RNA and VGAM289 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92052] VGAM282 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM282 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM282 host target RNA into VGAM282 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92053] VGAM283 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM283 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM283 host target RNA into VGAM283 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92054] VGAM284 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM284 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM284 host target RNA into VGAM284 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92055] VGAM285 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM285 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM285 host target RNA into VGAM285 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92056] VGAM286 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM286 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM286 host target RNA into VGAM286 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92057] VGAM287 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM287 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM287 host target RNA into VGAM287 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92058] VGAM288 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM288 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM288 host target RNA into VGAM288 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92059] VGAM289 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM289 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM289 host target RNA into VGAM289 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92060] It is appreciated that a function of VGR2779 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2779 gene include diagnosis, prevention and treatment of viral infection by Epiphyas Postvittana Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2779 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs com-

prised in the `operon-like` cluster of VGR2779 gene: VGAM282 host target protein, VGAM283 host target protein, VGAM284 host target protein, VGAM285 host target protein, VGAM286 host target protein, VGAM287 host target protein, VGAM288 host target protein and VGAM289 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM282, VGAM283, VGAM284, VGAM285, VGAM286, VGAM287, VGAM288 and VGAM289.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2780(VGR2780) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92061] VGR2780 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2780 gene was detected is described hereinabove with reference to Figs. 1-9.

[92062] VGR2780 gene encodes VGR2780 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92063] VGR2780 precursor RNA folds spatially, forming VGR2780 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2780 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2780 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92064] VGR2780 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM290 precursor RNA, VGAM291 precursor RNA, VGAM292 precursor RNA, VGAM293 precursor RNA, VGAM294 precursor RNA, VGAM295 precursor RNA, VGAM296 precursor RNA and VGAM297 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA

segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92065] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM290 RNA, VGAM291 RNA, VGAM292 RNA, VGAM293 RNA, VGAM294 RNA, VGAM295 RNA, VGAM296 RNA and VGAM297 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92066] VGAM290 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM290 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM290 host target RNA into VGAM290 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92067] VGAM291 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM291 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM291 host target RNA into VGAM291 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92068] VGAM292 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM292 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM292 host target RNA into VGAM292 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92069] VGAM293 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM293 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM293 host target RNA into VGAM293 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92070] VGAM294 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM294 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM294 host target RNA into VGAM294 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92071] VGAM295 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM295 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM295 host target RNA into VGAM295 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92072] VGAM296 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM296 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM296 host target RNA into VGAM296 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92073] VGAM297 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM297 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM297 host target RNA into VGAM297 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92074] It is appreciated that a function of VGR2780 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2780 gene include diagnosis, prevention and treatment of viral infection by Epiphyas Postvittana Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2780 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs com-

prised in the `operon-like` cluster of VGR2780 gene: VGAM290 host target protein, VGAM291 host target protein, VGAM292 host target protein, VGAM293 host target protein, VGAM294 host target protein, VGAM295 host target protein, VGAM296 host target protein and VGAM297 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM290, VGAM291, VGAM292, VGAM293, VGAM294, VGAM295, VGAM296 and VGAM297.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2781(VGR2781) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92075] VGR2781 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2781 gene was detected is described hereinabove with reference to Figs. 1-9.

[92076] VGR2781 gene encodes VGR2781 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92077] VGR2781 precursor RNA folds spatially, forming VGR2781 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2781 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2781 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92078] VGR2781 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM298 precursor RNA, VGAM299 precursor RNA, VGAM300 precursor RNA, VGAM301 precursor RNA, VGAM302 precursor RNA and VGAM303 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED

PRECURSOR RNA of Fig. 1.

[92079] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM298 RNA, VGAM299 RNA, VGAM300 RNA, VGAM301 RNA, VGAM302 RNA and VGAM303 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92080] VGAM298 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM298 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM298 host target RNA into VGAM298 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92081] VGAM299 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM299 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM299 host target RNA into VGAM299 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92082] VGAM300 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM300 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM300 host target RNA into VGAM300 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92083] VGAM301 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM301 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM301 host target RNA into VGAM301 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92084] VGAM302 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM302 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM302 host target RNA into VGAM302 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92085] VGAM303 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM303 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM303 host target RNA into VGAM303 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92086] It is appreciated that a function of VGR2781 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2781 gene include diagnosis, prevention and treatment of viral infection by Epiphyas Postvittana Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2781 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2781 gene: VGAM298 host target protein, VGAM299 host target protein, VGAM300 host target protein, VGAM301 host target

protein, VGAM302 host target protein and VGAM303 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM298, VGAM299, VGAM300, VGAM301, VGAM302 and VGAM303.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2782(VGR2782) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92087] VGR2782 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2782 gene was detected is described hereinabove with reference to Figs. 1-9.

[92088] VGR2782 gene encodes VGR2782 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92089] VGR2782 precursor RNA folds spatially, forming VGR2782

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2782 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2782 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92090] VGR2782 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM304 precursor RNA, VGAM305 precursor RNA and VGAM306 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92091] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM304 RNA, VGAM305 RNA and VGAM306 RNA, herein schemati-

cally represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92092] VGAM304 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM304 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM304 host target RNA into VGAM304 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92093] VGAM305 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM305 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM305 host target RNA into VGAM305 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92094] VGAM306 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM306 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM306 host target RNA into VGAM306 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92095] It is appreciated that a function of VGR2782 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2782 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2782 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2782 gene: VGAM304 host target protein, VGAM305 host target protein and VGAM306 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM304, VGAM305 and VGAM306.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2783(VGR2783) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92096] VGR2783 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2783 gene was detected is described hereinabove with reference to Figs. 1-9.

[92097] VGR2783 gene encodes VGR2783 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[92098] VGR2783 precursor RNA folds spatially, forming VGR2783 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2783 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2783 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92099] VGR2783 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM310 precursor RNA, VGAM311 precursor RNA and VGAM312 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92100] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM310 RNA, VGAM311 RNA and VGAM312 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92101] VGAM310 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM310 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM310 host target RNA into VGAM310 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92102] VGAM311 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM311 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM311 host target RNA into VGAM311 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92103] VGAM312 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM312 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM312 host target RNA into VGAM312 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92104] It is appreciated that a function of VGR2783 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2783 gene include diagnosis, prevention and treatment of viral infection by

Pothos Latent Virus. Specific functions, and accordingly utilities, of VGR2783 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2783 gene: VGAM310 host target protein, VGAM311 host target protein and VGAM312 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM310, VGAM311 and VGAM312.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2784(VGR2784) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92105] VGR2784 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2784 gene was detected is described hereinabove with reference to Figs. 1-9.

[92106] VGR2784 gene encodes VGR2784 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92107] VGR2784 precursor RNA folds spatially, forming VGR2784 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2784 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2784 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92108] VGR2784 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM315 precursor RNA, VGAM316 precursor RNA, VGAM317 precursor RNA and VGAM318 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92109] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM315 RNA, VGAM316 RNA, VGAM317 RNA and VGAM318 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92110] VGAM315 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM315 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM315 host target RNA into VGAM315 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92111] VGAM316 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM316 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM316 host target RNA into VGAM316 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92112] VGAM317 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM317 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM317 host target RNA into VGAM317 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92113] VGAM318 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM318 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM318 host target RNA into VGAM318 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92114] It is appreciated that a function of VGR2784 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2784 gene include diagnosis, prevention and treatment of viral infection by Cryphonectria Hypovirus 3. Specific functions, and accordingly utilities, of VGR2784 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2784 gene: VGAM315 host target protein, VGAM316 host target protein, VGAM317 host target protein and VGAM318 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN.

The function of these host target genes is elaborated hereinabove with reference to VGAM315, VGAM316, VGAM317 and VGAM318.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2785(VGR2785) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92115] VGR2785 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2785 gene was detected is described hereinabove with reference to Figs. 1-9.

[92116] VGR2785 gene encodes VGR2785 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92117] VGR2785 precursor RNA folds spatially, forming VGR2785 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2785 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2785 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92118] VGR2785 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM319 precursor RNA and VGAM320 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92119] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM319 RNA and VGAM320 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92120] VGAM319 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM319 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM319 host target RNA into VGAM319 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92121] VGAM320 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM320 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM320 host target RNA into VGAM320 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92122] It is appreciated that a function of VGR2785 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2785 gene include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGR2785 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2785 gene: VGAM319 host target protein and VGAM320 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM319 and VGAM320.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2786(VGR2786) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92123] VGR2786 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2786 gene was

detected is described hereinabove with reference to Figs. 1-9.

[92124] VGR2786 gene encodes VGR2786 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92125] VGR2786 precursor RNA folds spatially, forming VGR2786 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2786 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2786 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92126] VGR2786 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM324 precursor RNA, VGAM325 precursor RNA and VGAM326 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment,

corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92127] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM324 RNA, VGAM325 RNA and VGAM326 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92128] VGAM324 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM324 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM324 host target RNA into VGAM324 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92129] VGAM325 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM325 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM325 host target RNA into VGAM325 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92130] VGAM326 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM326 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM326 host target RNA into VGAM326 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92131] It is appreciated that a function of VGR2786 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2786 gene include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGR2786 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2786 gene: VGAM324 host target protein, VGAM325 host target protein and VGAM326 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM324, VGAM325 and VGAM326.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2787(VGR2787) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92132] VGR2787 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2787 gene was detected is described hereinabove with reference to Figs. 1-9.

[92133] VGR2787 gene encodes VGR2787 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92134] VGR2787 precursor RNA folds spatially, forming VGR2787 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2787 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2787 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92135] VGR2787 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM333 precursor RNA and VGAM334 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92136] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM333 RNA and VGAM334 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92137] VGAM333 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM333 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM333 host target RNA into VGAM333 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92138] VGAM334 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM334 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM334 host target RNA into VGAM334 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92139] It is appreciated that a function of VGR2787 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2787 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2787 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2787 gene: VGAM333 host target protein and VGAM334 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The func-

tion of these host target genes is elaborated hereinabove with reference to VGAM333 and VGAM334.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2788(VGR2788) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92140] VGR2788 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2788 gene was detected is described hereinabove with reference to Figs. 1-9.

[92141] VGR2788 gene encodes VGR2788 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92142] VGR2788 precursor RNA folds spatially, forming VGR2788 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2788 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2788 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92143] VGR2788 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM335 precursor RNA, VGAM336 precursor RNA, VGAM337 precursor RNA, VGAM338 precursor RNA and VGAM339 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92144] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM335 RNA, VGAM336 RNA, VGAM337 RNA, VGAM338 RNA and VGAM339 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92145] VGAM335 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM335 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM335 host target RNA into VGAM335 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92146] VGAM336 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM336 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM336 host target RNA into VGAM336 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92147] VGAM337 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM337 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM337 host target RNA into VGAM337 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92148] VGAM338 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM338 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM338 host target RNA into VGAM338 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92149] VGAM339 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM339 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM339 host target RNA into VGAM339 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92150] It is appreciated that a function of VGR2788 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2788 gene include diagnosis, prevention and treatment of viral infection by Saimiriine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2788 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2788 gene: VGAM335 host target protein, VGAM336 host target protein, VGAM337

host target protein, VGAM338 host target protein and VGAM339 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM335, VGAM336, VGAM337, VGAM338 and VGAM339.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2789(VGR2789) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92151] VGR2789 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2789 gene was detected is described hereinabove with reference to Figs. 1-9.

[92152] VGR2789 gene encodes VGR2789 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92153] VGR2789 precursor RNA folds spatially, forming VGR2789

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2789 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2789 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92154] VGR2789 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM340 precursor RNA, VGAM341 precursor RNA, VGAM342 precursor RNA, VGAM343 precursor RNA and VGAM344 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92155] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM340 RNA, VGAM341 RNA, VGAM342 RNA, VGAM343 RNA and

VGAM344 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92156] VGAM340 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM340 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM340 host target RNA into VGAM340 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92157] VGAM341 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM341 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM341 host target RNA into VGAM341 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92158] VGAM342 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM342 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM342 host target RNA into VGAM342 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92159] VGAM343 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM343 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM343 host target RNA into VGAM343 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92160] VGAM344 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM344 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM344 host target RNA into VGAM344 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92161] It is appreciated that a function of VGR2789 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2789 gene include diagnosis, prevention and treatment of viral infection by Tobacco Mosaic Virus. Specific functions, and accordingly

utilities, of VGR2789 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2789 gene: VGAM340 host target protein, VGAM341 host target protein, VGAM342 host target protein, VGAM343 host target protein and VGAM344 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM340, VGAM341, VGAM342, VGAM343 and VGAM344.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2790(VGR2790) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92162] VGR2790 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2790 gene was detected is described hereinabove with reference to Figs.

1-9.

[92163] VGR2790 gene encodes VGR2790 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92164] VGR2790 precursor RNA folds spatially, forming VGR2790 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2790 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2790 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92165] VGR2790 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM346 precursor RNA and VGAM347 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92166] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM346 RNA and VGAM347 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92167] VGAM346 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM346 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM346 host target RNA into VGAM346 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92168] VGAM347 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM347 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM347 host target RNA into VGAM347 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92169] It is appreciated that a function of VGR2790 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2790 gene include diagnosis, prevention and treatment of viral infection by Black Beetle Virus. Specific functions, and accordingly utilities, of VGR2790 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2790 gene: VGAM346 host target protein and VGAM347 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM346 and VGAM347.Fig. 9 further provides a conceptual description of novel bioinformati-

cally detected regulatory viral gene, referred to here as Viral Genomic Record 2791(VGR2791) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92170] VGR2791 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2791 gene was detected is described hereinabove with reference to Figs. 1-9.

[92171] VGR2791 gene encodes VGR2791 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92172] VGR2791 precursor RNA folds spatially, forming VGR2791 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2791 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2791 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[92173] VGR2791 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM348 precursor RNA and VGAM349 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92174] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM348 RNA and VGAM349 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92175] VGAM348 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM348 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM348 host target RNA into VGAM348 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92176] VGAM349 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM349 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM349 host target RNA into VGAM349 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92177] It is appreciated that a function of VGR2791 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2791 gene include diagnosis, prevention and treatment of viral infection by Human Enterovirus C. Specific functions, and accordingly

utilities, of VGR2791 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2791 gene: VGAM348 host target protein and VGAM349 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM348 and VGAM349.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2792(VGR2792) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92178] VGR2792 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2792 gene was detected is described hereinabove with reference to Figs. 1-9.

[92179] VGR2792 gene encodes VGR2792 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[92180] VGR2792 precursor RNA folds spatially, forming VGR2792 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2792 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2792 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92181] VGR2792 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM350 precursor RNA, VGAM351 precursor RNA, VGAM352 precursor RNA, VGAM353 precursor RNA, VGAM354 precursor RNA, VGAM355 precursor RNA, VGAM356 precursor RNA and VGAM357 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92182] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM350 RNA, VGAM351 RNA, VGAM352 RNA, VGAM353 RNA, VGAM354 RNA, VGAM355 RNA, VGAM356 RNA and VGAM357 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92183] VGAM350 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM350 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM350 host target RNA into VGAM350 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92184] VGAM351 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM351 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM351 host target RNA into VGAM351 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92185] VGAM352 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM352 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM352 host target RNA into VGAM352 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92186] VGAM353 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM353 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM353 host target RNA into VGAM353 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92187] VGAM354 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM354 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM354 host target RNA into VGAM354 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92188] VGAM355 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM355 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM355 host target RNA into VGAM355 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92189] VGAM356 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM356 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM356 host target RNA into VGAM356 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92190] VGAM357 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM357 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM357 host target RNA into VGAM357 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92191] It is appreciated that a function of VGR2792 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2792 gene include diagnosis, prevention and treatment of viral infection by Avian Infectious Bronchitis Virus. Specific functions, and accordingly utilities, of VGR2792 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2792 gene: VGAM350 host target protein, VGAM351 host target protein,

VGAM352 host target protein, VGAM353 host target protein, VGAM354 host target protein, VGAM355 host target protein, VGAM356 host target protein and VGAM357 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM350, VGAM351, VGAM352, VGAM353, VGAM354, VGAM355, VGAM356 and VGAM357.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2793(VGR2793) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92192] VGR2793 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2793 gene was detected is described hereinabove with reference to Figs. 1-9.

[92193] VGR2793 gene encodes VGR2793 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[92194] VGR2793 precursor RNA folds spatially, forming VGR2793 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2793 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2793 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92195] VGR2793 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM358 precursor RNA, VGAM359 precursor RNA, VGAM360 precursor RNA, VGAM361 precursor RNA, VGAM362 precursor RNA, VGAM363 precursor RNA and VGAM364 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92196] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM358 RNA, VGAM359 RNA, VGAM360 RNA, VGAM361 RNA, VGAM362 RNA, VGAM363 RNA and VGAM364 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92197] VGAM358 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM358 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM358 host target RNA into VGAM358 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92198] VGAM359 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM359 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM359 host target RNA into VGAM359 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92199] VGAM360 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM360 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM360 host target RNA into VGAM360 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92200] VGAM361 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM361 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM361 host target RNA into VGAM361 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92201] VGAM362 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM362 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM362 host target RNA into VGAM362 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92202] VGAM363 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM363 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM363 host target RNA into VGAM363 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92203] VGAM364 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM364 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM364 host target RNA into VGAM364 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92204] It is appreciated that a function of VGR2793 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2793 gene include diagnosis, prevention and treatment of viral infection by Avian Infectious Bronchitis Virus. Specific functions, and accordingly utilities, of VGR2793 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2793 gene: VGAM358 host target protein, VGAM359 host target protein, VGAM360 host target protein, VGAM361 host target protein, VGAM362 host target protein, VGAM363 host target protein and VGAM364 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM358, VGAM359, VGAM360, VGAM361, VGAM362, VGAM363 and VGAM364.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2794(VGR2794) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expres-

sion of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92205] VGR2794 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2794 gene was detected is described hereinabove with reference to Figs. 1-9.

[92206] VGR2794 gene encodes VGR2794 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92207] VGR2794 precursor RNA folds spatially, forming VGR2794 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2794 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2794 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92208] VGR2794 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM365 precursor RNA, VGAM366 precursor RNA, VGAM367 precursor RNA and VGAM368 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92209] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM365 RNA, VGAM366 RNA, VGAM367 RNA and VGAM368 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92210] VGAM365 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM365 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM365 host target RNA into VGAM365 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92211] VGAM366 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM366 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM366 host target RNA into VGAM366 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92212] VGAM367 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM367 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM367 host target RNA into VGAM367 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92213] VGAM368 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM368 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM368 host target RNA into VGAM368 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92214] It is appreciated that a function of VGR2794 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2794 gene include diagnosis, prevention and treatment of viral infection by Avian Infectious Bronchitis Virus. Specific functions, and

accordingly utilities, of VGR2794 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2794 gene: VGAM365 host target protein, VGAM366 host target protein, VGAM367 host target protein and VGAM368 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM365, VGAM366, VGAM367 and VGAM368.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2795(VGR2795) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92215] VGR2795 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2795 gene was detected is described hereinabove with reference to Figs. 1-9.

[92216] VGR2795 gene encodes VGR2795 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92217] VGR2795 precursor RNA folds spatially, forming VGR2795 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2795 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2795 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92218] VGR2795 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM369 precursor RNA, VGAM370 precursor RNA, VGAM371 precursor RNA, VGAM372 precursor RNA, VGAM373 precursor RNA, VGAM374 precursor RNA and VGAM375 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corre-

sponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92219] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM369 RNA, VGAM370 RNA, VGAM371 RNA, VGAM372 RNA, VGAM373 RNA, VGAM374 RNA and VGAM375 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92220] VGAM369 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM369 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM369 host target RNA into VGAM369 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92221] VGAM370 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM370 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM370 host target RNA into VGAM370 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92222] VGAM371 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM371 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM371 host target RNA into VGAM371 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92223] VGAM372 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM372 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM372 host target RNA into VGAM372 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92224] VGAM373 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM373 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM373 host target RNA into VGAM373 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92225] VGAM374 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM374 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM374 host target RNA into VGAM374 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92226] VGAM375 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM375 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM375 host target RNA into VGAM375 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92227] It is appreciated that a function of VGR2795 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2795 gene include diagnosis, prevention and treatment of viral infection by Avian Infectious Bronchitis Virus. Specific functions, and accordingly utilities, of VGR2795 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2795 gene: VGAM369 host target protein, VGAM370 host target protein, VGAM371 host target protein, VGAM372 host target protein, VGAM373 host target protein, VGAM374 host target protein and VGAM375 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM369, VGAM370, VGAM371, VGAM372, VGAM373, VGAM374 and VGAM375.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2796(VGR2796) viral gene, which

encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92228] VGR2796 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2796 gene was detected is described hereinabove with reference to Figs. 1-9.

[92229] VGR2796 gene encodes VGR2796 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92230] VGR2796 precursor RNA folds spatially, forming VGR2796 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2796 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2796 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[92231] VGR2796 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM376 precursor RNA and VGAM377 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92232] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM376 RNA and VGAM377 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92233] VGAM376 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM376 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM376 host target RNA into VGAM376 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92234] VGAM377 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM377 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM377 host target RNA into VGAM377 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92235] It is appreciated that a function of VGR2796 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2796 gene include diagnosis, prevention and treatment of viral infection by Eggplant Mosaic Virus. Specific functions, and accordingly utilities, of VGR2796 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2796 gene: VGAM376 host target protein and VGAM377 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM376 and VGAM377.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2797(VGR2797) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92236] VGR2797 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2797 gene was detected is described hereinabove with reference to Figs. 1-9.

[92237] VGR2797 gene encodes VGR2797 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92238] VGR2797 precursor RNA folds spatially, forming VGR2797 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2797 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2797 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92239] VGR2797 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM378 precursor RNA, VGAM379 precursor RNA, VGAM380 precursor RNA and VGAM381 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92240] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM378

RNA, VGAM379 RNA, VGAM380 RNA and VGAM381 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92241] VGAM378 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM378 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM378 host target RNA into VGAM378 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92242] VGAM379 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM379 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM379 host target RNA into VGAM379 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92243] VGAM380 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM380 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM380 host target RNA into VGAM380 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92244] VGAM381 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM381 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM381 host target RNA into VGAM381 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92245] It is appreciated that a function of VGR2797 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2797 gene include diagnosis, prevention and treatment of viral infection by Feline Immunodeficiency Virus. Specific functions, and accordingly utilities, of VGR2797 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2797 gene: VGAM378 host target protein, VGAM379 host target protein, VGAM380 host target protein and VGAM381 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM378, VGAM379, VGAM380 and VGAM381.Fig. 9 further provides a concep-

tual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2798(VGR2798) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92246] VGR2798 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2798 gene was detected is described hereinabove with reference to Figs. 1-9.

[92247] VGR2798 gene encodes VGR2798 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92248] VGR2798 precursor RNA folds spatially, forming VGR2798 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2798 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2798 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92249] VGR2798 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM382 precursor RNA, VGAM383 precursor RNA, VGAM384 precursor RNA, VGAM385 precursor RNA and VGAM386 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92250] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM382 RNA, VGAM383 RNA, VGAM384 RNA, VGAM385 RNA and VGAM386 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92251] VGAM382 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM382 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM382 host target RNA into VGAM382 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92252] VGAM383 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM383 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM383 host target RNA into VGAM383 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92253] VGAM384 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM384 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM384 host target RNA into VGAM384 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92254] VGAM385 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM385 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM385 host target RNA into VGAM385 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92255] VGAM386 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM386 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM386 host target RNA into VGAM386 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92256] It is appreciated that a function of VGR2798 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2798 gene include diagnosis, prevention and treatment of viral infection by Hepatitis A Virus. Specific functions, and accordingly utilities, of VGR2798 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2798 gene: VGAM382 host target protein, VGAM383 host target protein, VGAM384 host target protein, VGAM385 host target protein and VGAM386 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM382, VGAM383, VGAM384, VGAM385 and VGAM386.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2799(VGR2799) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92257] VGR2799 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2799 gene was detected is described hereinabove with reference to Figs. 1-9.

[92258] VGR2799 gene encodes VGR2799 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92259] VGR2799 precursor RNA folds spatially, forming VGR2799 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2799 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2799 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92260] VGR2799 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM387 precursor RNA, VGAM388 precursor RNA, VGAM389 precursor RNA, VGAM390 precursor RNA and VGAM391 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92261] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM387 RNA, VGAM388 RNA, VGAM389 RNA, VGAM390 RNA and VGAM391 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[92262] VGAM387 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM387 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM387 host target RNA into VGAM387 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92263] VGAM388 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM388 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM388 host target RNA into VGAM388 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92264] VGAM389 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM389 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM389 host target RNA into VGAM389 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92265] VGAM390 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM390 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM390 host target RNA into

VGAM390 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92266] VGAM391 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM391 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM391 host target RNA into VGAM391 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92267] It is appreciated that a function of VGR2799 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2799 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2799 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2799 gene: VGAM387 host target protein, VGAM388 host target protein, VGAM389 host target protein, VGAM390 host target protein and VGAM391 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM387, VGAM388, VGAM389, VGAM390 and VGAM391.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2800(VGR2800) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92268] VGR2800 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2800 gene was detected is described hereinabove with reference to Figs. 1-9.

[92269] VGR2800 gene encodes VGR2800 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92270] VGR2800 precursor RNA folds spatially, forming VGR2800 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2800 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2800 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92271] VGR2800 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM393 precursor RNA, VGAM394 precursor RNA, VGAM395 precursor RNA, VGAM396 precursor RNA, VGAM397 precursor RNA, VGAM398 precursor RNA, VGAM399 precursor RNA and VGAM400 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR

RNA of Fig. 1.

[92272] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM393 RNA, VGAM394 RNA, VGAM395 RNA, VGAM396 RNA, VGAM397 RNA, VGAM398 RNA, VGAM399 RNA and VGAM400 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92273] VGAM393 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM393 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM393 host target RNA into VGAM393 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92274] VGAM394 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM394 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM394 host target RNA into VGAM394 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92275] VGAM395 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM395 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM395 host target RNA into VGAM395 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92276] VGAM396 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM396 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM396 host target RNA into VGAM396 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92277] VGAM397 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM397 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM397 host target RNA into VGAM397 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92278] VGAM398 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM398 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM398 host target RNA into VGAM398 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92279] VGAM399 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM399 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM399 host target RNA into VGAM399 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92280] VGAM400 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM400 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM400 host target RNA into VGAM400 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92281] It is appreciated that a function of VGR2800 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2800 gene include diagnosis, prevention and treatment of viral infection by Cryphonectria Hypovirus 1. Specific functions, and accordingly utilities, of VGR2800 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2800 gene: VGAM393

host target protein, VGAM394 host target protein, VGAM395 host target protein, VGAM396 host target protein, VGAM397 host target protein, VGAM398 host target protein, VGAM399 host target protein and VGAM400 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM393, VGAM394, VGAM395, VGAM396, VGAM397, VGAM398, VGAM399 and VGAM400.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2801(VGR2801) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92282] VGR2801 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2801 gene was detected is described hereinabove with reference to Figs. 1-9.

[92283] VGR2801 gene encodes VGR2801 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92284] VGR2801 precursor RNA folds spatially, forming VGR2801 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2801 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2801 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92285] VGR2801 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM401 precursor RNA, VGAM402 precursor RNA, VGAM403 precursor RNA, VGAM404 precursor RNA, VGAM405 precursor RNA and VGAM406 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92286] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM401 RNA, VGAM402 RNA, VGAM403 RNA, VGAM404 RNA, VGAM405 RNA and VGAM406 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92287] VGAM401 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM401 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM401 host target RNA into VGAM401 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92288] VGAM402 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM402 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM402 host target RNA into VGAM402 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92289] VGAM403 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM403 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM403 host target RNA into VGAM403 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92290] VGAM404 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM404 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM404 host target RNA into VGAM404 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92291] VGAM405 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM405 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM405 host target RNA into VGAM405 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92292] VGAM406 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM406 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM406 host target RNA into VGAM406 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92293] It is appreciated that a function of VGR2801 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2801 gene include diagnosis, prevention and treatment of viral infection by Cryphonectria Hypovirus 1. Specific functions, and accordingly utilities, of VGR2801 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2801 gene: VGAM401 host target protein, VGAM402 host target protein, VGAM403 host target protein, VGAM404 host target protein, VGAM405 host target protein and VGAM406 host

target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM401, VGAM402, VGAM403, VGAM404, VGAM405 and VGAM406.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2802(VGR2802) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92294] VGR2802 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2802 gene was detected is described hereinabove with reference to Figs. 1-9.

[92295] VGR2802 gene encodes VGR2802 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92296] VGR2802 precursor RNA folds spatially, forming VGR2802 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2802 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2802 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92297] VGR2802 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM407 precursor RNA, VGAM408 precursor RNA and VGAM409 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92298] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM407 RNA, VGAM408 RNA and VGAM409 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92299] VGAM407 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM407 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM407 host target RNA into VGAM407 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92300] VGAM408 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM408 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM408 host target RNA into

VGAM408 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92301] VGAM409 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM409 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM409 host target RNA into VGAM409 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92302] It is appreciated that a function of VGR2802 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2802 gene include diagnosis, prevention and treatment of viral infection by Melon Necrotic Spot Virus. Specific functions, and accordingly utilities, of VGR2802 gene correlate with, and may be deduced from, the identity of the host target genes,

which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2802 gene: VGAM407 host target protein, VGAM408 host target protein and VGAM409 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM407, VGAM408 and VGAM409.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2803(VGR2803) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92303] VGR2803 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2803 gene was detected is described hereinabove with reference to Figs. 1-9.

[92304] VGR2803 gene encodes VGR2803 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92305] VGR2803 precursor RNA folds spatially, forming VGR2803 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2803 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2803 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92306] VGR2803 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM410 precursor RNA, VGAM411 precursor RNA and VGAM412 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92307] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM410

RNA, VGAM411 RNA and VGAM412 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92308] VGAM410 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM410 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM410 host target RNA into VGAM410 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92309] VGAM411 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM411 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM411 host target RNA into VGAM411 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92310] VGAM412 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM412 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM412 host target RNA into VGAM412 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92311] It is appreciated that a function of VGR2803 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2803 gene include diagnosis, prevention and treatment of viral infection by O'nyong-nyong Virus. Specific functions, and accordingly

utilities, of VGR2803 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2803 gene: VGAM410 host target protein, VGAM411 host target protein and VGAM412 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM410, VGAM411 and VGAM412.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2804(VGR2804) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92312] VGR2804 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2804 gene was detected is described hereinabove with reference to Figs. 1-9.

[92313] VGR2804 gene encodes VGR2804 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92314] VGR2804 precursor RNA folds spatially, forming VGR2804 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2804 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2804 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92315] VGR2804 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM413 precursor RNA, VGAM414 precursor RNA, VGAM415 precursor RNA, VGAM416 precursor RNA, VGAM417 precursor RNA, VGAM418 precursor RNA and VGAM419 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92316] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM413 RNA, VGAM414 RNA, VGAM415 RNA, VGAM416 RNA, VGAM417 RNA, VGAM418 RNA and VGAM419 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92317] VGAM413 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM413 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM413 host target RNA into VGAM413 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92318] VGAM414 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM414 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM414 host target RNA into VGAM414 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92319] VGAM415 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM415 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM415 host target RNA into VGAM415 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92320] VGAM416 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM416 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM416 host target RNA into VGAM416 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92321] VGAM417 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM417 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM417 host target RNA into VGAM417 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92322] VGAM418 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM418 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM418 host target RNA into VGAM418 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92323] VGAM419 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM419 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM419 host target RNA into VGAM419 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92324] It is appreciated that a function of VGR2804 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2804 gene include diagnosis, prevention and treatment of viral infection by Pepper Mottle Virus. Specific functions, and accordingly utilities, of VGR2804 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2804 gene: VGAM413 host target protein, VGAM414 host target protein, VGAM415 host target protein, VGAM416 host target protein, VGAM417 host target protein, VGAM418 host target protein and VGAM419 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM413, VGAM414, VGAM415, VGAM416, VGAM417, VGAM418 and VGAM419.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2805(VGR2805) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-

like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92325] VGR2805 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2805 gene was detected is described hereinabove with reference to Figs. 1-9.

[92326] VGR2805 gene encodes VGR2805 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92327] VGR2805 precursor RNA folds spatially, forming VGR2805 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2805 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2805 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92328] VGR2805 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM420 precursor RNA and VGAM421 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92329] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM420 RNA and VGAM421 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92330] VGAM420 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM420 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM420 host target RNA into VGAM420 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92331] VGAM421 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM421 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM421 host target RNA into VGAM421 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92332] It is appreciated that a function of VGR2805 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2805 gene include diagnosis, prevention and treatment of viral infection by Human Papillomavirus Type 39. Specific functions, and accordingly utilities, of VGR2805 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR2805 gene: VGAM420 host target protein and VGAM421 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM420 and VGAM421.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2806(VGR2806) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92333] VGR2806 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2806 gene was detected is described hereinabove with reference to Figs. 1-9.

[92334] VGR2806 gene encodes VGR2806 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92335] VGR2806 precursor RNA folds spatially, forming VGR2806

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2806 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2806 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92336] VGR2806 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM422 precursor RNA and VGAM423 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92337] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM422 RNA and VGAM423 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[92338] VGAM422 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM422 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM422 host target RNA into VGAM422 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92339] VGAM423 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM423 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM423 host target RNA into VGAM423 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92340] It is appreciated that a function of VGR2806 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2806 gene include diagnosis, prevention and treatment of viral infection by Canine Parvovirus. Specific functions, and accordingly utilities, of VGR2806 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2806 gene: VGAM422 host target protein and VGAM423 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM422 and VGAM423.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2807(VGR2807) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of

which at least one host target gene is known in the art.

[92341] VGR2807 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2807 gene was detected is described hereinabove with reference to Figs. 1-9.

[92342] VGR2807 gene encodes VGR2807 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92343] VGR2807 precursor RNA folds spatially, forming VGR2807 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2807 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2807 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92344] VGR2807 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM424 precursor RNA, VGAM425 pre-

cursor RNA, VGAM426 precursor RNA, VGAM427 precursor RNA and VGAM428 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92345] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM424 RNA, VGAM425 RNA, VGAM426 RNA, VGAM427 RNA and VGAM428 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92346] VGAM424 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM424 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM424 host target RNA into VGAM424 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92347] VGAM425 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM425 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM425 host target RNA into VGAM425 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92348] VGAM426 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM426 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM426 host target RNA into

VGAM426 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92349] VGAM427 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM427 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM427 host target RNA into VGAM427 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92350] VGAM428 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM428 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM428 host target RNA into VGAM428 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92351] It is appreciated that a function of VGR2807 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2807 gene include diagnosis, prevention and treatment of viral infection by Rabies Virus. Specific functions, and accordingly utilities, of VGR2807 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2807 gene: VGAM424 host target protein, VGAM425 host target protein, VGAM426 host target protein, VGAM427 host target protein and VGAM428 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM424, VGAM425, VGAM426, VGAM427 and VGAM428.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here

as Viral Genomic Record 2808(VGR2808) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92352] VGR2808 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2808 gene was detected is described hereinabove with reference to Figs. 1-9.

[92353] VGR2808 gene encodes VGR2808 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92354] VGR2808 precursor RNA folds spatially, forming VGR2808 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2808 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2808 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[92355] VGR2808 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM429 precursor RNA, VGAM430 precursor RNA, VGAM431 precursor RNA, VGAM432 precursor RNA and VGAM433 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92356] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM429 RNA, VGAM430 RNA, VGAM431 RNA, VGAM432 RNA and VGAM433 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92357] VGAM429 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM429 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM429 host target RNA into VGAM429 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92358] VGAM430 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM430 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM430 host target RNA into VGAM430 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92359] VGAM431 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM431 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM431 host target RNA into VGAM431 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92360] VGAM432 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM432 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM432 host target RNA into VGAM432 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92361] VGAM433 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM433 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM433 host target RNA into VGAM433 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92362] It is appreciated that a function of VGR2808 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2808 gene include diagnosis, prevention and treatment of viral infection by Rabbit Hemorrhagic Disease Virus. Specific functions, and accordingly utilities, of VGR2808 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2808 gene: VGAM429 host target protein, VGAM430 host target protein, VGAM431 host target protein, VGAM432 host target protein and VGAM433 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN

through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM429, VGAM430, VGAM431, VGAM432 and VGAM433.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2809(VGR2809) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92363] VGR2809 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2809 gene was detected is described hereinabove with reference to Figs. 1-9.

[92364] VGR2809 gene encodes VGR2809 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92365] VGR2809 precursor RNA folds spatially, forming VGR2809 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2809 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2809 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92366] VGR2809 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM434 precursor RNA, VGAM435 precursor RNA and VGAM436 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92367] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM434 RNA, VGAM435 RNA and VGAM436 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92368] VGAM434 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM434 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM434 host target RNA into VGAM434 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92369] VGAM435 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM435 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM435 host target RNA into VGAM435 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92370] VGAM436 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM436 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM436 host target RNA into VGAM436 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92371] It is appreciated that a function of VGR2809 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2809 gene include diagnosis, prevention and treatment of viral infection by Sendai Virus. Specific functions, and accordingly utilities, of VGR2809 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2809 gene: VGAM434 host target protein,

VGAM435 host target protein and VGAM436 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM434, VGAM435 and VGAM436.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2810(VGR2810) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92372] VGR2810 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2810 gene was detected is described hereinabove with reference to Figs. 1-9.

[92373] VGR2810 gene encodes VGR2810 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92374] VGR2810 precursor RNA folds spatially, forming VGR2810 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2810 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2810 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92375] VGR2810 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM437 precursor RNA, VGAM438 precursor RNA and VGAM439 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92376] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM437 RNA, VGAM438 RNA and VGAM439 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92377] VGAM437 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM437 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM437 host target RNA into VGAM437 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92378] VGAM438 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM438 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM438 host target RNA into

VGAM438 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92379] VGAM439 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM439 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM439 host target RNA into VGAM439 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92380] It is appreciated that a function of VGR2810 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2810 gene include diagnosis, prevention and treatment of viral infection by Tomato Bushy Stunt Virus. Specific functions, and accordingly utilities, of VGR2810 gene correlate with, and may be deduced from, the identity of the host target genes,

which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2810 gene: VGAM437 host target protein, VGAM438 host target protein and VGAM439 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM437, VGAM438 and VGAM439.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2811(VGR2811) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92381] VGR2811 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2811 gene was detected is described hereinabove with reference to Figs. 1-9.

[92382] VGR2811 gene encodes VGR2811 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92383] VGR2811 precursor RNA folds spatially, forming VGR2811 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2811 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2811 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92384] VGR2811 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM441 precursor RNA and VGAM442 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92385] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM441 RNA and VGAM442 RNA, herein schematically represented

by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92386] VGAM441 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM441 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM441 host target RNA into VGAM441 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92387] VGAM442 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM442 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM442 host target RNA into

VGAM442 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92388] It is appreciated that a function of VGR2811 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2811 gene include diagnosis, prevention and treatment of viral infection by Vaccinia Virus. Specific functions, and accordingly utilities, of VGR2811 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2811 gene: VGAM441 host target protein and VGAM442 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM441 and VGAM442.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2812(VGR2812) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one

host target gene, the function and utility of which at least one host target gene is known in the art.

[92389] VGR2812 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2812 gene was detected is described hereinabove with reference to Figs. 1-9.

[92390] VGR2812 gene encodes VGR2812 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92391] VGR2812 precursor RNA folds spatially, forming VGR2812 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2812 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2812 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92392] VGR2812 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM443 precursor RNA and VGAM444 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92393] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM443 RNA and VGAM444 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92394] VGAM443 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM443 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM443 host target RNA into VGAM443 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92395] VGAM444 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM444 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM444 host target RNA into VGAM444 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92396] It is appreciated that a function of VGR2812 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2812 gene include diagnosis, prevention and treatment of viral infection by Vaccinia Virus. Specific functions, and accordingly utilities, of VGR2812 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2812 gene: VGAM443 host target protein

and VGAM444 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM443 and VGAM444.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2813(VGR2813) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92397] VGR2813 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2813 gene was detected is described hereinabove with reference to Figs. 1-9.

[92398] VGR2813 gene encodes VGR2813 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92399] VGR2813 precursor RNA folds spatially, forming VGR2813 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2813 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2813 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92400] VGR2813 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM445 precursor RNA and VGAM446 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92401] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM445 RNA and VGAM446 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92402] VGAM445 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM445 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM445 host target RNA into VGAM445 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92403] VGAM446 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM446 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM446 host target RNA into VGAM446 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92404] It is appreciated that a function of VGR2813 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2813 gene include diagnosis, prevention and treatment of viral infection by Human Papillomavirus Type 17. Specific functions, and accordingly utilities, of VGR2813 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2813 gene: VGAM445 host target protein and VGAM446 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM445 and VGAM446.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2814(VGR2814) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92405] VGR2814 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2814 gene was detected is described hereinabove with reference to Figs. 1-9.

[92406] VGR2814 gene encodes VGR2814 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92407] VGR2814 precursor RNA folds spatially, forming VGR2814 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2814 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2814 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92408] VGR2814 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM447 precursor RNA and VGAM448 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92409] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM447 RNA and VGAM448 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92410] VGAM447 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM447 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM447 host target RNA into VGAM447 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92411] VGAM448 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM448 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM448 host target RNA into VGAM448 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92412] It is appreciated that a function of VGR2814 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2814 gene include diagnosis, prevention and treatment of viral infection by Human Papillomavirus Type 40. Specific functions, and accordingly utilities, of VGR2814 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2814 gene: VGAM447 host target protein and VGAM448 host target protein, herein schematically represented by VGAM1 HOST TARGET

PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM447 and VGAM448.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2815(VGR2815) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92413] VGR2815 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2815 gene was detected is described hereinabove with reference to Figs. 1-9.

[92414] VGR2815 gene encodes VGR2815 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92415] VGR2815 precursor RNA folds spatially, forming VGR2815 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2815 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2815 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92416] VGR2815 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM450 precursor RNA, VGAM451 precursor RNA and VGAM452 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92417] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM450 RNA, VGAM451 RNA and VGAM452 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92418] VGAM450 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM450 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM450 host target RNA into VGAM450 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92419] VGAM451 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM451 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM451 host target RNA into VGAM451 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92420] VGAM452 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM452 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM452 host target RNA into VGAM452 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92421] It is appreciated that a function of VGR2815 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2815 gene include diagnosis, prevention and treatment of viral infection by Cardamine Chlorotic Fleck Virus. Specific functions, and accordingly utilities, of VGR2815 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2815 gene: VGAM450

host target protein, VGAM451 host target protein and VGAM452 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM450, VGAM451 and VGAM452.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2816(VGR2816) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92422] VGR2816 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2816 gene was detected is described hereinabove with reference to Figs. 1-9.

[92423] VGR2816 gene encodes VGR2816 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92424] VGR2816 precursor RNA folds spatially, forming VGR2816 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2816 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2816 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92425] VGR2816 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM453 precursor RNA, VGAM454 precursor RNA and VGAM455 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92426] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM453 RNA, VGAM454 RNA and VGAM455 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92427] VGAM453 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM453 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM453 host target RNA into VGAM453 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92428] VGAM454 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM454 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM454 host target RNA into

VGAM454 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92429] VGAM455 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM455 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM455 host target RNA into VGAM455 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92430] It is appreciated that a function of VGR2816 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2816 gene include diagnosis, prevention and treatment of viral infection by Borna Disease Virus. Specific functions, and accordingly utilities, of VGR2816 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2816 gene: VGAM453 host target protein, VGAM454 host target protein and VGAM455 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM453, VGAM454 and VGAM455.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2817(VGR2817) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92431] VGR2817 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2817 gene was detected is described hereinabove with reference to Figs. 1-9.

[92432] VGR2817 gene encodes VGR2817 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92433] VGR2817 precursor RNA folds spatially, forming VGR2817 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2817 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2817 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92434] VGR2817 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM456 precursor RNA and VGAM457 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92435] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM456 RNA and VGAM457 RNA, herein schematically represented

by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92436] VGAM456 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM456 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM456 host target RNA into VGAM456 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92437] VGAM457 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM457 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM457 host target RNA into

VGAM457 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92438] It is appreciated that a function of VGR2817 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2817 gene include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGR2817 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2817 gene: VGAM456 host target protein and VGAM457 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM456 and VGAM457.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2818(VGR2818) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one

host target gene, the function and utility of which at least one host target gene is known in the art.

[92439] VGR2818 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2818 gene was detected is described hereinabove with reference to Figs. 1-9.

[92440] VGR2818 gene encodes VGR2818 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92441] VGR2818 precursor RNA folds spatially, forming VGR2818 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2818 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2818 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92442] VGR2818 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM458 precursor RNA and VGAM459 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92443] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM458 RNA and VGAM459 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92444] VGAM458 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM458 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM458 host target RNA into VGAM458 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92445] VGAM459 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM459 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM459 host target RNA into VGAM459 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92446] It is appreciated that a function of VGR2818 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2818 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR2818 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2818 gene: VGAM458 host

target protein and VGAM459 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM458 and VGAM459.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2819(VGR2819) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92447] VGR2819 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2819 gene was detected is described hereinabove with reference to Figs. 1-9.

[92448] VGR2819 gene encodes VGR2819 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92449] VGR2819 precursor RNA folds spatially, forming VGR2819 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2819 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2819 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92450] VGR2819 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM462 precursor RNA, VGAM463 precursor RNA and VGAM464 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92451] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM462 RNA, VGAM463 RNA and VGAM464 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 1.

[92452] VGAM462 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM462 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM462 host target RNA into VGAM462 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92453] VGAM463 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM463 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM463 host target RNA into VGAM463 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92454] VGAM464 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM464 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM464 host target RNA into VGAM464 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92455] It is appreciated that a function of VGR2819 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2819 gene include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGR2819 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like`

cluster of VGR2819 gene: VGAM462 host target protein, VGAM463 host target protein and VGAM464 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM462, VGAM463 and VGAM464.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2820(VGR2820) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92456] VGR2820 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2820 gene was detected is described hereinabove with reference to Figs. 1-9.

[92457] VGR2820 gene encodes VGR2820 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92458] VGR2820 precursor RNA folds spatially, forming VGR2820

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2820 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2820 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92459] VGR2820 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM466 precursor RNA and VGAM467 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92460] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM466 RNA and VGAM467 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[92461] VGAM466 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM466 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM466 host target RNA into VGAM466 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92462] VGAM467 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM467 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM467 host target RNA into VGAM467 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92463] It is appreciated that a function of VGR2820 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2820 gene include diagnosis, prevention and treatment of viral infection by Autographa Californica Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2820 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2820 gene: VGAM466 host target protein and VGAM467 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM466 and VGAM467.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2821(VGR2821) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the

function and utility of which at least one host target gene is known in the art.

[92464] VGR2821 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2821 gene was detected is described hereinabove with reference to Figs. 1-9.

[92465] VGR2821 gene encodes VGR2821 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92466] VGR2821 precursor RNA folds spatially, forming VGR2821 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2821 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2821 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92467] VGR2821 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM

precursor RNAs, VGAM472 precursor RNA, VGAM473 precursor RNA, VGAM474 precursor RNA, VGAM475 precursor RNA and VGAM476 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92468] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM472 RNA, VGAM473 RNA, VGAM474 RNA, VGAM475 RNA and VGAM476 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92469] VGAM472 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM472 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM472 host target RNA into

VGAM472 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92470] VGAM473 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM473 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM473 host target RNA into VGAM473 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92471] VGAM474 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM474 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM474 host target RNA into VGAM474 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92472] VGAM475 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM475 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM475 host target RNA into VGAM475 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92473] VGAM476 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM476 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM476 host target RNA into VGAM476 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92474] It is appreciated that a function of VGR2821 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2821 gene include diagnosis, prevention and treatment of viral infection by Tick-borne Encephalitis Virus. Specific functions, and accordingly utilities, of VGR2821 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2821 gene: VGAM472 host target protein, VGAM473 host target protein, VGAM474 host target protein, VGAM475 host target protein and VGAM476 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM472, VGAM473, VGAM474, VGAM475 and VGAM476.Fig. 9 further provides a conceptual de-

scription of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2822(VGR2822) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92475] VGR2822 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2822 gene was detected is described hereinabove with reference to Figs. 1-9.

[92476] VGR2822 gene encodes VGR2822 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92477] VGR2822 precursor RNA folds spatially, forming VGR2822 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2822 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2822 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92478] VGR2822 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM477 precursor RNA, VGAM478 precursor RNA, VGAM479 precursor RNA, VGAM480 precursor RNA, VGAM481 precursor RNA, VGAM482 precursor RNA, VGAM483 precursor RNA and VGAM484 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92479] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM477 RNA, VGAM478 RNA, VGAM479 RNA, VGAM480 RNA, VGAM481 RNA, VGAM482 RNA, VGAM483 RNA and VGAM484 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92480] VGAM477 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM477 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM477 host target RNA into VGAM477 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92481] VGAM478 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM478 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM478 host target RNA into VGAM478 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92482] VGAM479 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM479 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM479 host target RNA into VGAM479 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92483] VGAM480 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM480 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM480 host target RNA into VGAM480 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92484] VGAM481 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM481 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM481 host target RNA into VGAM481 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92485] VGAM482 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM482 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM482 host target RNA into VGAM482 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92486] VGAM483 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM483 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM483 host target RNA into VGAM483 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92487] VGAM484 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM484 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM484 host target RNA into

VGAM484 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92488] It is appreciated that a function of VGR2822 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2822 gene include diagnosis, prevention and treatment of viral infection by Hepatitis G Virus. Specific functions, and accordingly utilities, of VGR2822 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2822 gene: VGAM477 host target protein, VGAM478 host target protein, VGAM479 host target protein, VGAM480 host target protein, VGAM481 host target protein, VGAM482 host target protein, VGAM483 host target protein and VGAM484 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM477, VGAM478, VGAM479, VGAM480, VGAM481, VGAM482, VGAM483 and VGAM484.Fig. 9 further provides a concep-

tual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2823(VGR2823) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92489] VGR2823 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2823 gene was detected is described hereinabove with reference to Figs. 1-9.

[92490] VGR2823 gene encodes VGR2823 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92491] VGR2823 precursor RNA folds spatially, forming VGR2823 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2823 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2823 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92492] VGR2823 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM485 precursor RNA, VGAM486 precursor RNA, VGAM487 precursor RNA, VGAM488 precursor RNA, VGAM489 precursor RNA, VGAM490 precursor RNA, VGAM491 precursor RNA and VGAM492 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92493] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM485 RNA, VGAM486 RNA, VGAM487 RNA, VGAM488 RNA, VGAM489 RNA, VGAM490 RNA, VGAM491 RNA and VGAM492 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92494] VGAM485 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM485 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM485 host target RNA into VGAM485 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92495] VGAM486 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM486 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM486 host target RNA into VGAM486 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92496] VGAM487 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM487 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM487 host target RNA into VGAM487 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92497] VGAM488 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM488 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM488 host target RNA into VGAM488 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92498] VGAM489 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM489 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM489 host target RNA into VGAM489 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92499] VGAM490 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM490 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM490 host target RNA into VGAM490 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92500] VGAM491 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM491 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM491 host target RNA into VGAM491 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92501] VGAM492 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM492 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM492 host target RNA into

VGAM492 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92502] It is appreciated that a function of VGR2823 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2823 gene include diagnosis, prevention and treatment of viral infection by Hepatitis G Virus. Specific functions, and accordingly utilities, of VGR2823 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2823 gene: VGAM485 host target protein, VGAM486 host target protein, VGAM487 host target protein, VGAM488 host target protein, VGAM489 host target protein, VGAM490 host target protein, VGAM491 host target protein and VGAM492 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM485, VGAM486, VGAM487, VGAM488, VGAM489, VGAM490, VGAM491 and VGAM492.Fig. 9 further provides a concep-

tual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2824(VGR2824) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92503] VGR2824 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2824 gene was detected is described hereinabove with reference to Figs. 1-9.

[92504] VGR2824 gene encodes VGR2824 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92505] VGR2824 precursor RNA folds spatially, forming VGR2824 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2824 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2824 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92506] VGR2824 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM493 precursor RNA, VGAM494 precursor RNA and VGAM495 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92507] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM493 RNA, VGAM494 RNA and VGAM495 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92508] VGAM493 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM493 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM493 host target RNA into VGAM493 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92509] VGAM494 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM494 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM494 host target RNA into VGAM494 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92510] VGAM495 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM495 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM495 host target RNA into VGAM495 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92511] It is appreciated that a function of VGR2824 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2824 gene include diagnosis, prevention and treatment of viral infection by Hepatitis G Virus. Specific functions, and accordingly utilities, of VGR2824 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2824 gene: VGAM493 host target protein, VGAM494 host target protein and VGAM495 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target

genes is elaborated hereinabove with reference to VGAM493, VGAM494 and VGAM495.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2825(VGR2825) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92512] VGR2825 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2825 gene was detected is described hereinabove with reference to Figs. 1-9.

[92513] VGR2825 gene encodes VGR2825 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92514] VGR2825 precursor RNA folds spatially, forming VGR2825 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2825 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2825 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92515] VGR2825 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM496 precursor RNA and VGAM497 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92516] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM496 RNA and VGAM497 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92517] VGAM496 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM496 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM496 host target RNA into VGAM496 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92518] VGAM497 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM497 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM497 host target RNA into VGAM497 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92519] It is appreciated that a function of VGR2825 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2825 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 7. Specific functions, and accordingly utilities, of VGR2825 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2825 gene: VGAM496 host target protein and VGAM497 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM496 and VGAM497.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2826(VGR2826) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92520] VGR2826 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2826 gene was detected is described hereinabove with reference to Figs.

1-9.

[92521] VGR2826 gene encodes VGR2826 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92522] VGR2826 precursor RNA folds spatially, forming VGR2826 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2826 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2826 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92523] VGR2826 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM499 precursor RNA and VGAM500 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92524] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM499 RNA and VGAM500 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92525] VGAM499 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM499 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM499 host target RNA into VGAM499 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92526] VGAM500 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM500 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM500 host target RNA into VGAM500 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92527] It is appreciated that a function of VGR2826 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2826 gene include diagnosis, prevention and treatment of viral infection by Strawberry Vein Banding Virus (SVBV). Specific functions, and accordingly utilities, of VGR2826 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2826 gene: VGAM499 host target protein and VGAM500 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM499 and VGAM500.Fig. 9 further provides a conceptual description of novel bioin-

formatically detected regulatory viral gene, referred to here as Viral Genomic Record 2827(VGR2827) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92528] VGR2827 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2827 gene was detected is described hereinabove with reference to Figs. 1-9.

[92529] VGR2827 gene encodes VGR2827 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92530] VGR2827 precursor RNA folds spatially, forming VGR2827 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2827 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2827 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92531] VGR2827 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM501 precursor RNA and VGAM502 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92532] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM501 RNA and VGAM502 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92533] VGAM501 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM501 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM501 host target RNA into VGAM501 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92534] VGAM502 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM502 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM502 host target RNA into VGAM502 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92535] It is appreciated that a function of VGR2827 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2827 gene include diagnosis, prevention and treatment of viral infection by

Carrot Mottle Mimic Virus. Specific functions, and accordingly utilities, of VGR2827 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2827 gene: VGAM501 host target protein and VGAM502 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM501 and VGAM502.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2828(VGR2828) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92536] VGR2828 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2828 gene was detected is described hereinabove with reference to Figs. 1-9.

[92537] VGR2828 gene encodes VGR2828 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92538] VGR2828 precursor RNA folds spatially, forming VGR2828 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2828 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2828 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92539] VGR2828 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM506 precursor RNA, VGAM507 precursor RNA and VGAM508 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92540] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM506 RNA, VGAM507 RNA and VGAM508 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92541] VGAM506 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM506 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM506 host target RNA into VGAM506 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92542] VGAM507 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM507 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM507 host target RNA into VGAM507 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92543] VGAM508 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM508 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM508 host target RNA into VGAM508 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92544] It is appreciated that a function of VGR2828 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2828 gene include

diagnosis, prevention and treatment of viral infection by Saguaro Cactus Virus. Specific functions, and accordingly utilities, of VGR2828 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2828 gene: VGAM506 host target protein, VGAM507 host target protein and VGAM508 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM506, VGAM507 and VGAM508.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2829(VGR2829) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92545] VGR2829 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2829 gene was detected is described hereinabove with reference to Figs.

1-9.

[92546] VGR2829 gene encodes VGR2829 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92547] VGR2829 precursor RNA folds spatially, forming VGR2829 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2829 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2829 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92548] VGR2829 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM509 precursor RNA and VGAM510 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92549] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM509 RNA and VGAM510 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92550] VGAM509 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM509 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM509 host target RNA into VGAM509 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92551] VGAM510 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM510 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM510 host target RNA into VGAM510 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92552] It is appreciated that a function of VGR2829 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2829 gene include diagnosis, prevention and treatment of viral infection by Papaya Ringspot Virus. Specific functions, and accordingly utilities, of VGR2829 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2829 gene: VGAM509 host target protein and VGAM510 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM509 and VGAM510.Fig. 9 further provides a conceptual description of novel bioinformati-

cally detected regulatory viral gene, referred to here as Viral Genomic Record 2830(VGR2830) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92553] VGR2830 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2830 gene was detected is described hereinabove with reference to Figs. 1-9.

[92554] VGR2830 gene encodes VGR2830 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92555] VGR2830 precursor RNA folds spatially, forming VGR2830 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2830 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2830 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[92556] VGR2830 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM511 precursor RNA, VGAM512 precursor RNA, VGAM513 precursor RNA, VGAM514 precursor RNA and VGAM515 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92557] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM511 RNA, VGAM512 RNA, VGAM513 RNA, VGAM514 RNA and VGAM515 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92558] VGAM511 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM511 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM511 host target RNA into VGAM511 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92559] VGAM512 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM512 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM512 host target RNA into VGAM512 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92560] VGAM513 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM513 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM513 host target RNA into VGAM513 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92561] VGAM514 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM514 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM514 host target RNA into VGAM514 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92562] VGAM515 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM515 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM515 host target RNA into VGAM515 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92563] It is appreciated that a function of VGR2830 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2830 gene include diagnosis, prevention and treatment of viral infection by Cucumber Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGR2830 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2830 gene: VGAM511 host target protein, VGAM512 host target protein, VGAM513 host target protein, VGAM514 host target protein and VGAM515 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN

through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM511, VGAM512, VGAM513, VGAM514 and VGAM515.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2831(VGR2831) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92564] VGR2831 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2831 gene was detected is described hereinabove with reference to Figs. 1-9.

[92565] VGR2831 gene encodes VGR2831 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92566] VGR2831 precursor RNA folds spatially, forming VGR2831 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2831 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2831 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92567] VGR2831 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM516 precursor RNA and VGAM517 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92568] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM516 RNA and VGAM517 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92569] VGAM516 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM516 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM516 host target RNA into VGAM516 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92570] VGAM517 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM517 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM517 host target RNA into VGAM517 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92571] It is appreciated that a function of VGR2831 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2831 gene include diagnosis, prevention and treatment of viral infection by Galinsoga Mosaic Virus. Specific functions, and accordingly utilities, of VGR2831 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2831 gene: VGAM516 host target protein and VGAM517 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM516 and VGAM517.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2832(VGR2832) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92572] VGR2832 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2832 gene was detected is described hereinabove with reference to Figs. 1-9.

[92573] VGR2832 gene encodes VGR2832 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92574] VGR2832 precursor RNA folds spatially, forming VGR2832 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2832 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2832 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92575] VGR2832 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM519 precursor RNA and VGAM520 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92576] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM519 RNA and VGAM520 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92577] VGAM519 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM519 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM519 host target RNA into VGAM519 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92578] VGAM520 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM520 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM520 host target RNA into VGAM520 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92579] It is appreciated that a function of VGR2832 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2832 gene include diagnosis, prevention and treatment of viral infection by Lymphocystis Disease Virus 1. Specific functions, and accordingly utilities, of VGR2832 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2832 gene: VGAM519 host target protein and VGAM520 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-

above with reference to VGAM519 and VGAM520.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2833(VGR2833) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92580] VGR2833 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2833 gene was detected is described hereinabove with reference to Figs. 1-9.

[92581] VGR2833 gene encodes VGR2833 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92582] VGR2833 precursor RNA folds spatially, forming VGR2833 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2833 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2833 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92583] VGR2833 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM521 precursor RNA and VGAM522 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92584] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM521 RNA and VGAM522 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92585] VGAM521 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM521 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM521 host target RNA into VGAM521 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92586] VGAM522 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM522 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM522 host target RNA into VGAM522 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92587] It is appreciated that a function of VGR2833 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2833 gene include diagnosis, prevention and treatment of viral infection by Lymphocystis Disease Virus 1. Specific functions, and accordingly utilities, of VGR2833 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2833 gene: VGAM521 host target protein and VGAM522 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM521 and VGAM522.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2834(VGR2834) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92588] VGR2834 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2834 gene was

detected is described hereinabove with reference to Figs. 1-9.

[92589] VGR2834 gene encodes VGR2834 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92590] VGR2834 precursor RNA folds spatially, forming VGR2834 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2834 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2834 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92591] VGR2834 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM523 precursor RNA and VGAM524 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM

FOLDED PRECURSOR RNA of Fig. 1.

[92592] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM523 RNA and VGAM524 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92593] VGAM523 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM523 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM523 host target RNA into VGAM523 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92594] VGAM524 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM524 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM524 host target RNA into VGAM524 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92595] It is appreciated that a function of VGR2834 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2834 gene include diagnosis, prevention and treatment of viral infection by Murid Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2834 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2834 gene: VGAM523 host target protein and VGAM524 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM523 and VGAM524.Fig. 9 further

provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2835(VGR2835) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92596] VGR2835 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2835 gene was detected is described hereinabove with reference to Figs. 1-9.

[92597] VGR2835 gene encodes VGR2835 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92598] VGR2835 precursor RNA folds spatially, forming VGR2835 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2835 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2835 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92599] VGR2835 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM525 precursor RNA and VGAM526 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92600] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM525 RNA and VGAM526 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92601] VGAM525 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM525 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM525 host target RNA into VGAM525 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92602] VGAM526 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM526 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM526 host target RNA into VGAM526 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92603] It is appreciated that a function of VGR2835 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2835 gene include diagnosis, prevention and treatment of viral infection by

Murid Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2835 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2835 gene: VGAM525 host target protein and VGAM526 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM525 and VGAM526.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2836(VGR2836) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92604] VGR2836 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2836 gene was detected is described hereinabove with reference to Figs. 1-9.

[92605] VGR2836 gene encodes VGR2836 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92606] VGR2836 precursor RNA folds spatially, forming VGR2836 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2836 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2836 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92607] VGR2836 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM536 precursor RNA and VGAM537 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92608] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM536 RNA and VGAM537 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92609] VGAM536 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM536 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM536 host target RNA into VGAM536 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92610] VGAM537 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM537 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM537 host target RNA into VGAM537 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92611] It is appreciated that a function of VGR2836 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2836 gene include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2836 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2836 gene: VGAM536 host target protein and VGAM537 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM536 and VGAM537.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2837(VGR2837) viral gene, which en-

codes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92612] VGR2837 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2837 gene was detected is described hereinabove with reference to Figs. 1-9.

[92613] VGR2837 gene encodes VGR2837 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92614] VGR2837 precursor RNA folds spatially, forming VGR2837 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2837 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2837 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92615] VGR2837 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM539 precursor RNA, VGAM540 precursor RNA and VGAM541 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92616] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM539 RNA, VGAM540 RNA and VGAM541 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92617] VGAM539 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM539 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM539 host target RNA into VGAM539 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92618] VGAM540 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM540 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM540 host target RNA into VGAM540 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92619] VGAM541 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM541 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM541 host target RNA into VGAM541 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92620] It is appreciated that a function of VGR2837 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2837 gene include diagnosis, prevention and treatment of viral infection by Bovine Respiratory Syncytial Virus. Specific functions, and accordingly utilities, of VGR2837 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2837 gene: VGAM539 host target protein, VGAM540 host target protein and VGAM541 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM539, VGAM540 and VGAM541.Fig. 9 further provides a conceptual description of novel bioinformatically

detected regulatory viral gene, referred to here as Viral Genomic Record 2838(VGR2838) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92621] VGR2838 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2838 gene was detected is described hereinabove with reference to Figs. 1-9.

[92622] VGR2838 gene encodes VGR2838 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92623] VGR2838 precursor RNA folds spatially, forming VGR2838 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2838 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2838 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[92624] VGR2838 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM546 precursor RNA and VGAM547 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92625] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM546 RNA and VGAM547 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92626] VGAM546 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM546 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM546 host target RNA into VGAM546 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92627] VGAM547 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM547 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM547 host target RNA into VGAM547 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92628] It is appreciated that a function of VGR2838 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2838 gene include diagnosis, prevention and treatment of viral infection by Peanut Stunt Virus. Specific functions, and accordingly

utilities, of VGR2838 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2838 gene: VGAM546 host target protein and VGAM547 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM546 and VGAM547.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2839(VGR2839) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92629] VGR2839 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2839 gene was detected is described hereinabove with reference to Figs. 1-9.

[92630] VGR2839 gene encodes VGR2839 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[92631] VGR2839 precursor RNA folds spatially, forming VGR2839 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2839 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2839 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92632] VGR2839 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM550 precursor RNA and VGAM551 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92633] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM550

RNA and VGAM551 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92634] VGAM550 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM550 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM550 host target RNA into VGAM550 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92635] VGAM551 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM551 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM551 host target RNA into VGAM551 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92636] It is appreciated that a function of VGR2839 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2839 gene include diagnosis, prevention and treatment of viral infection by Leishmania RNA Virus 2-1. Specific functions, and accordingly utilities, of VGR2839 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2839 gene: VGAM550 host target protein and VGAM551 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM550 and VGAM551.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2840(VGR2840) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-

like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92637] VGR2840 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2840 gene was detected is described hereinabove with reference to Figs. 1-9.

[92638] VGR2840 gene encodes VGR2840 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92639] VGR2840 precursor RNA folds spatially, forming VGR2840 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2840 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2840 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92640] VGR2840 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM554 precursor RNA, VGAM555 precursor RNA and VGAM556 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92641] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM554 RNA, VGAM555 RNA and VGAM556 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92642] VGAM554 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM554 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM554 host target RNA into VGAM554 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92643] VGAM555 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM555 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM555 host target RNA into VGAM555 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92644] VGAM556 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM556 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM556 host target RNA into VGAM556 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92645] It is appreciated that a function of VGR2840 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2840 gene include diagnosis, prevention and treatment of viral infection by Spodoptera Exigua Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2840 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2840 gene: VGAM554 host target protein, VGAM555 host target protein and VGAM556 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM554, VGAM555 and VGAM556.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to

here as Viral Genomic Record 2841(VGR2841) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92646] VGR2841 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2841 gene was detected is described hereinabove with reference to Figs. 1-9.

[92647] VGR2841 gene encodes VGR2841 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92648] VGR2841 precursor RNA folds spatially, forming VGR2841 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2841 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2841 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[92649] VGR2841 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM562 precursor RNA, VGAM563 precursor RNA and VGAM564 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92650] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM562 RNA, VGAM563 RNA and VGAM564 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92651] VGAM562 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM562 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM562 host target RNA into VGAM562 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92652] VGAM563 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM563 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM563 host target RNA into VGAM563 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92653] VGAM564 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM564 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM564 host target RNA into VGAM564 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92654] It is appreciated that a function of VGR2841 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2841 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2841 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2841 gene: VGAM562 host target protein, VGAM563 host target protein and VGAM564 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to

VGAM562, VGAM563 and VGAM564.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2842(VGR2842) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92655] VGR2842 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2842 gene was detected is described hereinabove with reference to Figs. 1-9.

[92656] VGR2842 gene encodes VGR2842 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92657] VGR2842 precursor RNA folds spatially, forming VGR2842 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2842 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2842 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92658] VGR2842 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM565 precursor RNA and VGAM566 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92659] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM565 RNA and VGAM566 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92660] VGAM565 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM565 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM565 host target RNA into VGAM565 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92661] VGAM566 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM566 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM566 host target RNA into VGAM566 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92662] It is appreciated that a function of VGR2842 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2842 gene include

diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2842 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2842 gene: VGAM565 host target protein and VGAM566 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM565 and VGAM566.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2843(VGR2843) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92663] VGR2843 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2843 gene was detected is described hereinabove with reference to Figs. 1-9.

[92664] VGR2843 gene encodes VGR2843 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92665] VGR2843 precursor RNA folds spatially, forming VGR2843 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2843 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2843 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92666] VGR2843 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM567 precursor RNA, VGAM568 precursor RNA, VGAM569 precursor RNA and VGAM570 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92667] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM567 RNA, VGAM568 RNA, VGAM569 RNA and VGAM570 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92668] VGAM567 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM567 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM567 host target RNA into VGAM567 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92669] VGAM568 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM568 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM568 host target RNA into VGAM568 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92670] VGAM569 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM569 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM569 host target RNA into VGAM569 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92671] VGAM570 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM570 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM570 host target RNA into VGAM570 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92672] It is appreciated that a function of VGR2843 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2843 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2843 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2843 gene: VGAM567 host target protein, VGAM568 host target protein, VGAM569 host target protein and VGAM570 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The

function of these host target genes is elaborated herein-above with reference to VGAM567, VGAM568, VGAM569 and VGAM570.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2844(VGR2844) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92673] VGR2844 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2844 gene was detected is described hereinabove with reference to Figs. 1-9.

[92674] VGR2844 gene encodes VGR2844 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92675] VGR2844 precursor RNA folds spatially, forming VGR2844 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2844 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2844 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92676] VGR2844 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM571 precursor RNA, VGAM572 precursor RNA, VGAM573 precursor RNA and VGAM574 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92677] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM571 RNA, VGAM572 RNA, VGAM573 RNA and VGAM574 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92678] VGAM571 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM571 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM571 host target RNA into VGAM571 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92679] VGAM572 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM572 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM572 host target RNA into VGAM572 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92680] VGAM573 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM573 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM573 host target RNA into VGAM573 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92681] VGAM574 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM574 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM574 host target RNA into VGAM574 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92682] It is appreciated that a function of VGR2844 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2844 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2844 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2844 gene: VGAM571 host target protein, VGAM572 host target protein, VGAM573 host target protein and VGAM574 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM571, VGAM572, VGAM573 and VGAM574.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2845(VGR2845) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one

host target gene, the function and utility of which at least one host target gene is known in the art.

[92683] VGR2845 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2845 gene was detected is described hereinabove with reference to Figs. 1-9.

[92684] VGR2845 gene encodes VGR2845 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92685] VGR2845 precursor RNA folds spatially, forming VGR2845 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2845 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2845 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92686] VGR2845 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM575 precursor RNA and VGAM576 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92687] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM575 RNA and VGAM576 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92688] VGAM575 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM575 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM575 host target RNA into VGAM575 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92689] VGAM576 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM576 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM576 host target RNA into VGAM576 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92690] It is appreciated that a function of VGR2845 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2845 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2845 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2845 gene: VGAM575 host

target protein and VGAM576 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM575 and VGAM576.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2846(VGR2846) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92691] VGR2846 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2846 gene was detected is described hereinabove with reference to Figs. 1-9.

[92692] VGR2846 gene encodes VGR2846 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92693] VGR2846 precursor RNA folds spatially, forming VGR2846 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2846 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2846 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92694] VGR2846 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM577 precursor RNA and VGAM578 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92695] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM577 RNA and VGAM578 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92696] VGAM577 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM577 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM577 host target RNA into VGAM577 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92697] VGAM578 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM578 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM578 host target RNA into VGAM578 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92698] It is appreciated that a function of VGR2846 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2846 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2846 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2846 gene: VGAM577 host target protein and VGAM578 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM577 and VGAM578.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2847(VGR2847) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92699] VGR2847 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2847 gene was detected is described hereinabove with reference to Figs. 1-9.

[92700] VGR2847 gene encodes VGR2847 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92701] VGR2847 precursor RNA folds spatially, forming VGR2847 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2847 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2847 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92702] VGR2847 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM580 precursor RNA and VGAM581 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92703] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM580 RNA and VGAM581 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92704] VGAM580 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM580 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM580 host target RNA into VGAM580 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92705] VGAM581 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM581 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM581 host target RNA into VGAM581 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92706] It is appreciated that a function of VGR2847 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2847 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2847 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2847 gene: VGAM580 host target protein and VGAM581 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The func-

tion of these host target genes is elaborated hereinabove with reference to VGAM580 and VGAM581.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2848(VGR2848) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92707] VGR2848 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2848 gene was detected is described hereinabove with reference to Figs. 1-9.

[92708] VGR2848 gene encodes VGR2848 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92709] VGR2848 precursor RNA folds spatially, forming VGR2848 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2848 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2848 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92710] VGR2848 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM585 precursor RNA, VGAM586 precursor RNA and VGAM587 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92711] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM585 RNA, VGAM586 RNA and VGAM587 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92712] VGAM585 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM585 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM585 host target RNA into VGAM585 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92713] VGAM586 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM586 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM586 host target RNA into VGAM586 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92714] VGAM587 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM587 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM587 host target RNA into VGAM587 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92715] It is appreciated that a function of VGR2848 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2848 gene include diagnosis, prevention and treatment of viral infection by Gallid Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2848 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2848 gene: VGAM585 host target protein, VGAM586 host target protein and VGAM587 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM585, VGAM586 and VGAM587.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2849(VGR2849) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92716] VGR2849 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2849 gene was detected is described hereinabove with reference to Figs. 1-9.

[92717] VGR2849 gene encodes VGR2849 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92718] VGR2849 precursor RNA folds spatially, forming VGR2849 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2849 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2849 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92719] VGR2849 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM588 precursor RNA, VGAM589 precursor RNA and VGAM590 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92720] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM588 RNA, VGAM589 RNA and VGAM590 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92721] VGAM588 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM588 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM588 host target RNA into VGAM588 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92722] VGAM589 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM589 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM589 host target RNA into VGAM589 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92723] VGAM590 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM590 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM590 host target RNA into VGAM590 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92724] It is appreciated that a function of VGR2849 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2849 gene include diagnosis, prevention and treatment of viral infection by Gallid Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2849 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2849 gene: VGAM588 host

target protein, VGAM589 host target protein and VGAM590 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM588, VGAM589 and VGAM590.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2850(VGR2850) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92725] VGR2850 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2850 gene was detected is described hereinabove with reference to Figs. 1-9.

[92726] VGR2850 gene encodes VGR2850 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92727] VGR2850 precursor RNA folds spatially, forming VGR2850 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2850 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2850 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92728] VGR2850 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM591 precursor RNA and VGAM592 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92729] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM591 RNA and VGAM592 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92730] VGAM591 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM591 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM591 host target RNA into VGAM591 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92731] VGAM592 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM592 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM592 host target RNA into VGAM592 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92732] It is appreciated that a function of VGR2850 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2850 gene include diagnosis, prevention and treatment of viral infection by Gallid Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2850 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2850 gene: VGAM591 host target protein and VGAM592 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM591 and VGAM592.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2851(VGR2851) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92733] VGR2851 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2851 gene was detected is described hereinabove with reference to Figs. 1-9.

[92734] VGR2851 gene encodes VGR2851 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92735] VGR2851 precursor RNA folds spatially, forming VGR2851 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2851 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2851 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92736] VGR2851 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM594 precursor RNA, VGAM595 precursor RNA and VGAM596 precursor RNA, herein

schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92737] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM594 RNA, VGAM595 RNA and VGAM596 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92738] VGAM594 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM594 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM594 host target RNA into VGAM594 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92739] VGAM595 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM595 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM595 host target RNA into VGAM595 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92740] VGAM596 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM596 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM596 host target RNA into VGAM596 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92741] It is appreciated that a function of VGR2851 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2851 gene include diagnosis, prevention and treatment of viral infection by Northern Cereal Mosaic Virus. Specific functions, and accordingly utilities, of VGR2851 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2851 gene: VGAM594 host target protein, VGAM595 host target protein and VGAM596 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM594, VGAM595 and VGAM596.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2852(VGR2852) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of

at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92742] VGR2852 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2852 gene was detected is described hereinabove with reference to Figs. 1-9.

[92743] VGR2852 gene encodes VGR2852 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92744] VGR2852 precursor RNA folds spatially, forming VGR2852 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2852 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2852 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92745] VGR2852 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM597 precursor RNA, VGAM598 precursor RNA, VGAM599 precursor RNA, VGAM600 precursor RNA, VGAM601 precursor RNA, VGAM602 precursor RNA, VGAM603 precursor RNA and VGAM604 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92746] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM597 RNA, VGAM598 RNA, VGAM599 RNA, VGAM600 RNA, VGAM601 RNA, VGAM602 RNA, VGAM603 RNA and VGAM604 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92747] VGAM597 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM597 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM597 host target RNA into VGAM597 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92748] VGAM598 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM598 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM598 host target RNA into VGAM598 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92749] VGAM599 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM599 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM599 host target RNA into VGAM599 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92750] VGAM600 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM600 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM600 host target RNA into VGAM600 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92751] VGAM601 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM601 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM601 host target RNA into VGAM601 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92752] VGAM602 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM602 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM602 host target RNA into VGAM602 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92753] VGAM603 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM603 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM603 host target RNA into VGAM603 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92754] VGAM604 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM604 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM604 host target RNA into VGAM604 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92755] It is appreciated that a function of VGR2852 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2852 gene include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGR2852 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2852 gene: VGAM597 host target protein, VGAM598 host target protein, VGAM599 host target protein, VGAM600 host target protein, VGAM601 host target protein, VGAM602 host target protein, VGAM603 host target protein and VGAM604 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM597, VGAM598, VGAM599, VGAM600, VGAM601, VGAM602, VGAM603 and VGAM604.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2853(VGR2853) viral gene, which encodes an

`operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92756] VGR2853 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2853 gene was detected is described hereinabove with reference to Figs. 1-9.

[92757] VGR2853 gene encodes VGR2853 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92758] VGR2853 precursor RNA folds spatially, forming VGR2853 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2853 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2853 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92759] VGR2853 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM605 precursor RNA and VGAM606 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92760] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM605 RNA and VGAM606 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92761] VGAM605 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM605 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM605 host target RNA into

VGAM605 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92762] VGAM606 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM606 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM606 host target RNA into VGAM606 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92763] It is appreciated that a function of VGR2853 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2853 gene include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGR2853 gene correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2853 gene: VGAM605 host target protein and VGAM606 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM605 and VGAM606.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2854(VGR2854) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92764] VGR2854 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2854 gene was detected is described hereinabove with reference to Figs. 1-9.

[92765] VGR2854 gene encodes VGR2854 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92766] VGR2854 precursor RNA folds spatially, forming VGR2854 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2854 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2854 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92767] VGR2854 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM607 precursor RNA, VGAM608 precursor RNA, VGAM609 precursor RNA and VGAM610 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92768] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM607

RNA, VGAM608 RNA, VGAM609 RNA and VGAM610 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92769] VGAM607 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM607 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM607 host target RNA into VGAM607 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92770] VGAM608 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM608 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM608 host target RNA into VGAM608 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92771] VGAM609 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM609 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM609 host target RNA into VGAM609 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92772] VGAM610 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM610 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM610 host target RNA into VGAM610 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92773] It is appreciated that a function of VGR2854 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2854 gene include diagnosis, prevention and treatment of viral infection by Rice Grassy Stunt Virus. Specific functions, and accordingly utilities, of VGR2854 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2854 gene: VGAM607 host target protein, VGAM608 host target protein, VGAM609 host target protein and VGAM610 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM607, VGAM608, VGAM609 and VGAM610.Fig. 9 further provides a conceptual de-

scription of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2855(VGR2855) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92774] VGR2855 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2855 gene was detected is described hereinabove with reference to Figs. 1-9.

[92775] VGR2855 gene encodes VGR2855 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92776] VGR2855 precursor RNA folds spatially, forming VGR2855 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2855 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2855 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92777] VGR2855 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM613 precursor RNA and VGAM614 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92778] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM613 RNA and VGAM614 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92779] VGAM613 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM613 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM613 host target RNA into VGAM613 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92780] VGAM614 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM614 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM614 host target RNA into VGAM614 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92781] It is appreciated that a function of VGR2855 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2855 gene include diagnosis, prevention and treatment of viral infection by

Xestia C-nigrum Granulovirus. Specific functions, and accordingly utilities, of VGR2855 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2855 gene: VGAM613 host target protein and VGAM614 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM613 and VGAM614.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2856(VGR2856) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92782] VGR2856 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2856 gene was detected is described hereinabove with reference to Figs. 1-9.

[92783] VGR2856 gene encodes VGR2856 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92784] VGR2856 precursor RNA folds spatially, forming VGR2856 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2856 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2856 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92785] VGR2856 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM615 precursor RNA and VGAM616 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92786] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM615 RNA and VGAM616 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92787] VGAM615 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM615 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM615 host target RNA into VGAM615 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92788] VGAM616 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM616 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM616 host target RNA into VGAM616 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92789] It is appreciated that a function of VGR2856 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2856 gene include diagnosis, prevention and treatment of viral infection by Xestia C-nigrum Granulovirus. Specific functions, and accordingly utilities, of VGR2856 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2856 gene: VGAM615 host target protein and VGAM616 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM615 and VGAM616.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to

here as Viral Genomic Record 2857(VGR2857) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92790] VGR2857 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2857 gene was detected is described hereinabove with reference to Figs. 1-9.

[92791] VGR2857 gene encodes VGR2857 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92792] VGR2857 precursor RNA folds spatially, forming VGR2857 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2857 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2857 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[92793] VGR2857 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM619 precursor RNA, VGAM620 precursor RNA, VGAM621 precursor RNA, VGAM622 precursor RNA, VGAM623 precursor RNA, VGAM624 precursor RNA, VGAM625 precursor RNA and VGAM626 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92794] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM619 RNA, VGAM620 RNA, VGAM621 RNA, VGAM622 RNA, VGAM623 RNA, VGAM624 RNA, VGAM625 RNA and VGAM626 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92795] VGAM619 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM619 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM619 host target RNA into VGAM619 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92796] VGAM620 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM620 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM620 host target RNA into VGAM620 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92797] VGAM621 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM621 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM621 host target RNA into VGAM621 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92798] VGAM622 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM622 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM622 host target RNA into VGAM622 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92799] VGAM623 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM623 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM623 host target RNA into VGAM623 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92800] VGAM624 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM624 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM624 host target RNA into VGAM624 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92801] VGAM625 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM625 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM625 host target RNA into VGAM625 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92802] VGAM626 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM626 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM626 host target RNA into VGAM626 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92803] It is appreciated that a function of VGR2857 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2857 gene include diagnosis, prevention and treatment of viral infection by Hepatitis GB Virus C. Specific functions, and accordingly utilities, of VGR2857 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2857 gene: VGAM619 host target protein, VGAM620 host target protein, VGAM621 host target protein, VGAM622 host target protein, VGAM623 host target protein, VGAM624 host target protein, VGAM625 host target protein and VGAM626 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM619, VGAM620, VGAM621, VGAM622, VGAM623, VGAM624, VGAM625 and VGAM626.Fig. 9 further provides a conceptual description of novel bioinformatically detected regu-

latory viral gene, referred to here as Viral Genomic Record 2858(VGR2858) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92804] VGR2858 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2858 gene was detected is described hereinabove with reference to Figs. 1-9.

[92805] VGR2858 gene encodes VGR2858 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92806] VGR2858 precursor RNA folds spatially, forming VGR2858 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2858 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2858 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[92807] VGR2858 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM627 precursor RNA, VGAM628 precursor RNA, VGAM629 precursor RNA and VGAM630 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92808] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM627 RNA, VGAM628 RNA, VGAM629 RNA and VGAM630 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92809] VGAM627 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM627 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM627 host target RNA into VGAM627 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92810] VGAM628 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM628 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM628 host target RNA into VGAM628 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92811] VGAM629 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM629 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM629 host target RNA into VGAM629 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92812] VGAM630 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM630 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM630 host target RNA into VGAM630 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92813] It is appreciated that a function of VGR2858 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2858 gene include diagnosis, prevention and treatment of viral infection by Hepatitis GB Virus C. Specific functions, and accordingly utilities, of VGR2858 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2858 gene: VGAM627 host target protein, VGAM628 host target protein, VGAM629 host target protein and VGAM630 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM627, VGAM628, VGAM629 and VGAM630.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2859(VGR2859) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92814] VGR2859 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2859 gene was detected is described hereinabove with reference to Figs. 1-9.

[92815] VGR2859 gene encodes VGR2859 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92816] VGR2859 precursor RNA folds spatially, forming VGR2859 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2859 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2859 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92817] VGR2859 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM631 precursor RNA and VGAM632 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92818] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM631 RNA and VGAM632 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92819] VGAM631 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM631 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM631 host target RNA into VGAM631 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92820] VGAM632 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM632 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM632 host target RNA into VGAM632 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92821] It is appreciated that a function of VGR2859 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2859 gene include diagnosis, prevention and treatment of viral infection by Ovine Astrovirus. Specific functions, and accordingly utilities, of VGR2859 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2859 gene: VGAM631 host target protein and VGAM632 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove

with reference to VGAM631 and VGAM632.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2860(VGR2860) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92822] VGR2860 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2860 gene was detected is described hereinabove with reference to Figs. 1-9.

[92823] VGR2860 gene encodes VGR2860 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92824] VGR2860 precursor RNA folds spatially, forming VGR2860 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2860 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2860 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92825] VGR2860 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM633 precursor RNA and VGAM634 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92826] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM633 RNA and VGAM634 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92827] VGAM633 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM633 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM633 host target RNA into VGAM633 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92828] VGAM634 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM634 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM634 host target RNA into VGAM634 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92829] It is appreciated that a function of VGR2860 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2860 gene include

diagnosis, prevention and treatment of viral infection by Turkey Astrovirus. Specific functions, and accordingly utilities, of VGR2860 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2860 gene: VGAM633 host target protein and VGAM634 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM633 and VGAM634.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2861(VGR2861) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92830] VGR2861 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2861 gene was detected is described hereinabove with reference to Figs. 1-9.

[92831] VGR2861 gene encodes VGR2861 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92832] VGR2861 precursor RNA folds spatially, forming VGR2861 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2861 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2861 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92833] VGR2861 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM635 precursor RNA and VGAM636 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92834] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM635 RNA and VGAM636 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92835] VGAM635 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM635 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM635 host target RNA into VGAM635 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92836] VGAM636 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM636 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM636 host target RNA into VGAM636 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92837] It is appreciated that a function of VGR2861 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2861 gene include diagnosis, prevention and treatment of viral infection by Cherry Mottle Leaf Virus. Specific functions, and accordingly utilities, of VGR2861 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2861 gene: VGAM635 host target protein and VGAM636 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM635 and VGAM636.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Vi-

ral Genomic Record 2862(VGR2862) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92838] VGR2862 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2862 gene was detected is described hereinabove with reference to Figs. 1-9.

[92839] VGR2862 gene encodes VGR2862 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92840] VGR2862 precursor RNA folds spatially, forming VGR2862 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2862 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2862 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[92841] VGR2862 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM638 precursor RNA, VGAM639 precursor RNA and VGAM640 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92842] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM638 RNA, VGAM639 RNA and VGAM640 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92843] VGAM638 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM638 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM638 host target RNA into VGAM638 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92844] VGAM639 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM639 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM639 host target RNA into VGAM639 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92845] VGAM640 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM640 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM640 host target RNA into VGAM640 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92846] It is appreciated that a function of VGR2862 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2862 gene include diagnosis, prevention and treatment of viral infection by Turnip Mosaic Virus. Specific functions, and accordingly utilities, of VGR2862 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2862 gene: VGAM638 host target protein, VGAM639 host target protein and VGAM640 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM638, VGAM639 and VGAM640.Fig. 9 further pro-

vides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2863(VGR2863) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92847] VGR2863 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2863 gene was detected is described hereinabove with reference to Figs. 1-9.

[92848] VGR2863 gene encodes VGR2863 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92849] VGR2863 precursor RNA folds spatially, forming VGR2863 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2863 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2863 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92850] VGR2863 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM644 precursor RNA and VGAM645 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92851] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM644 RNA and VGAM645 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92852] VGAM644 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM644 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM644 host target RNA into VGAM644 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92853] VGAM645 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM645 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM645 host target RNA into VGAM645 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92854] It is appreciated that a function of VGR2863 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2863 gene include diagnosis, prevention and treatment of viral infection by

Parvovirus H1. Specific functions, and accordingly utilities, of VGR2863 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2863 gene: VGAM644 host target protein and VGAM645 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM644 and VGAM645.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2864(VGR2864) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92855] VGR2864 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2864 gene was detected is described hereinabove with reference to Figs. 1-9.

[92856] VGR2864 gene encodes VGR2864 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92857] VGR2864 precursor RNA folds spatially, forming VGR2864 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2864 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2864 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92858] VGR2864 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM647 precursor RNA, VGAM648 precursor RNA and VGAM649 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92859] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM647 RNA, VGAM648 RNA and VGAM649 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92860] VGAM647 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM647 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM647 host target RNA into VGAM647 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92861] VGAM648 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM648 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM648 host target RNA into VGAM648 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92862] VGAM649 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM649 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM649 host target RNA into VGAM649 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92863] It is appreciated that a function of VGR2864 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2864 gene include

diagnosis, prevention and treatment of viral infection by Acute Bee Paralysis Virus. Specific functions, and accordingly utilities, of VGR2864 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2864 gene: VGAM647 host target protein, VGAM648 host target protein and VGAM649 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM647, VGAM648 and VGAM649.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2865(VGR2865) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92864] VGR2865 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2865 gene was detected is described hereinabove with reference to Figs.

1-9.

[92865] VGR2865 gene encodes VGR2865 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92866] VGR2865 precursor RNA folds spatially, forming VGR2865 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2865 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2865 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92867] VGR2865 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM652 precursor RNA and VGAM653 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92868] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM652 RNA and VGAM653 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92869] VGAM652 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM652 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM652 host target RNA into VGAM652 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92870] VGAM653 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM653 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM653 host target RNA into VGAM653 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92871] It is appreciated that a function of VGR2865 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2865 gene include diagnosis, prevention and treatment of viral infection by Meleagrid Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2865 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2865 gene: VGAM652 host target protein and VGAM653 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM652 and VGAM653.Fig. 9 further provides a conceptual description of novel bioinformati-

cally detected regulatory viral gene, referred to here as Viral Genomic Record 2866(VGR2866) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92872] VGR2866 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2866 gene was detected is described hereinabove with reference to Figs. 1-9.

[92873] VGR2866 gene encodes VGR2866 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92874] VGR2866 precursor RNA folds spatially, forming VGR2866 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2866 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2866 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[92875] VGR2866 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM654 precursor RNA, VGAM655 precursor RNA, VGAM656 precursor RNA and VGAM657 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92876] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM654 RNA, VGAM655 RNA, VGAM656 RNA and VGAM657 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92877] VGAM654 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM654 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM654 host target RNA into VGAM654 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92878] VGAM655 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM655 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM655 host target RNA into VGAM655 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92879] VGAM656 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM656 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM656 host target RNA into VGAM656 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92880] VGAM657 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM657 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM657 host target RNA into VGAM657 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92881] It is appreciated that a function of VGR2866 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2866 gene include diagnosis, prevention and treatment of viral infection by Meleagrid Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2866 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2866 gene: VGAM654 host target protein, VGAM655 host target protein, VGAM656 host target protein and VGAM657 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM654, VGAM655, VGAM656 and VGAM657.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2867(VGR2867) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92882] VGR2867 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2867 gene was detected is described hereinabove with reference to Figs. 1-9.

[92883] VGR2867 gene encodes VGR2867 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92884] VGR2867 precursor RNA folds spatially, forming VGR2867 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2867 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2867 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92885] VGR2867 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM658 precursor RNA, VGAM659 precursor RNA and VGAM660 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92886] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM658 RNA, VGAM659 RNA and VGAM660 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92887] VGAM658 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM658 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM658 host target RNA into VGAM658 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92888] VGAM659 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM659 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM659 host target RNA into VGAM659 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92889] VGAM660 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM660 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM660 host target RNA into VGAM660 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92890] It is appreciated that a function of VGR2867 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2867 gene include diagnosis, prevention and treatment of viral infection by Meleagrid Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2867 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2867 gene: VGAM658 host target protein, VGAM659 host target protein and VGAM660 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM658, VGAM659 and VGAM660.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2868(VGR2868) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92891] VGR2868 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2868 gene was detected is described hereinabove with reference to Figs. 1-9.

[92892] VGR2868 gene encodes VGR2868 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92893] VGR2868 precursor RNA folds spatially, forming VGR2868 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2868 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2868 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92894] VGR2868 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM663 precursor RNA, VGAM664 precursor RNA and VGAM665 precursor RNA, herein

schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92895] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM663 RNA, VGAM664 RNA and VGAM665 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92896] VGAM663 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM663 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM663 host target RNA into VGAM663 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[92897] VGAM664 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM664 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM664 host target RNA into VGAM664 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92898] VGAM665 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM665 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM665 host target RNA into VGAM665 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92899] It is appreciated that a function of VGR2868 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2868 gene include diagnosis, prevention and treatment of viral infection by Rachiplusia Ou Multiple Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR2868 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2868 gene: VGAM663 host target protein, VGAM664 host target protein and VGAM665 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM663, VGAM664 and VGAM665.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2869(VGR2869) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates ex-

pression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92900] VGR2869 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2869 gene was detected is described hereinabove with reference to Figs. 1-9.

[92901] VGR2869 gene encodes VGR2869 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92902] VGR2869 precursor RNA folds spatially, forming VGR2869 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2869 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2869 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92903] VGR2869 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM671 precursor RNA and VGAM672 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92904] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM671 RNA and VGAM672 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92905] VGAM671 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM671 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM671 host target RNA into VGAM671 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92906] VGAM672 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM672 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM672 host target RNA into VGAM672 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92907] It is appreciated that a function of VGR2869 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2869 gene include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGR2869 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR2869 gene: VGAM671 host target protein and VGAM672 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM671 and VGAM672.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2870(VGR2870) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92908] VGR2870 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2870 gene was detected is described hereinabove with reference to Figs. 1-9.

[92909] VGR2870 gene encodes VGR2870 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92910] VGR2870 precursor RNA folds spatially, forming VGR2870 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2870 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2870 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92911] VGR2870 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM673 precursor RNA, VGAM674 precursor RNA, VGAM675 precursor RNA, VGAM676 precursor RNA, VGAM677 precursor RNA, VGAM678 precursor RNA, VGAM679 precursor RNA and VGAM680 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92912] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM673

RNA, VGAM674 RNA, VGAM675 RNA, VGAM676 RNA, VGAM677 RNA, VGAM678 RNA, VGAM679 RNA and VGAM680 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92913] VGAM673 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM673 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM673 host target RNA into VGAM673 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92914] VGAM674 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM674 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM674 host target RNA into VGAM674 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92915] VGAM675 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM675 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM675 host target RNA into VGAM675 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92916] VGAM676 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM676 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM676 host target RNA into VGAM676 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92917] VGAM677 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM677 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM677 host target RNA into VGAM677 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92918] VGAM678 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM678 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM678 host target RNA into VGAM678 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92919] VGAM679 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM679 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM679 host target RNA into VGAM679 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92920] VGAM680 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM680 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM680 host target RNA into VGAM680 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92921] It is appreciated that a function of VGR2870 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2870 gene include diagnosis, prevention and treatment of viral infection by Human Coronavirus 229E. Specific functions, and accordingly utilities, of VGR2870 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2870 gene: VGAM673 host target protein, VGAM674 host target protein, VGAM675 host target protein, VGAM676 host target protein, VGAM677 host target protein, VGAM678 host target protein, VGAM679 host target protein and VGAM680 host

target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM673, VGAM674, VGAM675, VGAM676, VGAM677, VGAM678, VGAM679 and VGAM680.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2871(VGR2871) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92922] VGR2871 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2871 gene was detected is described hereinabove with reference to Figs. 1-9.

[92923] VGR2871 gene encodes VGR2871 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92924] VGR2871 precursor RNA folds spatially, forming VGR2871 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2871 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2871 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92925] VGR2871 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM681 precursor RNA, VGAM682 precursor RNA, VGAM683 precursor RNA, VGAM684 precursor RNA, VGAM685 precursor RNA, VGAM686 precursor RNA, VGAM687 precursor RNA and VGAM688 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92926] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM681

RNA, VGAM682 RNA, VGAM683 RNA, VGAM684 RNA, VGAM685 RNA, VGAM686 RNA, VGAM687 RNA and VGAM688 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92927] VGAM681 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM681 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM681 host target RNA into VGAM681 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92928] VGAM682 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM682 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM682 host target RNA into VGAM682 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92929] VGAM683 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM683 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM683 host target RNA into VGAM683 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92930] VGAM684 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM684 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM684 host target RNA into VGAM684 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92931] VGAM685 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM685 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM685 host target RNA into VGAM685 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92932] VGAM686 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM686 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM686 host target RNA into VGAM686 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92933] VGAM687 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM687 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM687 host target RNA into VGAM687 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92934] VGAM688 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM688 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM688 host target RNA into VGAM688 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92935] It is appreciated that a function of VGR2871 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2871 gene include diagnosis, prevention and treatment of viral infection by Human Coronavirus 229E. Specific functions, and accordingly utilities, of VGR2871 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2871 gene: VGAM681 host target protein, VGAM682 host target protein, VGAM683 host target protein, VGAM684 host target protein, VGAM685 host target protein, VGAM686 host target protein, VGAM687 host target protein and VGAM688 host

target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM681, VGAM682, VGAM683, VGAM684, VGAM685, VGAM686, VGAM687 and VGAM688.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2872(VGR2872) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92936] VGR2872 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2872 gene was detected is described hereinabove with reference to Figs. 1-9.

[92937] VGR2872 gene encodes VGR2872 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92938] VGR2872 precursor RNA folds spatially, forming VGR2872 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2872 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2872 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92939] VGR2872 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM689 precursor RNA, VGAM690 precursor RNA, VGAM691 precursor RNA, VGAM692 precursor RNA, VGAM693 precursor RNA, VGAM694 precursor RNA, VGAM695 precursor RNA and VGAM696 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92940] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM689

RNA, VGAM690 RNA, VGAM691 RNA, VGAM692 RNA, VGAM693 RNA, VGAM694 RNA, VGAM695 RNA and VGAM696 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92941] VGAM689 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM689 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM689 host target RNA into VGAM689 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92942] VGAM690 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM690 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM690 host target RNA into VGAM690 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92943] VGAM691 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM691 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM691 host target RNA into VGAM691 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92944] VGAM692 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM692 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM692 host target RNA into VGAM692 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92945] VGAM693 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM693 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM693 host target RNA into VGAM693 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92946] VGAM694 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM694 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM694 host target RNA into VGAM694 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92947] VGAM695 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM695 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM695 host target RNA into VGAM695 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92948] VGAM696 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM696 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM696 host target RNA into VGAM696 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92949] It is appreciated that a function of VGR2872 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2872 gene include diagnosis, prevention and treatment of viral infection by Human Coronavirus 229E. Specific functions, and accordingly utilities, of VGR2872 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2872 gene: VGAM689 host target protein, VGAM690 host target protein, VGAM691 host target protein, VGAM692 host target protein, VGAM693 host target protein, VGAM694 host target protein, VGAM695 host target protein and VGAM696 host

target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM689, VGAM690, VGAM691, VGAM692, VGAM693, VGAM694, VGAM695 and VGAM696.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2873(VGR2873) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92950] VGR2873 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2873 gene was detected is described hereinabove with reference to Figs. 1-9.

[92951] VGR2873 gene encodes VGR2873 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92952] VGR2873 precursor RNA folds spatially, forming VGR2873 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2873 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2873 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92953] VGR2873 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM697 precursor RNA, VGAM698 precursor RNA, VGAM699 precursor RNA and VGAM700 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92954] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM697 RNA, VGAM698 RNA, VGAM699 RNA and VGAM700 RNA, herein schematically represented by VGAM1 RNA through

VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92955] VGAM697 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM697 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM697 host target RNA into VGAM697 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92956] VGAM698 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM698 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM698 host target RNA into

VGAM698 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92957] VGAM699 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM699 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM699 host target RNA into VGAM699 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92958] VGAM700 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM700 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM700 host target RNA into VGAM700 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92959] It is appreciated that a function of VGR2873 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2873 gene include diagnosis, prevention and treatment of viral infection by Human Coronavirus 229E. Specific functions, and accordingly utilities, of VGR2873 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2873 gene: VGAM697 host target protein, VGAM698 host target protein, VGAM699 host target protein and VGAM700 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM697, VGAM698, VGAM699 and VGAM700.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record

2874(VGR2874) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92960] VGR2874 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2874 gene was detected is described hereinabove with reference to Figs. 1-9.

[92961] VGR2874 gene encodes VGR2874 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92962] VGR2874 precursor RNA folds spatially, forming VGR2874 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2874 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2874 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[92963] VGR2874 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM701 precursor RNA, VGAM702 precursor RNA, VGAM703 precursor RNA, VGAM704 precursor RNA, VGAM705 precursor RNA and VGAM706 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92964] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM701 RNA, VGAM702 RNA, VGAM703 RNA, VGAM704 RNA, VGAM705 RNA and VGAM706 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92965] VGAM701 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM701 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM701 host target RNA into VGAM701 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92966] VGAM702 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM702 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM702 host target RNA into VGAM702 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92967] VGAM703 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM703 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM703 host target RNA into VGAM703 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92968] VGAM704 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM704 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM704 host target RNA into VGAM704 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92969] VGAM705 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM705 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM705 host target RNA into VGAM705 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92970] VGAM706 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM706 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM706 host target RNA into VGAM706 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92971] It is appreciated that a function of VGR2874 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2874 gene include diagnosis, prevention and treatment of viral infection by Human Coronavirus 229E. Specific functions, and accordingly utilities, of VGR2874 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2874 gene: VGAM701 host target protein, VGAM702 host target protein, VGAM703 host target protein, VGAM704 host target protein, VGAM705 host target protein and VGAM706 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM701, VGAM702, VGAM703, VGAM704, VGAM705 and VGAM706.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2875(VGR2875) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[92972] VGR2875 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2875 gene was detected is described hereinabove with reference to Figs. 1-9.

[92973] VGR2875 gene encodes VGR2875 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92974] VGR2875 precursor RNA folds spatially, forming VGR2875 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2875 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2875 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92975] VGR2875 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM710 precursor RNA, VGAM711 pre-

cursor RNA and VGAM712 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92976] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM710 RNA, VGAM711 RNA and VGAM712 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92977] VGAM710 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM710 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM710 host target RNA into VGAM710 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92978] VGAM711 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM711 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM711 host target RNA into VGAM711 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92979] VGAM712 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM712 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM712 host target RNA into

VGAM712 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92980] It is appreciated that a function of VGR2875 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2875 gene include diagnosis, prevention and treatment of viral infection by Pestivirus Type 2. Specific functions, and accordingly utilities, of VGR2875 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2875 gene: VGAM710 host target protein, VGAM711 host target protein and VGAM712 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM710, VGAM711 and VGAM712.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2876(VGR2876) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-

like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92981] VGR2876 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2876 gene was detected is described hereinabove with reference to Figs. 1-9.

[92982] VGR2876 gene encodes VGR2876 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92983] VGR2876 precursor RNA folds spatially, forming VGR2876 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2876 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2876 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92984] VGR2876 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM713 precursor RNA and VGAM714 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92985] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM713 RNA and VGAM714 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92986] VGAM713 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM713 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM713 host target RNA into VGAM713 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92987] VGAM714 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM714 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM714 host target RNA into VGAM714 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92988] It is appreciated that a function of VGR2876 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2876 gene include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2876 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR2876 gene: VGAM713 host target protein and VGAM714 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM713 and VGAM714.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2877(VGR2877) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92989] VGR2877 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2877 gene was detected is described hereinabove with reference to Figs. 1-9.

[92990] VGR2877 gene encodes VGR2877 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[92991] VGR2877 precursor RNA folds spatially, forming VGR2877 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2877 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2877 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[92992] VGR2877 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM715 precursor RNA, VGAM716 precursor RNA, VGAM717 precursor RNA and VGAM718 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[92993] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM715 RNA, VGAM716 RNA, VGAM717 RNA and VGAM718 RNA, herein schematically represented by VGAM1 RNA through

VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[92994] VGAM715 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM715 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM715 host target RNA into VGAM715 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92995] VGAM716 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM716 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM716 host target RNA into

VGAM716 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92996] VGAM717 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM717 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM717 host target RNA into VGAM717 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92997] VGAM718 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM718 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM718 host target RNA into VGAM718 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[92998] It is appreciated that a function of VGR2877 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2877 gene include diagnosis, prevention and treatment of viral infection by Cercopithecine Herpesvirus 7. Specific functions, and accordingly utilities, of VGR2877 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2877 gene: VGAM715 host target protein, VGAM716 host target protein, VGAM717 host target protein and VGAM718 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM715, VGAM716, VGAM717 and VGAM718.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record

2878(VGR2878) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[92999] VGR2878 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2878 gene was detected is described hereinabove with reference to Figs. 1-9.

[93000] VGR2878 gene encodes VGR2878 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93001] VGR2878 precursor RNA folds spatially, forming VGR2878 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2878 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2878 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[93002] VGR2878 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM719 precursor RNA and VGAM720 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93003] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM719 RNA and VGAM720 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93004] VGAM719 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM719 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM719 host target RNA into VGAM719 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93005] VGAM720 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM720 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM720 host target RNA into VGAM720 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93006] It is appreciated that a function of VGR2878 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2878 gene include diagnosis, prevention and treatment of viral infection by Ectocarpus Siliculosus Virus. Specific functions, and accordingly utilities, of VGR2878 gene correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2878 gene: VGAM719 host target protein and VGAM720 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM719 and VGAM720.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2879(VGR2879) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93007] VGR2879 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2879 gene was detected is described hereinabove with reference to Figs. 1-9.

[93008] VGR2879 gene encodes VGR2879 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[93009] VGR2879 precursor RNA folds spatially, forming VGR2879 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2879 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2879 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93010] VGR2879 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM721 precursor RNA, VGAM722 precursor RNA, VGAM723 precursor RNA, VGAM724 precursor RNA and VGAM725 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93011] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM721 RNA, VGAM722 RNA, VGAM723 RNA, VGAM724 RNA and VGAM725 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93012] VGAM721 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM721 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM721 host target RNA into VGAM721 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93013] VGAM722 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM722 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM722 host target RNA into VGAM722 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93014] VGAM723 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM723 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM723 host target RNA into VGAM723 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93015] VGAM724 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM724 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM724 host target RNA into VGAM724 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93016] VGAM725 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM725 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM725 host target RNA into VGAM725 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93017] It is appreciated that a function of VGR2879 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2879 gene include

diagnosis, prevention and treatment of viral infection by Tomato Mosaic Virus. Specific functions, and accordingly utilities, of VGR2879 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2879 gene: VGAM721 host target protein, VGAM722 host target protein, VGAM723 host target protein, VGAM724 host target protein and VGAM725 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM721, VGAM722, VGAM723, VGAM724 and VGAM725.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2880(VGR2880) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93018] VGR2880 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2880 gene was detected is described hereinabove with reference to Figs. 1-9.

[93019] VGR2880 gene encodes VGR2880 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93020] VGR2880 precursor RNA folds spatially, forming VGR2880 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2880 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2880 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93021] VGR2880 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM727 precursor RNA and VGAM728 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93022] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM727 RNA and VGAM728 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93023] VGAM727 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM727 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM727 host target RNA into VGAM727 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93024] VGAM728 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM728 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM728 host target RNA into VGAM728 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93025] It is appreciated that a function of VGR2880 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2880 gene include diagnosis, prevention and treatment of viral infection by Aconitum Latent Virus. Specific functions, and accordingly utilities, of VGR2880 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2880 gene: VGAM727 host target protein and VGAM728 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove

with reference to VGAM727 and VGAM728.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2881(VGR2881) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93026] VGR2881 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2881 gene was detected is described hereinabove with reference to Figs. 1-9.

[93027] VGR2881 gene encodes VGR2881 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93028] VGR2881 precursor RNA folds spatially, forming VGR2881 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2881 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2881 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93029] VGR2881 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM729 precursor RNA, VGAM730 precursor RNA, VGAM731 precursor RNA and VGAM732 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93030] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM729 RNA, VGAM730 RNA, VGAM731 RNA and VGAM732 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93031] VGAM729 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM729 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM729 host target RNA into VGAM729 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93032] VGAM730 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM730 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM730 host target RNA into VGAM730 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93033] VGAM731 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM731 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM731 host target RNA into VGAM731 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93034] VGAM732 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM732 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM732 host target RNA into VGAM732 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93035] It is appreciated that a function of VGR2881 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2881 gene include diagnosis, prevention and treatment of viral infection by Cydia Pomonella Granulovirus. Specific functions, and accordingly utilities, of VGR2881 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2881 gene: VGAM729 host target protein, VGAM730 host target protein, VGAM731 host target protein and VGAM732 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM729, VGAM730, VGAM731 and VGAM732.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2882(VGR2882) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93036] VGR2882 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2882 gene was detected is described hereinabove with reference to Figs. 1-9.

[93037] VGR2882 gene encodes VGR2882 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93038] VGR2882 precursor RNA folds spatially, forming VGR2882 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2882 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2882 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93039] VGR2882 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM733 precursor RNA, VGAM734 precursor RNA, VGAM735 precursor RNA, VGAM736 precur-

sor RNA, VGAM737 precursor RNA and VGAM738 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93040] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM733 RNA, VGAM734 RNA, VGAM735 RNA, VGAM736 RNA, VGAM737 RNA and VGAM738 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93041] VGAM733 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM733 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM733 host target RNA into VGAM733 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93042] VGAM734 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM734 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM734 host target RNA into VGAM734 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93043] VGAM735 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM735 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM735 host target RNA into

VGAM735 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93044] VGAM736 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM736 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM736 host target RNA into VGAM736 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93045] VGAM737 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM737 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM737 host target RNA into VGAM737 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93046] VGAM738 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM738 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM738 host target RNA into VGAM738 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93047] It is appreciated that a function of VGR2882 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2882 gene include diagnosis, prevention and treatment of viral infection by Barley Yellow Mosaic Virus. Specific functions, and accordingly utilities, of VGR2882 gene correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2882 gene: VGAM733 host target protein, VGAM734 host target protein, VGAM735 host target protein, VGAM736 host target protein, VGAM737 host target protein and VGAM738 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM733, VGAM734, VGAM735, VGAM736, VGAM737 and VGAM738.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2883(VGR2883) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93048] VGR2883 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2883 gene was detected is described hereinabove with reference to Figs.

1-9.

[93049] VGR2883 gene encodes VGR2883 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93050] VGR2883 precursor RNA folds spatially, forming VGR2883 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2883 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2883 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93051] VGR2883 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM739 precursor RNA, VGAM740 precursor RNA, VGAM741 precursor RNA and VGAM742 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED

PRECURSOR RNA of Fig. 1.

[93052] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM739 RNA, VGAM740 RNA, VGAM741 RNA and VGAM742 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93053] VGAM739 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM739 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM739 host target RNA into VGAM739 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93054] VGAM740 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM740 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM740 host target RNA into VGAM740 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93055] VGAM741 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM741 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM741 host target RNA into VGAM741 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93056] VGAM742 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM742 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM742 host target RNA into VGAM742 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93057] It is appreciated that a function of VGR2883 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2883 gene include diagnosis, prevention and treatment of viral infection by Taura Syndrome Virus. Specific functions, and accordingly utilities, of VGR2883 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2883 gene: VGAM739 host target protein, VGAM740 host target protein, VGAM741 host target protein and VGAM742 host target protein, herein schematically represented by VGAM1 HOST TARGET

PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM739, VGAM740, VGAM741 and VGAM742.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2884(VGR2884) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93058] VGR2884 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2884 gene was detected is described hereinabove with reference to Figs. 1-9.

[93059] VGR2884 gene encodes VGR2884 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93060] VGR2884 precursor RNA folds spatially, forming VGR2884 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2884 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2884 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93061] VGR2884 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM744 precursor RNA, VGAM745 precursor RNA, VGAM746 precursor RNA, VGAM747 precursor RNA, VGAM748 precursor RNA, VGAM749 precursor RNA, VGAM750 precursor RNA and VGAM751 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93062] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM744 RNA, VGAM745 RNA, VGAM746 RNA, VGAM747 RNA, VGAM748 RNA, VGAM749 RNA, VGAM750 RNA and

VGAM751 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93063] VGAM744 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM744 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM744 host target RNA into VGAM744 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93064] VGAM745 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM745 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM745 host target RNA into VGAM745 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93065] VGAM746 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM746 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM746 host target RNA into VGAM746 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93066] VGAM747 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM747 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM747 host target RNA into VGAM747 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93067] VGAM748 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM748 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM748 host target RNA into VGAM748 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93068] VGAM749 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM749 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM749 host target RNA into VGAM749 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93069] VGAM750 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM750 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM750 host target RNA into VGAM750 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93070] VGAM751 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM751 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM751 host target RNA into VGAM751 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93071] It is appreciated that a function of VGR2884 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2884 gene include diagnosis, prevention and treatment of viral infection by Bovine Coronavirus. Specific functions, and accordingly utilities, of VGR2884 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2884 gene: VGAM744 host target protein, VGAM745 host target protein, VGAM746 host target protein, VGAM747 host target protein, VGAM748 host target protein, VGAM749 host target protein, VGAM750 host target protein and VGAM751 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM744, VGAM745, VGAM746, VGAM747, VGAM748, VGAM749, VGAM750 and VGAM751.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2885(VGR2885) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93072] VGR2885 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2885 gene was detected is described hereinabove with reference to Figs. 1-9.

[93073] VGR2885 gene encodes VGR2885 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93074] VGR2885 precursor RNA folds spatially, forming VGR2885 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2885 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2885 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93075] VGR2885 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM752 precursor RNA, VGAM753 precursor RNA, VGAM754 precursor RNA, VGAM755 precursor RNA, VGAM756 precursor RNA, VGAM757 precursor RNA, VGAM758 precursor RNA and VGAM759 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93076] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM752 RNA, VGAM753 RNA, VGAM754 RNA, VGAM755 RNA, VGAM756 RNA, VGAM757 RNA, VGAM758 RNA and

VGAM759 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93077] VGAM752 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM752 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM752 host target RNA into VGAM752 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93078] VGAM753 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM753 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM753 host target RNA into VGAM753 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93079] VGAM754 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM754 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM754 host target RNA into VGAM754 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93080] VGAM755 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM755 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM755 host target RNA into VGAM755 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93081] VGAM756 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM756 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM756 host target RNA into VGAM756 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93082] VGAM757 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM757 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM757 host target RNA into VGAM757 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93083] VGAM758 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM758 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM758 host target RNA into VGAM758 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93084] VGAM759 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM759 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM759 host target RNA into VGAM759 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93085] It is appreciated that a function of VGR2885 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2885 gene include diagnosis, prevention and treatment of viral infection by Bovine Coronavirus. Specific functions, and accordingly utilities, of VGR2885 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2885 gene: VGAM752 host target protein, VGAM753 host target protein, VGAM754 host target protein, VGAM755 host target protein, VGAM756 host target protein, VGAM757 host target protein, VGAM758 host target protein and VGAM759 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM752, VGAM753, VGAM754, VGAM755, VGAM756, VGAM757, VGAM758 and VGAM759.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2886(VGR2886) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93086] VGR2886 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2886 gene was detected is described hereinabove with reference to Figs. 1-9.

[93087] VGR2886 gene encodes VGR2886 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93088] VGR2886 precursor RNA folds spatially, forming VGR2886 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2886 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2886 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93089] VGR2886 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM760 precursor RNA, VGAM761 precursor RNA, VGAM762 precursor RNA, VGAM763 precursor RNA, VGAM764 precursor RNA, VGAM765 precursor RNA, VGAM766 precursor RNA and VGAM767 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93090] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM760 RNA, VGAM761 RNA, VGAM762 RNA, VGAM763 RNA, VGAM764 RNA, VGAM765 RNA, VGAM766 RNA and

VGAM767 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93091] VGAM760 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM760 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM760 host target RNA into VGAM760 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93092] VGAM761 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM761 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM761 host target RNA into VGAM761 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93093] VGAM762 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM762 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM762 host target RNA into VGAM762 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93094] VGAM763 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM763 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM763 host target RNA into VGAM763 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93095] VGAM764 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM764 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM764 host target RNA into VGAM764 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93096] VGAM765 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM765 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM765 host target RNA into VGAM765 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93097] VGAM766 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM766 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM766 host target RNA into VGAM766 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93098] VGAM767 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM767 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM767 host target RNA into VGAM767 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93099] It is appreciated that a function of VGR2886 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2886 gene include diagnosis, prevention and treatment of viral infection by Bovine Coronavirus. Specific functions, and accordingly utilities, of VGR2886 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2886 gene: VGAM760 host target protein, VGAM761 host target protein, VGAM762 host target protein, VGAM763 host target protein, VGAM764 host target protein, VGAM765 host target protein, VGAM766 host target protein and VGAM767 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM760, VGAM761, VGAM762, VGAM763, VGAM764, VGAM765, VGAM766 and VGAM767.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2887(VGR2887) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93100] VGR2887 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2887 gene was detected is described hereinabove with reference to Figs. 1-9.

[93101] VGR2887 gene encodes VGR2887 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93102] VGR2887 precursor RNA folds spatially, forming VGR2887 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2887 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2887 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93103] VGR2887 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM768 precursor RNA and VGAM769 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93104] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM768 RNA and VGAM769 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93105] VGAM768 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM768 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM768 host target RNA into VGAM768 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93106] VGAM769 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM769 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM769 host target RNA into VGAM769 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93107] It is appreciated that a function of VGR2887 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2887 gene include diagnosis, prevention and treatment of viral infection by Bovine Coronavirus. Specific functions, and accordingly utilities, of VGR2887 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2887 gene: VGAM768 host target protein and VGAM769 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM768 and VGAM769.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2888(VGR2888) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93108] VGR2888 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2888 gene was detected is described hereinabove with reference to Figs. 1-9.

[93109] VGR2888 gene encodes VGR2888 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93110] VGR2888 precursor RNA folds spatially, forming VGR2888 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2888 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2888 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93111] VGR2888 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM771 precursor RNA, VGAM772 precursor RNA, VGAM773 precursor RNA, VGAM774 precursor RNA and VGAM775 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through

VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93112] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM771 RNA, VGAM772 RNA, VGAM773 RNA, VGAM774 RNA and VGAM775 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93113] VGAM771 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM771 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM771 host target RNA into VGAM771 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93114] VGAM772 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM772 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM772 host target RNA into VGAM772 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93115] VGAM773 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM773 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM773 host target RNA into VGAM773 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93116] VGAM774 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM774 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM774 host target RNA into VGAM774 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93117] VGAM775 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM775 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM775 host target RNA into VGAM775 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93118] It is appreciated that a function of VGR2888 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2888 gene include diagnosis, prevention and treatment of viral infection by Bovine Coronavirus. Specific functions, and accordingly utilities, of VGR2888 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2888 gene: VGAM771 host target protein, VGAM772 host target protein, VGAM773 host target protein, VGAM774 host target protein and VGAM775 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM771, VGAM772, VGAM773, VGAM774 and VGAM775.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2889(VGR2889) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn

modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93119] VGR2889 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2889 gene was detected is described hereinabove with reference to Figs. 1-9.

[93120] VGR2889 gene encodes VGR2889 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93121] VGR2889 precursor RNA folds spatially, forming VGR2889 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2889 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2889 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93122] VGR2889 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM781 precursor RNA, VGAM782 precursor RNA, VGAM783 precursor RNA and VGAM784 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93123] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM781 RNA, VGAM782 RNA, VGAM783 RNA and VGAM784 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93124] VGAM781 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM781 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM781 host target RNA into VGAM781 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93125] VGAM782 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM782 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM782 host target RNA into VGAM782 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93126] VGAM783 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM783 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM783 host target RNA into VGAM783 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93127] VGAM784 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM784 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM784 host target RNA into VGAM784 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93128] It is appreciated that a function of VGR2889 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2889 gene include diagnosis, prevention and treatment of viral infection by Deer Tick Virus. Specific functions, and accordingly utili-

ties, of VGR2889 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2889 gene: VGAM781 host target protein, VGAM782 host target protein, VGAM783 host target protein and VGAM784 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM781, VGAM782, VGAM783 and VGAM784.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2890(VGR2890) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93129] VGR2890 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2890 gene was detected is described hereinabove with reference to Figs. 1-9.

[93130] VGR2890 gene encodes VGR2890 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93131] VGR2890 precursor RNA folds spatially, forming VGR2890 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2890 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2890 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93132] VGR2890 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM785 precursor RNA, VGAM786 precursor RNA, VGAM787 precursor RNA and VGAM788 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93133] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM785 RNA, VGAM786 RNA, VGAM787 RNA and VGAM788 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93134] VGAM785 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM785 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM785 host target RNA into VGAM785 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93135] VGAM786 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM786 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM786 host target RNA into VGAM786 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93136] VGAM787 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM787 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM787 host target RNA into VGAM787 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93137] VGAM788 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM788 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM788 host target RNA into VGAM788 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93138] It is appreciated that a function of VGR2890 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2890 gene include diagnosis, prevention and treatment of viral infection by Zucchini Yellow Mosaic Virus. Specific functions, and accordingly utilities, of VGR2890 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2890 gene: VGAM785 host target protein, VGAM786 host target protein, VGAM787 host target protein and VGAM788 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN.

The function of these host target genes is elaborated hereinabove with reference to VGAM785, VGAM786, VGAM787 and VGAM788.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2891(VGR2891) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93139] VGR2891 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2891 gene was detected is described hereinabove with reference to Figs. 1-9.

[93140] VGR2891 gene encodes VGR2891 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93141] VGR2891 precursor RNA folds spatially, forming VGR2891 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2891 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2891 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93142] VGR2891 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM789 precursor RNA, VGAM790 precursor RNA and VGAM791 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93143] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM789 RNA, VGAM790 RNA and VGAM791 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93144] VGAM789 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM789 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM789 host target RNA into VGAM789 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93145] VGAM790 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM790 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM790 host target RNA into VGAM790 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93146] VGAM791 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM791 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM791 host target RNA into VGAM791 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93147] It is appreciated that a function of VGR2891 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2891 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2891 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2891 gene: VGAM789 host target protein, VGAM790

host target protein and VGAM791 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM789, VGAM790 and VGAM791.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2892(VGR2892) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93148] VGR2892 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2892 gene was detected is described hereinabove with reference to Figs. 1-9.

[93149] VGR2892 gene encodes VGR2892 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[93150] VGR2892 precursor RNA folds spatially, forming VGR2892 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2892 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2892 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93151] VGR2892 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM792 precursor RNA and VGAM793 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93152] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM792 RNA and VGAM793 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93153] VGAM792 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM792 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM792 host target RNA into VGAM792 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93154] VGAM793 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM793 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM793 host target RNA into VGAM793 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93155] It is appreciated that a function of VGR2892 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2892 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2892 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2892 gene: VGAM792 host target protein and VGAM793 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM792 and VGAM793.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2893(VGR2893) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[93156] VGR2893 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2893 gene was detected is described hereinabove with reference to Figs. 1-9.

[93157] VGR2893 gene encodes VGR2893 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93158] VGR2893 precursor RNA folds spatially, forming VGR2893 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2893 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2893 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93159] VGR2893 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM795 precursor RNA and VGAM796

precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93160] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM795 RNA and VGAM796 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93161] VGAM795 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM795 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM795 host target RNA into VGAM795 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93162] VGAM796 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM796 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM796 host target RNA into VGAM796 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93163] It is appreciated that a function of VGR2893 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2893 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2893 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2893 gene: VGAM795 host target protein and

VGAM796 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM795 and VGAM796.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2894(VGR2894) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93164] VGR2894 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2894 gene was detected is described hereinabove with reference to Figs. 1-9.

[93165] VGR2894 gene encodes VGR2894 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93166] VGR2894 precursor RNA folds spatially, forming VGR2894 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2894 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2894 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93167] VGR2894 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM797 precursor RNA and VGAM798 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93168] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM797 RNA and VGAM798 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93169] VGAM797 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM797 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM797 host target RNA into VGAM797 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93170] VGAM798 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM798 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM798 host target RNA into VGAM798 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93171] It is appreciated that a function of VGR2894 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2894 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2894 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2894 gene: VGAM797 host target protein and VGAM798 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM797 and VGAM798.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2895(VGR2895) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93172] VGR2895 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2895 gene was detected is described hereinabove with reference to Figs. 1-9.

[93173] VGR2895 gene encodes VGR2895 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93174] VGR2895 precursor RNA folds spatially, forming VGR2895 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2895 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2895 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93175] VGR2895 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM799 precursor RNA and VGAM800 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93176] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM799 RNA and VGAM800 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93177] VGAM799 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM799 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM799 host target RNA into VGAM799 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93178] VGAM800 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM800 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM800 host target RNA into VGAM800 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93179] It is appreciated that a function of VGR2895 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2895 gene include diagnosis, prevention and treatment of viral infection by Shrimp White Spot Syndrome Virus (white spot bacilliform virus). Specific functions, and accordingly utilities, of VGR2895 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2895 gene: VGAM799 host target protein and VGAM800 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM799 and VGAM800.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2896(VGR2896) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93180] VGR2896 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2896 gene was detected is described hereinabove with reference to Figs. 1-9.

[93181] VGR2896 gene encodes VGR2896 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93182] VGR2896 precursor RNA folds spatially, forming VGR2896 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2896 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2896 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93183] VGR2896 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM801 precursor RNA, VGAM802 precursor RNA and VGAM803 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93184] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM801 RNA, VGAM802 RNA and VGAM803 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93185] VGAM801 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM801 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM801 host target RNA into VGAM801 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93186] VGAM802 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM802 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM802 host target RNA into VGAM802 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93187] VGAM803 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM803 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM803 host target RNA into VGAM803 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93188] It is appreciated that a function of VGR2896 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2896 gene include diagnosis, prevention and treatment of viral infection by Murid Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2896 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2896 gene: VGAM801 host

target protein, VGAM802 host target protein and VGAM803 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM801, VGAM802 and VGAM803.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2897(VGR2897) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93189] VGR2897 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2897 gene was detected is described hereinabove with reference to Figs. 1-9.

[93190] VGR2897 gene encodes VGR2897 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93191] VGR2897 precursor RNA folds spatially, forming VGR2897 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2897 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2897 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93192] VGR2897 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM807 precursor RNA, VGAM808 precursor RNA and VGAM809 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93193] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM807 RNA, VGAM808 RNA and VGAM809 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93194] VGAM807 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM807 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM807 host target RNA into VGAM807 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93195] VGAM808 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM808 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM808 host target RNA into

VGAM808 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93196] VGAM809 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM809 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM809 host target RNA into VGAM809 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93197] It is appreciated that a function of VGR2897 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2897 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2897 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2897 gene: VGAM807 host target protein, VGAM808 host target protein and VGAM809 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM807, VGAM808 and VGAM809.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2898(VGR2898) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93198] VGR2898 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2898 gene was detected is described hereinabove with reference to Figs. 1-9.

[93199] VGR2898 gene encodes VGR2898 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93200] VGR2898 precursor RNA folds spatially, forming VGR2898 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2898 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2898 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93201] VGR2898 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM812 precursor RNA, VGAM813 precursor RNA and VGAM814 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93202] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM812

RNA, VGAM813 RNA and VGAM814 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93203] VGAM812 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM812 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM812 host target RNA into VGAM812 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93204] VGAM813 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM813 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM813 host target RNA into VGAM813 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93205] VGAM814 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM814 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM814 host target RNA into VGAM814 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93206] It is appreciated that a function of VGR2898 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2898 gene include diagnosis, prevention and treatment of viral infection by Murid Herpesvirus 4. Specific functions, and accordingly

utilities, of VGR2898 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2898 gene: VGAM812 host target protein, VGAM813 host target protein and VGAM814 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM812, VGAM813 and VGAM814.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2899(VGR2899) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93207] VGR2899 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2899 gene was detected is described hereinabove with reference to Figs. 1-9.

[93208] VGR2899 gene encodes VGR2899 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93209] VGR2899 precursor RNA folds spatially, forming VGR2899 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2899 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2899 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93210] VGR2899 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM815 precursor RNA and VGAM816 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93211] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM815 RNA and VGAM816 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93212] VGAM815 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM815 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM815 host target RNA into VGAM815 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93213] VGAM816 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM816 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM816 host target RNA into VGAM816 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93214] It is appreciated that a function of VGR2899 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2899 gene include diagnosis, prevention and treatment of viral infection by Macaca Mulatta Rhadinovirus. Specific functions, and accordingly utilities, of VGR2899 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2899 gene: VGAM815 host target protein and VGAM816 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM815 and VGAM816.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2900(VGR2900) viral gene,

which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93215] VGR2900 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2900 gene was detected is described hereinabove with reference to Figs. 1-9.

[93216] VGR2900 gene encodes VGR2900 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93217] VGR2900 precursor RNA folds spatially, forming VGR2900 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2900 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2900 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[93218] VGR2900 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM821 precursor RNA and VGAM822 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93219] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM821 RNA and VGAM822 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93220] VGAM821 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM821 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM821 host target RNA into VGAM821 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93221] VGAM822 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM822 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM822 host target RNA into VGAM822 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93222] It is appreciated that a function of VGR2900 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2900 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 6. Specific functions, and accordingly utilities, of VGR2900 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2900 gene: VGAM821 host target protein and VGAM822 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM821 and VGAM822.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2901(VGR2901) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93223] VGR2901 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2901 gene was detected is described hereinabove with reference to Figs. 1-9.

[93224] VGR2901 gene encodes VGR2901 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93225] VGR2901 precursor RNA folds spatially, forming VGR2901 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2901 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2901 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93226] VGR2901 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM823 precursor RNA and VGAM824 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93227] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM823 RNA and VGAM824 RNA, herein schematically represented

by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93228] VGAM823 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM823 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM823 host target RNA into VGAM823 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93229] VGAM824 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM824 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM824 host target RNA into

VGAM824 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93230] It is appreciated that a function of VGR2901 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2901 gene include diagnosis, prevention and treatment of viral infection by African Swine Fever Virus. Specific functions, and accordingly utilities, of VGR2901 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2901 gene: VGAM823 host target protein and VGAM824 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM823 and VGAM824.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2902(VGR2902) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of

at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93231] VGR2902 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2902 gene was detected is described hereinabove with reference to Figs. 1-9.

[93232] VGR2902 gene encodes VGR2902 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93233] VGR2902 precursor RNA folds spatially, forming VGR2902 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2902 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2902 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93234] VGR2902 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM826 precursor RNA and VGAM827 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93235] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM826 RNA and VGAM827 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93236] VGAM826 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM826 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM826 host target RNA into VGAM826 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93237] VGAM827 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM827 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM827 host target RNA into VGAM827 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93238] It is appreciated that a function of VGR2902 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2902 gene include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2902 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2902 gene: VGAM826 host

target protein and VGAM827 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM826 and VGAM827.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2903(VGR2903) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93239] VGR2903 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2903 gene was detected is described hereinabove with reference to Figs. 1-9.

[93240] VGR2903 gene encodes VGR2903 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93241] VGR2903 precursor RNA folds spatially, forming VGR2903 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2903 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2903 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93242] VGR2903 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM828 precursor RNA, VGAM829 precursor RNA and VGAM830 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93243] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM828 RNA, VGAM829 RNA and VGAM830 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 1.

[93244] VGAM828 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM828 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM828 host target RNA into VGAM828 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93245] VGAM829 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM829 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM829 host target RNA into VGAM829 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93246] VGAM830 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM830 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM830 host target RNA into VGAM830 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93247] It is appreciated that a function of VGR2903 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2903 gene include diagnosis, prevention and treatment of viral infection by African Swine Fever Virus. Specific functions, and accordingly utilities, of VGR2903 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR2903 gene: VGAM828 host target protein, VGAM829 host target protein and VGAM830 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM828, VGAM829 and VGAM830.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2904(VGR2904) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93248] VGR2904 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2904 gene was detected is described hereinabove with reference to Figs. 1-9.

[93249] VGR2904 gene encodes VGR2904 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93250] VGR2904 precursor RNA folds spatially, forming VGR2904

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2904 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2904 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93251] VGR2904 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM831 precursor RNA and VGAM832 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93252] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM831 RNA and VGAM832 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[93253] VGAM831 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM831 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM831 host target RNA into VGAM831 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93254] VGAM832 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM832 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM832 host target RNA into VGAM832 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93255] It is appreciated that a function of VGR2904 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2904 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 6B. Specific functions, and accordingly utilities, of VGR2904 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2904 gene: VGAM831 host target protein and VGAM832 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM831 and VGAM832.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2905(VGR2905) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of

which at least one host target gene is known in the art.

[93256] VGR2905 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2905 gene was detected is described hereinabove with reference to Figs. 1-9.

[93257] VGR2905 gene encodes VGR2905 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93258] VGR2905 precursor RNA folds spatially, forming VGR2905 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2905 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2905 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93259] VGR2905 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM833 precursor RNA, VGAM834 pre-

cursor RNA, VGAM835 precursor RNA, VGAM836 precursor RNA, VGAM837 precursor RNA and VGAM838 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93260] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM833 RNA, VGAM834 RNA, VGAM835 RNA, VGAM836 RNA, VGAM837 RNA and VGAM838 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93261] VGAM833 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM833 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM833 host target RNA into

VGAM833 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93262] VGAM834 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM834 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM834 host target RNA into VGAM834 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93263] VGAM835 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM835 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM835 host target RNA into VGAM835 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93264] VGAM836 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM836 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM836 host target RNA into VGAM836 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93265] VGAM837 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM837 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM837 host target RNA into VGAM837 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93266] VGAM838 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM838 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM838 host target RNA into VGAM838 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93267] It is appreciated that a function of VGR2905 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2905 gene include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly util-

ities, of VGR2905 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2905 gene: VGAM833 host target protein, VGAM834 host target protein, VGAM835 host target protein, VGAM836 host target protein, VGAM837 host target protein and VGAM838 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM833, VGAM834, VGAM835, VGAM836, VGAM837 and VGAM838.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2906(VGR2906) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93268] VGR2906 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2906 gene was

detected is described hereinabove with reference to Figs. 1-9.

[93269] VGR2906 gene encodes VGR2906 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93270] VGR2906 precursor RNA folds spatially, forming VGR2906 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2906 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2906 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93271] VGR2906 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM841 precursor RNA and VGAM842 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM

FOLDED PRECURSOR RNA of Fig. 1.

[93272] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM841 RNA and VGAM842 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93273] VGAM841 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM841 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM841 host target RNA into VGAM841 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93274] VGAM842 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM842 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM842 host target RNA into VGAM842 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93275] It is appreciated that a function of VGR2906 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2906 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2906 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2906 gene: VGAM841 host target protein and VGAM842 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM841 and VGAM842.Fig. 9 further

provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2907(VGR2907) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93276] VGR2907 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2907 gene was detected is described hereinabove with reference to Figs. 1-9.

[93277] VGR2907 gene encodes VGR2907 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93278] VGR2907 precursor RNA folds spatially, forming VGR2907 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2907 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2907 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93279] VGR2907 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM843 precursor RNA and VGAM844 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93280] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM843 RNA and VGAM844 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93281] VGAM843 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM843 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM843 host target RNA into VGAM843 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93282] VGAM844 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM844 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM844 host target RNA into VGAM844 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93283] It is appreciated that a function of VGR2907 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2907 gene include diagnosis, prevention and treatment of viral infection by

Monkeypox Virus. Specific functions, and accordingly utilities, of VGR2907 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2907 gene: VGAM843 host target protein and VGAM844 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM843 and VGAM844.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2908(VGR2908) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93284] VGR2908 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2908 gene was detected is described hereinabove with reference to Figs. 1-9.

[93285] VGR2908 gene encodes VGR2908 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93286] VGR2908 precursor RNA folds spatially, forming VGR2908 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2908 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2908 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93287] VGR2908 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM845 precursor RNA, VGAM846 precursor RNA, VGAM847 precursor RNA and VGAM848 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93288] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM845 RNA, VGAM846 RNA, VGAM847 RNA and VGAM848 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93289] VGAM845 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM845 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM845 host target RNA into VGAM845 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93290] VGAM846 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM846 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM846 host target RNA into VGAM846 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93291] VGAM847 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM847 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM847 host target RNA into VGAM847 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93292] VGAM848 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM848 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM848 host target RNA into VGAM848 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93293] It is appreciated that a function of VGR2908 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2908 gene include diagnosis, prevention and treatment of viral infection by Gallid Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2908 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2908 gene: VGAM845 host target protein, VGAM846 host target protein, VGAM847 host target protein and VGAM848 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-

above with reference to VGAM845, VGAM846, VGAM847 and VGAM848.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2909(VGR2909) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93294] VGR2909 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2909 gene was detected is described hereinabove with reference to Figs. 1-9.

[93295] VGR2909 gene encodes VGR2909 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93296] VGR2909 precursor RNA folds spatially, forming VGR2909 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2909 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2909 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93297] VGR2909 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM849 precursor RNA, VGAM850 precursor RNA and VGAM851 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93298] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM849 RNA, VGAM850 RNA and VGAM851 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93299] VGAM849 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM849 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM849 host target RNA into VGAM849 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93300] VGAM850 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM850 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM850 host target RNA into VGAM850 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93301] VGAM851 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM851 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM851 host target RNA into VGAM851 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93302] It is appreciated that a function of VGR2909 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2909 gene include diagnosis, prevention and treatment of viral infection by Lymphocystis Disease Virus 1. Specific functions, and accordingly utilities, of VGR2909 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2909 gene: VGAM849 host target protein, VGAM850 host target protein and VGAM851 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM849, VGAM850 and VGAM851.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2910(VGR2910) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93303] VGR2910 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2910 gene was detected is described hereinabove with reference to Figs. 1-9.

[93304] VGR2910 gene encodes VGR2910 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93305] VGR2910 precursor RNA folds spatially, forming VGR2910 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2910 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2910 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93306] VGR2910 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM855 precursor RNA and VGAM856 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93307] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM855 RNA and VGAM856 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93308] VGAM855 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM855 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM855 host target RNA into VGAM855 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93309] VGAM856 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM856 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM856 host target RNA into VGAM856 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93310] It is appreciated that a function of VGR2910 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2910 gene include diagnosis, prevention and treatment of viral infection by African Swine Fever Virus. Specific functions, and accordingly utilities, of VGR2910 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2910 gene: VGAM855 host target protein and VGAM856 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM855 and VGAM856.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2911(VGR2911) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93311] VGR2911 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2911 gene was detected is described hereinabove with reference to Figs. 1-9.

[93312] VGR2911 gene encodes VGR2911 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93313] VGR2911 precursor RNA folds spatially, forming VGR2911 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2911 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2911 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93314] VGR2911 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM857 precursor RNA, VGAM858 precursor RNA and VGAM859 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93315] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM857 RNA, VGAM858 RNA and VGAM859 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93316] VGAM857 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM857 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM857 host target RNA into VGAM857 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93317] VGAM858 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM858 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM858 host target RNA into VGAM858 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93318] VGAM859 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM859 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM859 host target RNA into VGAM859 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93319] It is appreciated that a function of VGR2911 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2911 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR2911 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2911 gene: VGAM857 host target protein, VGAM858 host target protein and VGAM859 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM857, VGAM858 and VGAM859.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2912(VGR2912) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93320] VGR2912 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2912 gene was detected is described hereinabove with reference to Figs. 1-9.

[93321] VGR2912 gene encodes VGR2912 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93322] VGR2912 precursor RNA folds spatially, forming VGR2912 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2912 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2912 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93323] VGR2912 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM861 precursor RNA, VGAM862 precursor RNA, VGAM863 precursor RNA and VGAM864 pre-

cursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93324] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM861 RNA, VGAM862 RNA, VGAM863 RNA and VGAM864 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93325] VGAM861 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM861 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM861 host target RNA into VGAM861 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93326] VGAM862 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM862 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM862 host target RNA into VGAM862 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93327] VGAM863 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM863 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM863 host target RNA into VGAM863 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93328] VGAM864 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM864 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM864 host target RNA into VGAM864 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93329] It is appreciated that a function of VGR2912 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2912 gene include diagnosis, prevention and treatment of viral infection by Ictalurid Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2912 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR2912 gene: VGAM861 host target protein, VGAM862 host target protein, VGAM863 host target protein and VGAM864 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM861, VGAM862, VGAM863 and VGAM864.Fig. 9 further provides a conceptual de-scription of novel bioinformatically detected regulatory vi-ral gene, referred to here as Viral Genomic Record 2913(VGR2913) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93330] VGR2913 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2913 gene was detected is described hereinabove with reference to Figs. 1-9.

[93331] VGR2913 gene encodes VGR2913 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[93332] VGR2913 precursor RNA folds spatially, forming VGR2913 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2913 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2913 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93333] VGR2913 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM865 precursor RNA and VGAM866 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93334] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM865 RNA and VGAM866 RNA, herein schematically represented

by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93335] VGAM865 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM865 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM865 host target RNA into VGAM865 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93336] VGAM866 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM866 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM866 host target RNA into

VGAM866 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93337] It is appreciated that a function of VGR2913 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2913 gene include diagnosis, prevention and treatment of viral infection by Swinepox Virus. Specific functions, and accordingly utilities, of VGR2913 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2913 gene: VGAM865 host target protein and VGAM866 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM865 and VGAM866.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2914(VGR2914) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of

at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93338] VGR2914 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2914 gene was detected is described hereinabove with reference to Figs. 1-9.

[93339] VGR2914 gene encodes VGR2914 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93340] VGR2914 precursor RNA folds spatially, forming VGR2914 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2914 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2914 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93341] VGR2914 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM867 precursor RNA and VGAM868 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93342] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM867 RNA and VGAM868 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93343] VGAM867 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM867 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM867 host target RNA into VGAM867 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93344] VGAM868 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM868 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM868 host target RNA into VGAM868 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93345] It is appreciated that a function of VGR2914 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2914 gene include diagnosis, prevention and treatment of viral infection by Turkey Adenovirus 3. Specific functions, and accordingly utilities, of VGR2914 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2914 gene: VGAM867 host

target protein and VGAM868 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM867 and VGAM868.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2915(VGR2915) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93346] VGR2915 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2915 gene was detected is described hereinabove with reference to Figs. 1-9.

[93347] VGR2915 gene encodes VGR2915 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93348] VGR2915 precursor RNA folds spatially, forming VGR2915 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2915 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2915 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93349] VGR2915 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM869 precursor RNA, VGAM870 precursor RNA, VGAM871 precursor RNA, VGAM872 precursor RNA and VGAM873 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93350] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM869 RNA, VGAM870 RNA, VGAM871 RNA, VGAM872 RNA and VGAM873 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[93351] VGAM869 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM869 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM869 host target RNA into VGAM869 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93352] VGAM870 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM870 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM870 host target RNA into VGAM870 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93353] VGAM871 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM871 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM871 host target RNA into VGAM871 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93354] VGAM872 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM872 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM872 host target RNA into

VGAM872 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93355] VGAM873 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM873 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM873 host target RNA into VGAM873 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93356] It is appreciated that a function of VGR2915 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2915 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2915 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2915 gene: VGAM869 host target protein, VGAM870 host target protein, VGAM871 host target protein, VGAM872 host target protein and VGAM873 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM869, VGAM870, VGAM871, VGAM872 and VGAM873.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2916(VGR2916) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93357] VGR2916 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2916 gene was detected is described hereinabove with reference to Figs. 1-9.

[93358] VGR2916 gene encodes VGR2916 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93359] VGR2916 precursor RNA folds spatially, forming VGR2916 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2916 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2916 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93360] VGR2916 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM875 precursor RNA, VGAM876 precursor RNA and VGAM877 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93361] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM875 RNA, VGAM876 RNA and VGAM877 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93362] VGAM875 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM875 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM875 host target RNA into VGAM875 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93363] VGAM876 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM876 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM876 host target RNA into VGAM876 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93364] VGAM877 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM877 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM877 host target RNA into VGAM877 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93365] It is appreciated that a function of VGR2916 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2916 gene include

diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGR2916 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2916 gene: VGAM875 host target protein, VGAM876 host target protein and VGAM877 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM875, VGAM876 and VGAM877.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2917(VGR2917) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93366] VGR2917 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2917 gene was detected is described hereinabove with reference to Figs.

1-9.

[93367] VGR2917 gene encodes VGR2917 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93368] VGR2917 precursor RNA folds spatially, forming VGR2917 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2917 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2917 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93369] VGR2917 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM880 precursor RNA and VGAM881 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93370] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM880 RNA and VGAM881 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93371] VGAM880 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM880 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM880 host target RNA into VGAM880 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93372] VGAM881 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM881 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM881 host target RNA into VGAM881 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93373] It is appreciated that a function of VGR2917 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2917 gene include diagnosis, prevention and treatment of viral infection by Gallid Herpesvirus 3. Specific functions, and accordingly utilities, of VGR2917 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2917 gene: VGAM880 host target protein and VGAM881 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM880 and VGAM881.Fig. 9 further provides a conceptual description of novel bioinformati-

cally detected regulatory viral gene, referred to here as Viral Genomic Record 2918(VGR2918) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93374] VGR2918 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2918 gene was detected is described hereinabove with reference to Figs. 1-9.

[93375] VGR2918 gene encodes VGR2918 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93376] VGR2918 precursor RNA folds spatially, forming VGR2918 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2918 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2918 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[93377] VGR2918 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM886 precursor RNA and VGAM887 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93378] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM886 RNA and VGAM887 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93379] VGAM886 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM886 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM886 host target RNA into VGAM886 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93380] VGAM887 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM887 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM887 host target RNA into VGAM887 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93381] It is appreciated that a function of VGR2918 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2918 gene include diagnosis, prevention and treatment of viral infection by Vaccinia Virus. Specific functions, and accordingly utilities,

of VGR2918 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2918 gene: VGAM886 host target protein and VGAM887 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM886 and VGAM887.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2919(VGR2919) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93382] VGR2919 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2919 gene was detected is described hereinabove with reference to Figs. 1-9.

[93383] VGR2919 gene encodes VGR2919 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[93384] VGR2919 precursor RNA folds spatially, forming VGR2919 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2919 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2919 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93385] VGR2919 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM888 precursor RNA, VGAM889 precursor RNA, VGAM890 precursor RNA and VGAM891 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93386] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM888 RNA, VGAM889 RNA, VGAM890 RNA and VGAM891 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93387] VGAM888 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM888 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM888 host target RNA into VGAM888 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93388] VGAM889 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM889 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM889 host target RNA into VGAM889 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93389] VGAM890 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM890 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM890 host target RNA into VGAM890 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93390] VGAM891 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM891 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM891 host target RNA into VGAM891 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93391] It is appreciated that a function of VGR2919 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2919 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2919 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2919 gene: VGAM888 host target protein, VGAM889 host target protein, VGAM890 host target protein and VGAM891 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM888, VGAM889, VGAM890

and VGAM891.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2920(VGR2920) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93392] VGR2920 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2920 gene was detected is described hereinabove with reference to Figs. 1-9.

[93393] VGR2920 gene encodes VGR2920 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93394] VGR2920 precursor RNA folds spatially, forming VGR2920 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2920 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2920 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93395] VGR2920 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM892 precursor RNA, VGAM893 precursor RNA and VGAM894 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93396] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM892 RNA, VGAM893 RNA and VGAM894 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93397] VGAM892 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM892 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM892 host target RNA into VGAM892 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93398] VGAM893 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM893 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM893 host target RNA into VGAM893 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93399] VGAM894 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM894 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM894 host target RNA into VGAM894 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93400] It is appreciated that a function of VGR2920 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2920 gene include diagnosis, prevention and treatment of viral infection by Periplaneta Fuliginosa Densovirus. Specific functions, and accordingly utilities, of VGR2920 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2920 gene: VGAM892 host target protein, VGAM893 host target protein and VGAM894 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM892, VGAM893 and VGAM894.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2921(VGR2921) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93401] VGR2921 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2921 gene was detected is described hereinabove with reference to Figs. 1-9.

[93402] VGR2921 gene encodes VGR2921 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93403] VGR2921 precursor RNA folds spatially, forming VGR2921 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2921 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2921 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93404] VGR2921 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM895 precursor RNA, VGAM896 precursor RNA and VGAM897 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93405] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM895 RNA, VGAM896 RNA and VGAM897 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93406] VGAM895 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM895 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM895 host target RNA into VGAM895 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93407] VGAM896 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM896 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM896 host target RNA into VGAM896 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93408] VGAM897 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM897 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM897 host target RNA into VGAM897 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93409] It is appreciated that a function of VGR2921 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2921 gene include diagnosis, prevention and treatment of viral infection by Gallid Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2921 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2921 gene: VGAM895 host target protein, VGAM896 host target protein and

VGAM897 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM895, VGAM896 and VGAM897.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2922(VGR2922) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93410] VGR2922 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2922 gene was detected is described hereinabove with reference to Figs. 1-9.

[93411] VGR2922 gene encodes VGR2922 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93412] VGR2922 precursor RNA folds spatially, forming VGR2922 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2922 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2922 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93413] VGR2922 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM901 precursor RNA and VGAM902 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93414] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM901 RNA and VGAM902 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93415] VGAM901 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM901 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM901 host target RNA into VGAM901 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93416] VGAM902 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM902 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM902 host target RNA into VGAM902 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93417] It is appreciated that a function of VGR2922 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2922 gene include diagnosis, prevention and treatment of viral infection by Sulfolobus Virus SIRV-1. Specific functions, and accordingly utilities, of VGR2922 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2922 gene: VGAM901 host target protein and VGAM902 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM901 and VGAM902.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2923(VGR2923) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93418] VGR2923 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2923 gene was detected is described hereinabove with reference to Figs. 1-9.

[93419] VGR2923 gene encodes VGR2923 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93420] VGR2923 precursor RNA folds spatially, forming VGR2923 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2923 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2923 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93421] VGR2923 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM903 precursor RNA and VGAM904 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93422] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM903 RNA and VGAM904 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93423] VGAM903 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM903 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM903 host target RNA into VGAM903 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93424] VGAM904 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM904 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM904 host target RNA into VGAM904 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93425] It is appreciated that a function of VGR2923 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2923 gene include diagnosis, prevention and treatment of viral infection by Melanoplus Sanguinipes Entomopoxvirus. Specific functions, and accordingly utilities, of VGR2923 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2923 gene: VGAM903 host target protein and VGAM904 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN.

The function of these host target genes is elaborated hereinabove with reference to VGAM903 and VGAM904.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2924(VGR2924) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93426] VGR2924 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2924 gene was detected is described hereinabove with reference to Figs. 1-9.

[93427] VGR2924 gene encodes VGR2924 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93428] VGR2924 precursor RNA folds spatially, forming VGR2924 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2924 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2924 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93429] VGR2924 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM905 precursor RNA, VGAM906 precursor RNA, VGAM907 precursor RNA and VGAM908 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93430] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM905 RNA, VGAM906 RNA, VGAM907 RNA and VGAM908 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93431] VGAM905 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM905 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM905 host target RNA into VGAM905 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93432] VGAM906 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM906 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM906 host target RNA into VGAM906 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93433] VGAM907 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM907 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM907 host target RNA into VGAM907 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93434] VGAM908 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM908 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM908 host target RNA into VGAM908 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93435] It is appreciated that a function of VGR2924 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2924 gene include diagnosis, prevention and treatment of viral infection by Saimiriine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2924 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2924 gene: VGAM905 host target protein, VGAM906 host target protein, VGAM907 host target protein and VGAM908 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM905, VGAM906, VGAM907 and VGAM908.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2925(VGR2925) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one

host target gene, the function and utility of which at least one host target gene is known in the art.

[93436] VGR2925 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2925 gene was detected is described hereinabove with reference to Figs. 1-9.

[93437] VGR2925 gene encodes VGR2925 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93438] VGR2925 precursor RNA folds spatially, forming VGR2925 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2925 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2925 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93439] VGR2925 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM909 precursor RNA and VGAM910 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93440] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM909 RNA and VGAM910 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93441] VGAM909 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM909 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM909 host target RNA into VGAM909 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93442] VGAM910 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM910 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM910 host target RNA into VGAM910 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93443] It is appreciated that a function of VGR2925 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2925 gene include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2925 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2925 gene: VGAM909 host

target protein and VGAM910 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM909 and VGAM910.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2926(VGR2926) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93444] VGR2926 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2926 gene was detected is described hereinabove with reference to Figs. 1-9.

[93445] VGR2926 gene encodes VGR2926 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93446] VGR2926 precursor RNA folds spatially, forming VGR2926 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2926 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2926 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93447] VGR2926 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM911 precursor RNA and VGAM912 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93448] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM911 RNA and VGAM912 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93449] VGAM911 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM911 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM911 host target RNA into VGAM911 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93450] VGAM912 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM912 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM912 host target RNA into VGAM912 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93451] It is appreciated that a function of VGR2926 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2926 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 8. Specific functions, and accordingly utilities, of VGR2926 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2926 gene: VGAM911 host target protein and VGAM912 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM911 and VGAM912.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2927(VGR2927) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93452] VGR2927 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2927 gene was detected is described hereinabove with reference to Figs. 1-9.

[93453] VGR2927 gene encodes VGR2927 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93454] VGR2927 precursor RNA folds spatially, forming VGR2927 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2927 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2927 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93455] VGR2927 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM913 precursor RNA and VGAM914 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93456] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM913 RNA and VGAM914 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93457] VGAM913 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM913 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM913 host target RNA into VGAM913 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93458] VGAM914 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM914 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM914 host target RNA into VGAM914 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93459] It is appreciated that a function of VGR2927 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2927 gene include diagnosis, prevention and treatment of viral infection by Pothos Latent Virus. Specific functions, and accordingly utilities, of VGR2927 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2927 gene: VGAM913 host target protein and VGAM914 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The func-

tion of these host target genes is elaborated hereinabove with reference to VGAM913 and VGAM914.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2928(VGR2928) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93460] VGR2928 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2928 gene was detected is described hereinabove with reference to Figs. 1-9.

[93461] VGR2928 gene encodes VGR2928 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93462] VGR2928 precursor RNA folds spatially, forming VGR2928 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2928 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2928 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93463] VGR2928 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM915 precursor RNA and VGAM916 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93464] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM915 RNA and VGAM916 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93465] VGAM915 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM915 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM915 host target RNA into VGAM915 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93466] VGAM916 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM916 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM916 host target RNA into VGAM916 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93467] It is appreciated that a function of VGR2928 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2928 gene include diagnosis, prevention and treatment of viral infection by Trichoplusia Ni Cytoplasmic Polyhedrosis Virus 15. Specific functions, and accordingly utilities, of VGR2928 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2928 gene: VGAM915 host target protein and VGAM916 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM915 and VGAM916.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2929(VGR2929) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93468] VGR2929 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2929 gene was

detected is described hereinabove with reference to Figs. 1-9.

[93469] VGR2929 gene encodes VGR2929 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93470] VGR2929 precursor RNA folds spatially, forming VGR2929 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2929 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2929 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93471] VGR2929 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM918 precursor RNA and VGAM919 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM

FOLDED PRECURSOR RNA of Fig. 1.

[93472] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM918 RNA and VGAM919 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93473] VGAM918 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM918 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM918 host target RNA into VGAM918 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93474] VGAM919 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM919 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM919 host target RNA into VGAM919 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93475] It is appreciated that a function of VGR2929 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2929 gene include diagnosis, prevention and treatment of viral infection by Vaccinia Virus. Specific functions, and accordingly utilities, of VGR2929 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2929 gene: VGAM918 host target protein and VGAM919 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM918 and VGAM919.Fig. 9 further provides a

conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2930(VGR2930) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93476] VGR2930 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2930 gene was detected is described hereinabove with reference to Figs. 1-9.

[93477] VGR2930 gene encodes VGR2930 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93478] VGR2930 precursor RNA folds spatially, forming VGR2930 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2930 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2930 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93479] VGR2930 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM921 precursor RNA, VGAM922 precursor RNA and VGAM923 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93480] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM921 RNA, VGAM922 RNA and VGAM923 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93481] VGAM921 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM921 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM921 host target RNA into VGAM921 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93482] VGAM922 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM922 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM922 host target RNA into VGAM922 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93483] VGAM923 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM923 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM923 host target RNA into VGAM923 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93484] It is appreciated that a function of VGR2930 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2930 gene include diagnosis, prevention and treatment of viral infection by Peanut Clump Virus. Specific functions, and accordingly utilities, of VGR2930 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2930 gene: VGAM921 host target protein, VGAM922 host target protein and VGAM923 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target

genes is elaborated hereinabove with reference to VGAM921, VGAM922 and VGAM923.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2931(VGR2931) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93485] VGR2931 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2931 gene was detected is described hereinabove with reference to Figs. 1-9.

[93486] VGR2931 gene encodes VGR2931 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93487] VGR2931 precursor RNA folds spatially, forming VGR2931 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2931 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2931 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93488] VGR2931 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM924 precursor RNA, VGAM925 precursor RNA, VGAM926 precursor RNA, VGAM927 precursor RNA, VGAM928 precursor RNA and VGAM929 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93489] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM924 RNA, VGAM925 RNA, VGAM926 RNA, VGAM927 RNA, VGAM928 RNA and VGAM929 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93490] VGAM924 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM924 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM924 host target RNA into VGAM924 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93491] VGAM925 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM925 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM925 host target RNA into VGAM925 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93492] VGAM926 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM926 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM926 host target RNA into VGAM926 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93493] VGAM927 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM927 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM927 host target RNA into VGAM927 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93494] VGAM928 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM928 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM928 host target RNA into VGAM928 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93495] VGAM929 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM929 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM929 host target RNA into VGAM929 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93496] It is appreciated that a function of VGR2931 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2931 gene include diagnosis, prevention and treatment of viral infection by Infectious Spleen and Kidney Necrosis Virus. Specific functions, and accordingly utilities, of VGR2931 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2931 gene: VGAM924 host target protein, VGAM925 host target protein, VGAM926 host target protein, VGAM927 host target protein, VGAM928 host target protein and VGAM929 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM924, VGAM925, VGAM926, VGAM927, VGAM928 and VGAM929.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2932(VGR2932)

viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93497] VGR2932 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2932 gene was detected is described hereinabove with reference to Figs. 1-9.

[93498] VGR2932 gene encodes VGR2932 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93499] VGR2932 precursor RNA folds spatially, forming VGR2932 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2932 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2932 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[93500] VGR2932 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM932 precursor RNA, VGAM933 precursor RNA and VGAM934 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93501] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM932 RNA, VGAM933 RNA and VGAM934 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93502] VGAM932 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM932 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM932 host target RNA into VGAM932 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93503] VGAM933 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM933 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM933 host target RNA into VGAM933 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93504] VGAM934 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM934 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM934 host target RNA into VGAM934 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93505] It is appreciated that a function of VGR2932 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2932 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2932 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2932 gene: VGAM932 host target protein, VGAM933 host target protein and VGAM934 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM932, VGAM933 and VGAM934.Fig. 9 further pro-

vides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2933(VGR2933) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93506] VGR2933 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2933 gene was detected is described hereinabove with reference to Figs. 1-9.

[93507] VGR2933 gene encodes VGR2933 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93508] VGR2933 precursor RNA folds spatially, forming VGR2933 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2933 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2933 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93509] VGR2933 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM935 precursor RNA, VGAM936 precursor RNA and VGAM937 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93510] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM935 RNA, VGAM936 RNA and VGAM937 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93511] VGAM935 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM935 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM935 host target RNA into VGAM935 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93512] VGAM936 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM936 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM936 host target RNA into VGAM936 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93513] VGAM937 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM937 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM937 host target RNA into VGAM937 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93514] It is appreciated that a function of VGR2933 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2933 gene include diagnosis, prevention and treatment of viral infection by Melanoplus Sanguinipes Entomopoxvirus. Specific functions, and accordingly utilities, of VGR2933 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2933 gene: VGAM935 host target protein, VGAM936 host target protein and VGAM937 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of

these host target genes is elaborated hereinabove with reference to VGAM935, VGAM936 and VGAM937.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2934(VGR2934) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93515] VGR2934 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2934 gene was detected is described hereinabove with reference to Figs. 1-9.

[93516] VGR2934 gene encodes VGR2934 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93517] VGR2934 precursor RNA folds spatially, forming VGR2934 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2934 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2934 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93518] VGR2934 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM938 precursor RNA, VGAM939 precursor RNA and VGAM940 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93519] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM938 RNA, VGAM939 RNA and VGAM940 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93520] VGAM938 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM938 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM938 host target RNA into VGAM938 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93521] VGAM939 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM939 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM939 host target RNA into VGAM939 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93522] VGAM940 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM940 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM940 host target RNA into VGAM940 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93523] It is appreciated that a function of VGR2934 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2934 gene include diagnosis, prevention and treatment of viral infection by Beet Soil-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGR2934 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2934 gene: VGAM938 host target protein, VGAM939 host target protein and

VGAM940 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM938, VGAM939 and VGAM940.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2935(VGR2935) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93524] VGR2935 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2935 gene was detected is described hereinabove with reference to Figs. 1-9.

[93525] VGR2935 gene encodes VGR2935 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93526] VGR2935 precursor RNA folds spatially, forming VGR2935 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2935 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2935 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93527] VGR2935 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM941 precursor RNA, VGAM942 precursor RNA and VGAM943 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93528] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM941 RNA, VGAM942 RNA and VGAM943 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 1.

[93529] VGAM941 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM941 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM941 host target RNA into VGAM941 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93530] VGAM942 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM942 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM942 host target RNA into VGAM942 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93531] VGAM943 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM943 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM943 host target RNA into VGAM943 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93532] It is appreciated that a function of VGR2935 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2935 gene include diagnosis, prevention and treatment of viral infection by Infectious Spleen and Kidney Necrosis Virus. Specific functions, and accordingly utilities, of VGR2935 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs

comprised in the `operon-like` cluster of VGR2935 gene: VGAM941 host target protein, VGAM942 host target protein and VGAM943 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM941, VGAM942 and VGAM943.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2936(VGR2936) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93533] VGR2936 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2936 gene was detected is described hereinabove with reference to Figs. 1-9.

[93534] VGR2936 gene encodes VGR2936 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93535] VGR2936 precursor RNA folds spatially, forming VGR2936 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2936 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2936 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93536] VGR2936 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM944 precursor RNA and VGAM945 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93537] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM944 RNA and VGAM945 RNA, herein schematically represented

by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93538] VGAM944 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM944 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM944 host target RNA into VGAM944 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93539] VGAM945 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM945 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM945 host target RNA into

VGAM945 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93540] It is appreciated that a function of VGR2936 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2936 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 7. Specific functions, and accordingly utilities, of VGR2936 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2936 gene: VGAM944 host target protein and VGAM945 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM944 and VGAM945.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2937(VGR2937) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of

at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93541] VGR2937 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2937 gene was detected is described hereinabove with reference to Figs. 1-9.

[93542] VGR2937 gene encodes VGR2937 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93543] VGR2937 precursor RNA folds spatially, forming VGR2937 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2937 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2937 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93544] VGR2937 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM946 precursor RNA and VGAM947 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93545] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM946 RNA and VGAM947 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93546] VGAM946 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM946 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM946 host target RNA into VGAM946 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93547] VGAM947 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM947 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM947 host target RNA into VGAM947 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93548] It is appreciated that a function of VGR2937 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2937 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 6. Specific functions, and accordingly utilities, of VGR2937 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2937 gene: VGAM946 host

target protein and VGAM947 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM946 and VGAM947.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2938(VGR2938) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93549] VGR2938 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2938 gene was detected is described hereinabove with reference to Figs. 1-9.

[93550] VGR2938 gene encodes VGR2938 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93551] VGR2938 precursor RNA folds spatially, forming VGR2938 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2938 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2938 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93552] VGR2938 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM948 precursor RNA and VGAM949 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93553] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM948 RNA and VGAM949 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93554] VGAM948 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM948 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM948 host target RNA into VGAM948 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93555] VGAM949 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM949 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM949 host target RNA into VGAM949 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93556] It is appreciated that a function of VGR2938 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2938 gene include diagnosis, prevention and treatment of viral infection by Carnation Italian Ringspot Virus. Specific functions, and accordingly utilities, of VGR2938 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2938 gene: VGAM948 host target protein and VGAM949 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM948 and VGAM949.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2939(VGR2939) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93557] VGR2939 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2939 gene was detected is described hereinabove with reference to Figs. 1-9.

[93558] VGR2939 gene encodes VGR2939 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93559] VGR2939 precursor RNA folds spatially, forming VGR2939 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2939 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2939 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93560] VGR2939 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM950 precursor RNA, VGAM951 precursor RNA and VGAM952 precursor RNA, herein

schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93561] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM950 RNA, VGAM951 RNA and VGAM952 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93562] VGAM950 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM950 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM950 host target RNA into VGAM950 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93563] VGAM951 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM951 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM951 host target RNA into VGAM951 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93564] VGAM952 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM952 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM952 host target RNA into VGAM952 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93565] It is appreciated that a function of VGR2939 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2939 gene include diagnosis, prevention and treatment of viral infection by Tomato Bushy Stunt Virus. Specific functions, and accordingly utilities, of VGR2939 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2939 gene: VGAM950 host target protein, VGAM951 host target protein and VGAM952 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM950, VGAM951 and VGAM952.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2940(VGR2940) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of

at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93566] VGR2940 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2940 gene was detected is described hereinabove with reference to Figs. 1-9.

[93567] VGR2940 gene encodes VGR2940 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93568] VGR2940 precursor RNA folds spatially, forming VGR2940 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2940 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2940 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93569] VGR2940 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM

precursor RNAs, VGAM953 precursor RNA, VGAM954 precursor RNA, VGAM955 precursor RNA, VGAM956 precursor RNA, VGAM957 precursor RNA and VGAM958 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93570] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM953 RNA, VGAM954 RNA, VGAM955 RNA, VGAM956 RNA, VGAM957 RNA and VGAM958 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93571] VGAM953 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM953 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM953 host target RNA into VGAM953 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93572] VGAM954 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM954 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM954 host target RNA into VGAM954 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93573] VGAM955 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM955 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM955 host target RNA into VGAM955 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93574] VGAM956 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM956 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM956 host target RNA into VGAM956 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93575] VGAM957 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM957 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM957 host target RNA into VGAM957 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93576] VGAM958 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM958 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM958 host target RNA into VGAM958 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93577] It is appreciated that a function of VGR2940 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2940 gene include diagnosis, prevention and treatment of viral infection by

Tomato Spotted Wilt Virus. Specific functions, and accordingly utilities, of VGR2940 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2940 gene: VGAM953 host target protein, VGAM954 host target protein, VGAM955 host target protein, VGAM956 host target protein, VGAM957 host target protein and VGAM958 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM953, VGAM954, VGAM955, VGAM956, VGAM957 and VGAM958.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2941(VGR2941) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93578] VGR2941 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2941 gene was detected is described hereinabove with reference to Figs. 1-9.

[93579] VGR2941 gene encodes VGR2941 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93580] VGR2941 precursor RNA folds spatially, forming VGR2941 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2941 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2941 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93581] VGR2941 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM959 precursor RNA, VGAM960 precursor RNA and VGAM961 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93582] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM959 RNA, VGAM960 RNA and VGAM961 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93583] VGAM959 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM959 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM959 host target RNA into VGAM959 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93584] VGAM960 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM960 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM960 host target RNA into VGAM960 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93585] VGAM961 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM961 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM961 host target RNA into VGAM961 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93586] It is appreciated that a function of VGR2941 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2941 gene include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGR2941 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2941 gene: VGAM959 host target protein, VGAM960 host target protein and VGAM961 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM959, VGAM960 and VGAM961.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2942(VGR2942) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93587] VGR2942 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2942 gene was detected is described hereinabove with reference to Figs. 1-9.

[93588] VGR2942 gene encodes VGR2942 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93589] VGR2942 precursor RNA folds spatially, forming VGR2942 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2942 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2942 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93590] VGR2942 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM962 precursor RNA, VGAM963 precursor RNA, VGAM964 precursor RNA, VGAM965 precur-

sor RNA and VGAM966 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93591] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM962 RNA, VGAM963 RNA, VGAM964 RNA, VGAM965 RNA and VGAM966 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93592] VGAM962 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM962 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM962 host target RNA into VGAM962 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3

HOST TARGET PROTEIN, all of Fig. 1.

[93593] VGAM963 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM963 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM963 host target RNA into VGAM963 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93594] VGAM964 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM964 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM964 host target RNA into VGAM964 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93595] VGAM965 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM965 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM965 host target RNA into VGAM965 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93596] VGAM966 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM966 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM966 host target RNA into

VGAM966 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93597] It is appreciated that a function of VGR2942 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2942 gene include diagnosis, prevention and treatment of viral infection by Meleagrid Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2942 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2942 gene: VGAM962 host target protein, VGAM963 host target protein, VGAM964 host target protein, VGAM965 host target protein and VGAM966 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM962, VGAM963, VGAM964, VGAM965 and VGAM966.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2943(VGR2943)

viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93598] VGR2943 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2943 gene was detected is described hereinabove with reference to Figs. 1-9.

[93599] VGR2943 gene encodes VGR2943 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93600] VGR2943 precursor RNA folds spatially, forming VGR2943 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2943 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2943 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[93601] VGR2943 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM967 precursor RNA, VGAM968 precursor RNA, VGAM969 precursor RNA and VGAM970 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93602] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM967 RNA, VGAM968 RNA, VGAM969 RNA and VGAM970 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93603] VGAM967 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM967 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM967 host target RNA into VGAM967 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93604] VGAM968 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM968 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM968 host target RNA into VGAM968 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93605] VGAM969 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM969 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM969 host target RNA into VGAM969 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93606] VGAM970 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM970 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM970 host target RNA into VGAM970 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93607] It is appreciated that a function of VGR2943 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2943 gene include

diagnosis, prevention and treatment of viral infection by Sheeppox Virus. Specific functions, and accordingly utilities, of VGR2943 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2943 gene: VGAM967 host target protein, VGAM968 host target protein, VGAM969 host target protein and VGAM970 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM967, VGAM968, VGAM969 and VGAM970.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2944(VGR2944) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93608] VGR2944 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2944 gene was

detected is described hereinabove with reference to Figs. 1-9.

[93609] VGR2944 gene encodes VGR2944 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93610] VGR2944 precursor RNA folds spatially, forming VGR2944 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2944 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2944 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93611] VGR2944 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM971 precursor RNA and VGAM972 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM

FOLDED PRECURSOR RNA of Fig. 1.

[93612] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM971 RNA and VGAM972 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93613] VGAM971 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM971 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM971 host target RNA into VGAM971 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93614] VGAM972 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM972 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM972 host target RNA into VGAM972 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93615] It is appreciated that a function of VGR2944 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2944 gene include diagnosis, prevention and treatment of viral infection by Melanoplus Sanguinipes Entomopoxvirus. Specific functions, and accordingly utilities, of VGR2944 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2944 gene: VGAM971 host target protein and VGAM972 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM971 and

VGAM972.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2945(VGR2945) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93616] VGR2945 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2945 gene was detected is described hereinabove with reference to Figs. 1-9.

[93617] VGR2945 gene encodes VGR2945 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93618] VGR2945 precursor RNA folds spatially, forming VGR2945 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2945 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2945 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93619] VGR2945 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM975 precursor RNA, VGAM976 precursor RNA, VGAM977 precursor RNA, VGAM978 precursor RNA and VGAM979 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93620] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM975 RNA, VGAM976 RNA, VGAM977 RNA, VGAM978 RNA and VGAM979 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93621] VGAM975 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM975 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM975 host target RNA into VGAM975 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93622] VGAM976 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM976 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM976 host target RNA into VGAM976 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93623] VGAM977 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM977 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM977 host target RNA into VGAM977 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93624] VGAM978 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM978 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM978 host target RNA into VGAM978 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93625] VGAM979 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM979 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM979 host target RNA into VGAM979 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93626] It is appreciated that a function of VGR2945 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2945 gene include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGR2945 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2945 gene: VGAM975 host target protein, VGAM976 host target protein, VGAM977 host target protein, VGAM978 host target protein and VGAM979 host

target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM975, VGAM976, VGAM977, VGAM978 and VGAM979.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2946(VGR2946) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93627] VGR2946 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2946 gene was detected is described hereinabove with reference to Figs. 1-9.

[93628] VGR2946 gene encodes VGR2946 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93629] VGR2946 precursor RNA folds spatially, forming VGR2946 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2946 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2946 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93630] VGR2946 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM980 precursor RNA, VGAM981 precursor RNA, VGAM982 precursor RNA, VGAM983 precursor RNA and VGAM984 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93631] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM980 RNA, VGAM981 RNA, VGAM982 RNA, VGAM983 RNA and VGAM984 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93632] VGAM980 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM980 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM980 host target RNA into VGAM980 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93633] VGAM981 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM981 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM981 host target RNA into

VGAM981 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93634] VGAM982 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM982 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM982 host target RNA into VGAM982 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93635] VGAM983 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM983 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM983 host target RNA into VGAM983 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93636] VGAM984 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM984 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM984 host target RNA into VGAM984 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93637] It is appreciated that a function of VGR2946 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2946 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR2946 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2946 gene: VGAM980 host target protein, VGAM981 host target protein, VGAM982 host target protein, VGAM983 host target protein and VGAM984 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM980, VGAM981, VGAM982, VGAM983 and VGAM984.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2947(VGR2947) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93638] VGR2947 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2947 gene was detected is described hereinabove with reference to Figs. 1-9.

[93639] VGR2947 gene encodes VGR2947 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93640] VGR2947 precursor RNA folds spatially, forming VGR2947 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2947 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2947 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93641] VGR2947 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM986 precursor RNA, VGAM987 precursor RNA, VGAM988 precursor RNA, VGAM989 precursor RNA and VGAM990 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93642] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM986 RNA, VGAM987 RNA, VGAM988 RNA, VGAM989 RNA and VGAM990 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93643] VGAM986 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM986 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM986 host target RNA into VGAM986 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93644] VGAM987 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM987 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM987 host target RNA into VGAM987 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93645] VGAM988 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM988 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM988 host target RNA into VGAM988 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93646] VGAM989 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM989 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM989 host target RNA into VGAM989 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93647] VGAM990 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM990 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM990 host target RNA into VGAM990 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93648] It is appreciated that a function of VGR2947 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2947 gene include diagnosis, prevention and treatment of viral infection by Leishmania RNA Virus 1-4. Specific functions, and accordingly utilities, of VGR2947 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2947 gene: VGAM986 host target protein, VGAM987 host target protein, VGAM988 host target protein, VGAM989 host target protein and VGAM990 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM986, VGAM987, VGAM988, VGAM989 and VGAM990.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2948(VGR2948) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93649] VGR2948 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2948 gene was detected is described hereinabove with reference to Figs. 1-9.

[93650] VGR2948 gene encodes VGR2948 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93651] VGR2948 precursor RNA folds spatially, forming VGR2948 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2948 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2948 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93652] VGR2948 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM991 precursor RNA, VGAM992 precursor RNA, VGAM993 precursor RNA, VGAM994 precur-

sor RNA, VGAM995 precursor RNA and VGAM996 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93653] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM991 RNA, VGAM992 RNA, VGAM993 RNA, VGAM994 RNA, VGAM995 RNA and VGAM996 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93654] VGAM991 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM991 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM991 host target RNA into VGAM991 host target protein, herein schematically repre-

sented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93655] VGAM992 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM992 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM992 host target RNA into VGAM992 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93656] VGAM993 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM993 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM993 host target RNA into

VGAM993 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93657] VGAM994 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM994 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM994 host target RNA into VGAM994 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93658] VGAM995 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM995 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM995 host target RNA into VGAM995 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93659] VGAM996 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM996 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM996 host target RNA into VGAM996 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93660] It is appreciated that a function of VGR2948 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2948 gene include diagnosis, prevention and treatment of viral infection by Leishmania RNA Virus 1-1. Specific functions, and accordingly utilities, of VGR2948 gene correlate with, and may

be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2948 gene: VGAM991 host target protein, VGAM992 host target protein, VGAM993 host target protein, VGAM994 host target protein, VGAM995 host target protein and VGAM996 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM991, VGAM992, VGAM993, VGAM994, VGAM995 and VGAM996.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2949(VGR2949) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93661] VGR2949 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2949 gene was detected is described hereinabove with reference to Figs.

1-9.

[93662] VGR2949 gene encodes VGR2949 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93663] VGR2949 precursor RNA folds spatially, forming VGR2949 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2949 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2949 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93664] VGR2949 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM997 precursor RNA, VGAM998 precursor RNA, VGAM999 precursor RNA, VGAM1000 precursor RNA and VGAM1001 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corre-

sponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93665] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM997 RNA, VGAM998 RNA, VGAM999 RNA, VGAM1000 RNA and VGAM1001 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93666] VGAM997 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM997 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM997 host target RNA into VGAM997 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93667] VGAM998 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM998 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM998 host target RNA into VGAM998 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93668] VGAM999 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM999 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM999 host target RNA into VGAM999 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93669] VGAM1000 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1000 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1000 host target RNA into VGAM1000 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93670] VGAM1001 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1001 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1001 host target RNA into VGAM1001 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93671] It is appreciated that a function of VGR2949 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2949 gene include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGR2949 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2949 gene: VGAM997 host target protein, VGAM998 host target protein, VGAM999 host target protein, VGAM1000 host target protein and VGAM1001 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM997, VGAM998, VGAM999, VGAM1000 and VGAM1001.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2950(VGR2950) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[93672] VGR2950 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2950 gene was detected is described hereinabove with reference to Figs. 1-9.

[93673] VGR2950 gene encodes VGR2950 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93674] VGR2950 precursor RNA folds spatially, forming VGR2950 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2950 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2950 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93675] VGR2950 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1002 precursor RNA, VGAM1003

precursor RNA, VGAM1004 precursor RNA, VGAM1005 precursor RNA, VGAM1006 precursor RNA, VGAM1007 precursor RNA and VGAM1008 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93676] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1002 RNA, VGAM1003 RNA, VGAM1004 RNA, VGAM1005 RNA, VGAM1006 RNA, VGAM1007 RNA and VGAM1008 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93677] VGAM1002 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1002 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1002 host target RNA into VGAM1002 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93678] VGAM1003 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1003 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1003 host target RNA into VGAM1003 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93679] VGAM1004 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1004 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1004 host target RNA into VGAM1004 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93680] VGAM1005 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1005 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1005 host target RNA into VGAM1005 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93681] VGAM1006 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1006 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1006 host target RNA into VGAM1006 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93682] VGAM1007 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1007 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1007 host target RNA into VGAM1007 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93683] VGAM1008 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1008 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1008 host target RNA into VGAM1008 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93684] It is appreciated that a function of VGR2950 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2950 gene include diagnosis, prevention and treatment of viral infection by Chimpanzee Cytomegalovirus. Specific functions, and accordingly utilities, of VGR2950 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2950 gene: VGAM1002 host target protein, VGAM1003 host target protein, VGAM1004 host target protein, VGAM1005 host target protein, VGAM1006 host target protein, VGAM1007 host target protein and VGAM1008 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1002, VGAM1003, VGAM1004, VGAM1005, VGAM1006, VGAM1007 and VGAM1008.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2951(VGR2951) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93685] VGR2951 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2951 gene was detected is described hereinabove with reference to Figs. 1-9.

[93686] VGR2951 gene encodes VGR2951 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93687] VGR2951 precursor RNA folds spatially, forming VGR2951 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2951 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2951 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93688] VGR2951 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1009 precursor RNA, VGAM1010 precursor RNA and VGAM1011 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93689] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1009 RNA, VGAM1010 RNA and VGAM1011 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM

RNA of Fig. 1.

[93690] VGAM1009 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1009 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1009 host target RNA into VGAM1009 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93691] VGAM1010 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1010 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1010 host target RNA into VGAM1010 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93692] VGAM1011 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1011 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1011 host target RNA into VGAM1011 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93693] It is appreciated that a function of VGR2951 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2951 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2951 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR2951 gene: VGAM1009 host target protein, VGAM1010 host target protein and VGAM1011 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1009, VGAM1010 and VGAM1011.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2952(VGR2952) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93694] VGR2952 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2952 gene was detected is described hereinabove with reference to Figs. 1-9.

[93695] VGR2952 gene encodes VGR2952 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93696] VGR2952 precursor RNA folds spatially, forming VGR2952 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2952 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2952 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93697] VGR2952 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1012 precursor RNA and VGAM1013 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93698] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1012 RNA and VGAM1013 RNA, herein schematically repre-

sented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93699] VGAM1012 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1012 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1012 host target RNA into VGAM1012 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93700] VGAM1013 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1013 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1013 host target RNA into

VGAM1013 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93701] It is appreciated that a function of VGR2952 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2952 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2952 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2952 gene: VGAM1012 host target protein and VGAM1013 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1012 and VGAM1013.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2953(VGR2953) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expres-

sion of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93702] VGR2953 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2953 gene was detected is described hereinabove with reference to Figs. 1-9.

[93703] VGR2953 gene encodes VGR2953 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93704] VGR2953 precursor RNA folds spatially, forming VGR2953 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2953 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2953 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93705] VGR2953 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1015 precursor RNA and VGAM1016 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93706] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1015 RNA and VGAM1016 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93707] VGAM1015 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1015 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1015 host target RNA into VGAM1015 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93708] VGAM1016 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1016 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1016 host target RNA into VGAM1016 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93709] It is appreciated that a function of VGR2953 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2953 gene include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGR2953 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR2953 gene: VGAM1015 host target protein and VGAM1016 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1015 and VGAM1016.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2954(VGR2954) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93710] VGR2954 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2954 gene was detected is described hereinabove with reference to Figs. 1-9.

[93711] VGR2954 gene encodes VGR2954 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93712] VGR2954 precursor RNA folds spatially, forming VGR2954

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2954 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2954 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93713] VGR2954 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1017 precursor RNA, VGAM1018 precursor RNA and VGAM1019 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93714] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1017 RNA, VGAM1018 RNA and VGAM1019 RNA, herein

schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93715] VGAM1017 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1017 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1017 host target RNA into VGAM1017 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93716] VGAM1018 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1018 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1018 host target RNA into VGAM1018 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93717] VGAM1019 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1019 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1019 host target RNA into VGAM1019 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93718] It is appreciated that a function of VGR2954 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2954 gene include diagnosis, prevention and treatment of viral infection by Beet Western Yellows Virus. Specific functions, and accordingly utilities, of VGR2954 gene correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2954 gene: VGAM1017 host target protein, VGAM1018 host target protein and VGAM1019 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1017, VGAM1018 and VGAM1019.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2955(VGR2955) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93719] VGR2955 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2955 gene was detected is described hereinabove with reference to Figs. 1-9.

[93720] VGR2955 gene encodes VGR2955 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93721] VGR2955 precursor RNA folds spatially, forming VGR2955 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2955 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2955 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93722] VGR2955 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1020 precursor RNA, VGAM1021 precursor RNA, VGAM1022 precursor RNA, VGAM1023 precursor RNA, VGAM1024 precursor RNA, VGAM1025 precursor RNA and VGAM1026 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig.

1.

[93723] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1020 RNA, VGAM1021 RNA, VGAM1022 RNA, VGAM1023 RNA, VGAM1024 RNA, VGAM1025 RNA and VGAM1026 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93724] VGAM1020 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1020 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1020 host target RNA into VGAM1020 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93725] VGAM1021 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1021 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1021 host target RNA into VGAM1021 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93726] VGAM1022 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1022 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1022 host target RNA into VGAM1022 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93727] VGAM1023 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1023 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1023 host target RNA into VGAM1023 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93728] VGAM1024 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1024 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1024 host target RNA into VGAM1024 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93729] VGAM1025 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1025 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1025 host target RNA into VGAM1025 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93730] VGAM1026 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1026 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1026 host target RNA into VGAM1026 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93731] It is appreciated that a function of VGR2955 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2955 gene include diagnosis, prevention and treatment of viral infection by Cereal Yellow Dwarf Virus - RPV. Specific functions, and accordingly utilities, of VGR2955 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2955 gene: VGAM1020 host target protein, VGAM1021 host target protein, VGAM1022 host target protein, VGAM1023 host target protein, VGAM1024 host target protein, VGAM1025 host target protein and VGAM1026 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1020, VGAM1021, VGAM1022, VGAM1023, VGAM1024, VGAM1025 and VGAM1026.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2956(VGR2956) viral

gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93732] VGR2956 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2956 gene was detected is described hereinabove with reference to Figs. 1-9.

[93733] VGR2956 gene encodes VGR2956 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93734] VGR2956 precursor RNA folds spatially, forming VGR2956 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2956 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2956 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[93735] VGR2956 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1027 precursor RNA and VGAM1028 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93736] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1027 RNA and VGAM1028 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93737] VGAM1027 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1027 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1027 host target RNA into VGAM1027 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93738] VGAM1028 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1028 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1028 host target RNA into VGAM1028 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93739] It is appreciated that a function of VGR2956 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2956 gene include diagnosis, prevention and treatment of viral infection by Ictalurid Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2956 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2956 gene: VGAM1027 host target protein and VGAM1028 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1027 and VGAM1028.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2957(VGR2957) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93740] VGR2957 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2957 gene was detected is described hereinabove with reference to Figs. 1-9.

[93741] VGR2957 gene encodes VGR2957 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[93742] VGR2957 precursor RNA folds spatially, forming VGR2957 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2957 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2957 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93743] VGR2957 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1030 precursor RNA and VGAM1031 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93744] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1030

RNA and VGAM1031 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93745] VGAM1030 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1030 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1030 host target RNA into VGAM1030 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93746] VGAM1031 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1031 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1031 host target RNA into VGAM1031 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93747] It is appreciated that a function of VGR2957 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2957 gene include diagnosis, prevention and treatment of viral infection by Beet Mild Yellowing Virus. Specific functions, and accordingly utilities, of VGR2957 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2957 gene: VGAM1030 host target protein and VGAM1031 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1030 and VGAM1031.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2958(VGR2958) viral gene, which encodes an `operon-like` cluster of novel viral micro

RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93748] VGR2958 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2958 gene was detected is described hereinabove with reference to Figs. 1-9.

[93749] VGR2958 gene encodes VGR2958 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93750] VGR2958 precursor RNA folds spatially, forming VGR2958 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2958 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2958 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93751] VGR2958 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1032 precursor RNA, VGAM1033 precursor RNA, VGAM1034 precursor RNA, VGAM1035 precursor RNA and VGAM1036 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93752] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1032 RNA, VGAM1033 RNA, VGAM1034 RNA, VGAM1035 RNA and VGAM1036 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93753] VGAM1032 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1032 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1032 host target RNA into VGAM1032 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93754] VGAM1033 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1033 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1033 host target RNA into VGAM1033 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93755] VGAM1034 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1034 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1034 host target RNA into VGAM1034 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93756] VGAM1035 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1035 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1035 host target RNA into VGAM1035 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93757] VGAM1036 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1036 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1036 host target RNA into VGAM1036 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93758] It is appreciated that a function of VGR2958 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2958 gene include diagnosis, prevention and treatment of viral infection by Cercopithecine Herpesvirus 7. Specific functions, and accordingly utilities, of VGR2958 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2958 gene: VGAM1032 host target protein, VGAM1033 host target protein, VGAM1034 host target protein, VGAM1035 host target protein and VGAM1036 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The func-

tion of these host target genes is elaborated hereinabove with reference to VGAM1032, VGAM1033, VGAM1034, VGAM1035 and VGAM1036.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2959(VGR2959) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93759] VGR2959 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2959 gene was detected is described hereinabove with reference to Figs. 1-9.

[93760] VGR2959 gene encodes VGR2959 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93761] VGR2959 precursor RNA folds spatially, forming VGR2959 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2959 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2959 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93762] VGR2959 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1037 precursor RNA, VGAM1038 precursor RNA, VGAM1039 precursor RNA and VGAM1040 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93763] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1037 RNA, VGAM1038 RNA, VGAM1039 RNA and VGAM1040 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93764] VGAM1037 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1037 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1037 host target RNA into VGAM1037 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93765] VGAM1038 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1038 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1038 host target RNA into VGAM1038 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93766] VGAM1039 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1039 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1039 host target RNA into VGAM1039 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93767] VGAM1040 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1040 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1040 host target RNA into VGAM1040 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93768] It is appreciated that a function of VGR2959 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2959 gene include diagnosis, prevention and treatment of viral infection by Molluscum Contagiosum Virus. Specific functions, and accordingly utilities, of VGR2959 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2959 gene: VGAM1037 host target protein, VGAM1038 host target protein, VGAM1039 host target protein and VGAM1040 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1037, VGAM1038, VGAM1039 and VGAM1040.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2960(VGR2960) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes,

each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93769] VGR2960 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2960 gene was detected is described hereinabove with reference to Figs. 1-9.

[93770] VGR2960 gene encodes VGR2960 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93771] VGR2960 precursor RNA folds spatially, forming VGR2960 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2960 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2960 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93772] VGR2960 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1041 precursor RNA, VGAM1042 precursor RNA and VGAM1043 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93773] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1041 RNA, VGAM1042 RNA and VGAM1043 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93774] VGAM1041 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1041 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1041 host target RNA into VGAM1041 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93775] VGAM1042 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1042 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1042 host target RNA into VGAM1042 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93776] VGAM1043 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1043 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1043 host target RNA into VGAM1043 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93777] It is appreciated that a function of VGR2960 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2960 gene include diagnosis, prevention and treatment of viral infection by White Clover Mosaic Virus. Specific functions, and accordingly utilities, of VGR2960 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2960 gene: VGAM1041 host target protein, VGAM1042 host target protein and VGAM1043 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1041, VGAM1042 and VGAM1043.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to

here as Viral Genomic Record 2961(VGR2961) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93778] VGR2961 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2961 gene was detected is described hereinabove with reference to Figs. 1-9.

[93779] VGR2961 gene encodes VGR2961 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93780] VGR2961 precursor RNA folds spatially, forming VGR2961 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2961 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2961 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[93781] VGR2961 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1044 precursor RNA, VGAM1045 precursor RNA and VGAM1046 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93782] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1044 RNA, VGAM1045 RNA and VGAM1046 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93783] VGAM1044 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1044 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1044 host target RNA into VGAM1044 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93784] VGAM1045 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1045 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1045 host target RNA into VGAM1045 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93785] VGAM1046 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1046 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1046 host target RNA into VGAM1046 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93786] It is appreciated that a function of VGR2961 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2961 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 8. Specific functions, and accordingly utilities, of VGR2961 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2961 gene: VGAM1044 host target protein, VGAM1045 host target protein and VGAM1046 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with refer-

ence to VGAM1044, VGAM1045 and VGAM1046.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2962(VGR2962) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93787] VGR2962 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2962 gene was detected is described hereinabove with reference to Figs. 1-9.

[93788] VGR2962 gene encodes VGR2962 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93789] VGR2962 precursor RNA folds spatially, forming VGR2962 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2962 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2962 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93790] VGR2962 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1047 precursor RNA, VGAM1048 precursor RNA and VGAM1049 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93791] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1047 RNA, VGAM1048 RNA and VGAM1049 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93792] VGAM1047 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1047 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1047 host target RNA into VGAM1047 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93793] VGAM1048 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1048 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1048 host target RNA into VGAM1048 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93794] VGAM1049 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1049 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1049 host target RNA into VGAM1049 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93795] It is appreciated that a function of VGR2962 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2962 gene include diagnosis, prevention and treatment of viral infection by Strawberry Mild Yellow Edge Virus. Specific functions, and accordingly utilities, of VGR2962 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2962 gene: VGAM1047 host target protein, VGAM1048 host target protein and VGAM1049 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1047, VGAM1048 and VGAM1049.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2963(VGR2963) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93796] VGR2963 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2963 gene was detected is described hereinabove with reference to Figs. 1-9.

[93797] VGR2963 gene encodes VGR2963 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93798] VGR2963 precursor RNA folds spatially, forming VGR2963 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2963 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2963 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93799] VGR2963 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1050 precursor RNA, VGAM1051 precursor RNA, VGAM1052 precursor RNA and VGAM1053 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93800] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1050 RNA, VGAM1051 RNA, VGAM1052 RNA and VGAM1053 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corre-

sponding to VGAM RNA of Fig. 1.

[93801] VGAM1050 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1050 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1050 host target RNA into VGAM1050 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93802] VGAM1051 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1051 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1051 host target RNA into VGAM1051 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93803] VGAM1052 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1052 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1052 host target RNA into VGAM1052 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93804] VGAM1053 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1053 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1053 host target RNA into

VGAM1053 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93805] It is appreciated that a function of VGR2963 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2963 gene include diagnosis, prevention and treatment of viral infection by Meleagrid Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2963 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2963 gene: VGAM1050 host target protein, VGAM1051 host target protein, VGAM1052 host target protein and VGAM1053 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1050, VGAM1051, VGAM1052 and VGAM1053.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2964(VGR2964) viral gene, which encodes an

`operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93806] VGR2964 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2964 gene was detected is described hereinabove with reference to Figs. 1-9.

[93807] VGR2964 gene encodes VGR2964 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93808] VGR2964 precursor RNA folds spatially, forming VGR2964 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2964 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2964 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93809] VGR2964 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1055 precursor RNA and VGAM1056 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93810] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1055 RNA and VGAM1056 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93811] VGAM1055 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1055 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1055 host target RNA into

VGAM1055 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93812] VGAM1056 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1056 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1056 host target RNA into VGAM1056 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93813] It is appreciated that a function of VGR2964 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2964 gene include diagnosis, prevention and treatment of viral infection by Mayaro Virus. Specific functions, and accordingly utilities, of VGR2964 gene correlate with, and may be deduced from, the identity of the host target genes, which are in-

hibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2964 gene: VGAM1055 host target protein and VGAM1056 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1055 and VGAM1056.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2965(VGR2965) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93814] VGR2965 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2965 gene was detected is described hereinabove with reference to Figs. 1-9.

[93815] VGR2965 gene encodes VGR2965 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93816] VGR2965 precursor RNA folds spatially, forming VGR2965

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2965 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2965 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93817] VGR2965 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1057 precursor RNA, VGAM1058 precursor RNA and VGAM1059 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93818] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1057 RNA, VGAM1058 RNA and VGAM1059 RNA, herein

schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93819] VGAM1057 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1057 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1057 host target RNA into VGAM1057 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93820] VGAM1058 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1058 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1058 host target RNA into VGAM1058 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93821] VGAM1059 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1059 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1059 host target RNA into VGAM1059 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93822] It is appreciated that a function of VGR2965 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2965 gene include diagnosis, prevention and treatment of viral infection by Murid Herpesvirus 4. Specific functions, and accordingly utilities, of VGR2965 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2965 gene: VGAM1057 host target protein, VGAM1058 host target protein and VGAM1059 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1057, VGAM1058 and VGAM1059.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2966(VGR2966) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93823] VGR2966 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2966 gene was detected is described hereinabove with reference to Figs. 1-9.

[93824] VGR2966 gene encodes VGR2966 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93825] VGR2966 precursor RNA folds spatially, forming VGR2966 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2966 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2966 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93826] VGR2966 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1061 precursor RNA and VGAM1062 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93827] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1061 RNA and VGAM1062 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93828] VGAM1061 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1061 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1061 host target RNA into VGAM1061 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93829] VGAM1062 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1062 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1062 host target RNA into VGAM1062 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93830] It is appreciated that a function of VGR2966 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2966 gene include diagnosis, prevention and treatment of viral infection by Canine Adenovirus Type 1. Specific functions, and accordingly utilities, of VGR2966 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2966 gene: VGAM1061 host target protein and VGAM1062 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1061 and VGAM1062.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2967(VGR2967) viral gene, which

encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93831] VGR2967 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2967 gene was detected is described hereinabove with reference to Figs. 1-9.

[93832] VGR2967 gene encodes VGR2967 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93833] VGR2967 precursor RNA folds spatially, forming VGR2967 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2967 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2967 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[93834] VGR2967 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1063 precursor RNA, VGAM1064 precursor RNA, VGAM1065 precursor RNA and VGAM1066 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93835] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1063 RNA, VGAM1064 RNA, VGAM1065 RNA and VGAM1066 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93836] VGAM1063 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1063 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1063 host target RNA into VGAM1063 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93837] VGAM1064 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1064 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1064 host target RNA into VGAM1064 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93838] VGAM1065 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1065 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1065 host target RNA into VGAM1065 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93839] VGAM1066 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1066 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1066 host target RNA into VGAM1066 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93840] It is appreciated that a function of VGR2967 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2967 gene include

diagnosis, prevention and treatment of viral infection by Tulip Virus X. Specific functions, and accordingly utilities, of VGR2967 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2967 gene: VGAM1063 host target protein, VGAM1064 host target protein, VGAM1065 host target protein and VGAM1066 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1063, VGAM1064, VGAM1065 and VGAM1066.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2968(VGR2968) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93841] VGR2968 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2968 gene was

detected is described hereinabove with reference to Figs. 1-9.

[93842] VGR2968 gene encodes VGR2968 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93843] VGR2968 precursor RNA folds spatially, forming VGR2968 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2968 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2968 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93844] VGR2968 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1067 precursor RNA, VGAM1068 precursor RNA, VGAM1069 precursor RNA, VGAM1070 precursor RNA, VGAM1071 precursor RNA, VGAM1072 precursor RNA, VGAM1073 precursor RNA and VGAM1074 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93845] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1067 RNA, VGAM1068 RNA, VGAM1069 RNA, VGAM1070 RNA, VGAM1071 RNA, VGAM1072 RNA, VGAM1073 RNA and VGAM1074 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93846] VGAM1067 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1067 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1067 host target RNA into VGAM1067 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93847] VGAM1068 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1068 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1068 host target RNA into VGAM1068 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93848] VGAM1069 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1069 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1069 host target RNA into VGAM1069 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93849] VGAM1070 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1070 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1070 host target RNA into VGAM1070 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93850] VGAM1071 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1071 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1071 host target RNA into

VGAM1071 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93851] VGAM1072 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1072 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1072 host target RNA into VGAM1072 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93852] VGAM1073 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1073 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1073 host target RNA into VGAM1073 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93853] VGAM1074 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1074 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1074 host target RNA into VGAM1074 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93854] It is appreciated that a function of VGR2968 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2968 gene include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGR2968 gene correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2968 gene: VGAM1067 host target protein, VGAM1068 host target protein, VGAM1069 host target protein, VGAM1070 host target protein, VGAM1071 host target protein, VGAM1072 host target protein, VGAM1073 host target protein and VGAM1074 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1067, VGAM1068, VGAM1069, VGAM1070, VGAM1071, VGAM1072, VGAM1073 and VGAM1074.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2969(VGR2969) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93855] VGR2969 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2969 gene was detected is described hereinabove with reference to Figs. 1-9.

[93856] VGR2969 gene encodes VGR2969 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93857] VGR2969 precursor RNA folds spatially, forming VGR2969 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2969 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2969 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93858] VGR2969 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1075 precursor RNA, VGAM1076 precursor RNA, VGAM1077 precursor RNA, VGAM1078 precursor RNA, VGAM1079 precursor RNA, VGAM1080 precursor RNA, VGAM1081 precursor RNA and VGAM1082

precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93859] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1075 RNA, VGAM1076 RNA, VGAM1077 RNA, VGAM1078 RNA, VGAM1079 RNA, VGAM1080 RNA, VGAM1081 RNA and VGAM1082 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93860] VGAM1075 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1075 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1075 host target RNA into VGAM1075 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93861] VGAM1076 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1076 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1076 host target RNA into VGAM1076 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93862] VGAM1077 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1077 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1077 host target RNA into

VGAM1077 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93863] VGAM1078 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1078 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1078 host target RNA into VGAM1078 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93864] VGAM1079 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1079 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1079 host target RNA into VGAM1079 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93865] VGAM1080 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1080 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1080 host target RNA into VGAM1080 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93866] VGAM1081 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1081 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1081 host target RNA into VGAM1081 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93867] VGAM1082 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1082 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1082 host target RNA into VGAM1082 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93868] It is appreciated that a function of VGR2969 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2969 gene include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and

accordingly utilities, of VGR2969 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2969 gene: VGAM1075 host target protein, VGAM1076 host target protein, VGAM1077 host target protein, VGAM1078 host target protein, VGAM1079 host target protein, VGAM1080 host target protein, VGAM1081 host target protein and VGAM1082 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1075, VGAM1076, VGAM1077, VGAM1078, VGAM1079, VGAM1080, VGAM1081 and VGAM1082.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2970(VGR2970) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93869] VGR2970 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2970 gene was detected is described hereinabove with reference to Figs. 1-9.

[93870] VGR2970 gene encodes VGR2970 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93871] VGR2970 precursor RNA folds spatially, forming VGR2970 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2970 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2970 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93872] VGR2970 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1083 precursor RNA, VGAM1084 precursor RNA, VGAM1085 precursor RNA, VGAM1086 precursor RNA, VGAM1087 precursor RNA, VGAM1088

precursor RNA, VGAM1089 precursor RNA and VGAM1090 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93873] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1083 RNA, VGAM1084 RNA, VGAM1085 RNA, VGAM1086 RNA, VGAM1087 RNA, VGAM1088 RNA, VGAM1089 RNA and VGAM1090 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93874] VGAM1083 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1083 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1083 host target RNA into

VGAM1083 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93875] VGAM1084 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1084 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1084 host target RNA into VGAM1084 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93876] VGAM1085 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1085 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1085 host target RNA into VGAM1085 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93877] VGAM1086 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1086 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1086 host target RNA into VGAM1086 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93878] VGAM1087 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1087 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1087 host target RNA into VGAM1087 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93879] VGAM1088 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1088 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1088 host target RNA into VGAM1088 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93880] VGAM1089 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1089 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1089 host target RNA into VGAM1089 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93881] VGAM1090 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1090 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1090 host target RNA into VGAM1090 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93882] It is appreciated that a function of VGR2970 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2970 gene include diagnosis, prevention and treatment of viral infection by

Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGR2970 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2970 gene: VGAM1083 host target protein, VGAM1084 host target protein, VGAM1085 host target protein, VGAM1086 host target protein, VGAM1087 host target protein, VGAM1088 host target protein, VGAM1089 host target protein and VGAM1090 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1083, VGAM1084, VGAM1085, VGAM1086, VGAM1087, VGAM1088, VGAM1089 and VGAM1090.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2971(VGR2971) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93883] VGR2971 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2971 gene was detected is described hereinabove with reference to Figs. 1-9.

[93884] VGR2971 gene encodes VGR2971 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93885] VGR2971 precursor RNA folds spatially, forming VGR2971 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2971 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2971 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93886] VGR2971 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1091 precursor RNA, VGAM1092 precursor RNA, VGAM1093 precursor RNA, VGAM1094

precursor RNA and VGAM1095 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93887] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1091 RNA, VGAM1092 RNA, VGAM1093 RNA, VGAM1094 RNA and VGAM1095 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93888] VGAM1091 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1091 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1091 host target RNA into VGAM1091 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93889] VGAM1092 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1092 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1092 host target RNA into VGAM1092 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93890] VGAM1093 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1093 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1093 host target RNA into

VGAM1093 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93891] VGAM1094 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1094 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1094 host target RNA into VGAM1094 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93892] VGAM1095 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1095 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1095 host target RNA into VGAM1095 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93893] It is appreciated that a function of VGR2971 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2971 gene include diagnosis, prevention and treatment of viral infection by Poinsettia Mosaic Virus. Specific functions, and accordingly utilities, of VGR2971 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2971 gene: VGAM1091 host target protein, VGAM1092 host target protein, VGAM1093 host target protein, VGAM1094 host target protein and VGAM1095 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1091, VGAM1092, VGAM1093, VGAM1094 and VGAM1095.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory vi-

ral gene, referred to here as Viral Genomic Record 2972(VGR2972) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93894] VGR2972 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2972 gene was detected is described hereinabove with reference to Figs. 1-9.

[93895] VGR2972 gene encodes VGR2972 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93896] VGR2972 precursor RNA folds spatially, forming VGR2972 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2972 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2972 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[93897] VGR2972 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1096 precursor RNA, VGAM1097 precursor RNA, VGAM1098 precursor RNA, VGAM1099 precursor RNA, VGAM1100 precursor RNA, VGAM1101 precursor RNA, VGAM1102 precursor RNA and VGAM1103 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93898] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1096 RNA, VGAM1097 RNA, VGAM1098 RNA, VGAM1099 RNA, VGAM1100 RNA, VGAM1101 RNA, VGAM1102 RNA and VGAM1103 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93899] VGAM1096 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1096 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1096 host target RNA into VGAM1096 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93900] VGAM1097 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1097 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1097 host target RNA into VGAM1097 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93901] VGAM1098 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1098 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1098 host target RNA into VGAM1098 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93902] VGAM1099 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1099 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1099 host target RNA into VGAM1099 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93903] VGAM1100 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1100 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1100 host target RNA into VGAM1100 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93904] VGAM1101 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1101 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1101 host target RNA into VGAM1101 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93905] VGAM1102 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1102 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1102 host target RNA into VGAM1102 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93906] VGAM1103 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1103 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1103 host target RNA into VGAM1103 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93907] It is appreciated that a function of VGR2972 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2972 gene include diagnosis, prevention and treatment of viral infection by Strawberry Mottle Virus. Specific functions, and accordingly utilities, of VGR2972 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2972 gene: VGAM1096 host target protein, VGAM1097 host target protein, VGAM1098 host target protein, VGAM1099 host target protein, VGAM1100 host target protein, VGAM1101 host target protein, VGAM1102 host target protein and VGAM1103 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1096, VGAM1097, VGAM1098, VGAM1099, VGAM1100, VGAM1101, VGAM1102 and VGAM1103.Fig. 9 further provides a conceptual description of novel bioinformati-

cally detected regulatory viral gene, referred to here as Viral Genomic Record 2973(VGR2973) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93908] VGR2973 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2973 gene was detected is described hereinabove with reference to Figs. 1-9.

[93909] VGR2973 gene encodes VGR2973 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93910] VGR2973 precursor RNA folds spatially, forming VGR2973 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2973 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2973 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[93911] VGR2973 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1104 precursor RNA, VGAM1105 precursor RNA and VGAM1106 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93912] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1104 RNA, VGAM1105 RNA and VGAM1106 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93913] VGAM1104 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1104 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1104 host target RNA into VGAM1104 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93914] VGAM1105 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1105 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1105 host target RNA into VGAM1105 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93915] VGAM1106 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1106 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1106 host target RNA into VGAM1106 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93916] It is appreciated that a function of VGR2973 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2973 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2973 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2973 gene: VGAM1104 host target protein, VGAM1105 host target protein and VGAM1106 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with refer-

ence to VGAM1104, VGAM1105 and VGAM1106.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2974(VGR2974) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93917] VGR2974 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2974 gene was detected is described hereinabove with reference to Figs. 1-9.

[93918] VGR2974 gene encodes VGR2974 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93919] VGR2974 precursor RNA folds spatially, forming VGR2974 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2974 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2974 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93920] VGR2974 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1108 precursor RNA and VGAM1109 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93921] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1108 RNA and VGAM1109 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93922] VGAM1108 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1108 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1108 host target RNA into VGAM1108 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93923] VGAM1109 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1109 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1109 host target RNA into VGAM1109 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93924] It is appreciated that a function of VGR2974 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2974 gene include diagnosis, prevention and treatment of viral infection by Chimpanzee Cytomegalovirus. Specific functions, and accordingly utilities, of VGR2974 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2974 gene: VGAM1108 host target protein and VGAM1109 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1108 and VGAM1109.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2975(VGR2975) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93925] VGR2975 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2975 gene was

detected is described hereinabove with reference to Figs. 1-9.

[93926] VGR2975 gene encodes VGR2975 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93927] VGR2975 precursor RNA folds spatially, forming VGR2975 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2975 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2975 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93928] VGR2975 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1111 precursor RNA, VGAM1112 precursor RNA, VGAM1113 precursor RNA, VGAM1114 precursor RNA and VGAM1115 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93929] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1111 RNA, VGAM1112 RNA, VGAM1113 RNA, VGAM1114 RNA and VGAM1115 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93930] VGAM1111 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1111 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1111 host target RNA into VGAM1111 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93931] VGAM1112 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1112 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1112 host target RNA into VGAM1112 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93932] VGAM1113 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1113 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1113 host target RNA into VGAM1113 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93933] VGAM1114 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1114 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1114 host target RNA into VGAM1114 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93934] VGAM1115 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1115 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1115 host target RNA into VGAM1115 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93935] It is appreciated that a function of VGR2975 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2975 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR2975 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2975 gene: VGAM1111 host target protein, VGAM1112 host target protein, VGAM1113 host target protein, VGAM1114 host target protein and VGAM1115 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1111, VGAM1112, VGAM1113, VGAM1114 and VGAM1115.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2976(VGR2976) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes,

each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93936] VGR2976 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2976 gene was detected is described hereinabove with reference to Figs. 1-9.

[93937] VGR2976 gene encodes VGR2976 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93938] VGR2976 precursor RNA folds spatially, forming VGR2976 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2976 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2976 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93939] VGR2976 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1116 precursor RNA, VGAM1117 precursor RNA, VGAM1118 precursor RNA, VGAM1119 precursor RNA and VGAM1120 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93940] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1116 RNA, VGAM1117 RNA, VGAM1118 RNA, VGAM1119 RNA and VGAM1120 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93941] VGAM1116 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1116 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1116 host target RNA into VGAM1116 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93942] VGAM1117 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1117 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1117 host target RNA into VGAM1117 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93943] VGAM1118 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1118 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1118 host target RNA into VGAM1118 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93944] VGAM1119 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1119 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1119 host target RNA into VGAM1119 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93945] VGAM1120 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1120 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1120 host target RNA into VGAM1120 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93946] It is appreciated that a function of VGR2976 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2976 gene include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGR2976 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2976 gene: VGAM1116 host target protein, VGAM1117 host target protein, VGAM1118 host target protein, VGAM1119 host target protein and VGAM1120 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with refer-

ence to VGAM1116, VGAM1117, VGAM1118, VGAM1119 and VGAM1120.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2977(VGR2977) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93947] VGR2977 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2977 gene was detected is described hereinabove with reference to Figs. 1-9.

[93948] VGR2977 gene encodes VGR2977 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93949] VGR2977 precursor RNA folds spatially, forming VGR2977 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2977 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR2977 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93950] VGR2977 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1121 precursor RNA, VGAM1122 precursor RNA, VGAM1123 precursor RNA, VGAM1124 precursor RNA and VGAM1125 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93951] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1121 RNA, VGAM1122 RNA, VGAM1123 RNA, VGAM1124 RNA and VGAM1125 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93952] VGAM1121 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1121 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1121 host target RNA into VGAM1121 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93953] VGAM1122 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1122 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1122 host target RNA into VGAM1122 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93954] VGAM1123 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1123 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1123 host target RNA into VGAM1123 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93955] VGAM1124 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1124 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1124 host target RNA into VGAM1124 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93956] VGAM1125 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1125 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1125 host target RNA into VGAM1125 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93957] It is appreciated that a function of VGR2977 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2977 gene include diagnosis, prevention and treatment of viral infection by Saimiriine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR2977 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2977 gene: VGAM1121 host

target protein, VGAM1122 host target protein, VGAM1123 host target protein, VGAM1124 host target protein and VGAM1125 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1121, VGAM1122, VGAM1123, VGAM1124 and VGAM1125.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2978(VGR2978) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93958] VGR2978 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2978 gene was detected is described hereinabove with reference to Figs. 1-9.

[93959] VGR2978 gene encodes VGR2978 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93960] VGR2978 precursor RNA folds spatially, forming VGR2978 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2978 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2978 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93961] VGR2978 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1127 precursor RNA, VGAM1128 precursor RNA, VGAM1129 precursor RNA, VGAM1130 precursor RNA, VGAM1131 precursor RNA and VGAM1132 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93962] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1127 RNA, VGAM1128 RNA, VGAM1129 RNA, VGAM1130 RNA, VGAM1131 RNA and VGAM1132 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93963] VGAM1127 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1127 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1127 host target RNA into VGAM1127 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93964] VGAM1128 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1128 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1128 host target RNA into VGAM1128 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93965] VGAM1129 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1129 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1129 host target RNA into VGAM1129 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93966] VGAM1130 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1130 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1130 host target RNA into VGAM1130 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93967] VGAM1131 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1131 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1131 host target RNA into VGAM1131 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93968] VGAM1132 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1132 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1132 host target RNA into VGAM1132 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93969] It is appreciated that a function of VGR2978 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2978 gene include diagnosis, prevention and treatment of viral infection by Barley Stripe Mosaic Virus. Specific functions, and accordingly utilities, of VGR2978 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2978 gene: VGAM1127 host target protein, VGAM1128 host target protein, VGAM1129 host target protein, VGAM1130 host target protein, VGAM1131 host target protein and VGAM1132 host target protein, herein schematically represented by VGAM1 HOST

TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1127, VGAM1128, VGAM1129, VGAM1130, VGAM1131 and VGAM1132.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2979(VGR2979) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93970] VGR2979 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2979 gene was detected is described hereinabove with reference to Figs. 1-9.

[93971] VGR2979 gene encodes VGR2979 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93972] VGR2979 precursor RNA folds spatially, forming VGR2979 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2979 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2979 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93973] VGR2979 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1133 precursor RNA, VGAM1134 precursor RNA and VGAM1135 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93974] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1133 RNA, VGAM1134 RNA and VGAM1135 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM

RNA of Fig. 1.

[93975] VGAM1133 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1133 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1133 host target RNA into VGAM1133 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93976] VGAM1134 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1134 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1134 host target RNA into VGAM1134 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93977] VGAM1135 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1135 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1135 host target RNA into VGAM1135 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93978] It is appreciated that a function of VGR2979 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2979 gene include diagnosis, prevention and treatment of viral infection by Maize Rayado Fino Virus. Specific functions, and accordingly utilities, of VGR2979 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR2979 gene: VGAM1133 host target protein, VGAM1134 host target protein and VGAM1135 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1133, VGAM1134 and VGAM1135.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2980(VGR2980) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93979] VGR2980 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2980 gene was detected is described hereinabove with reference to Figs. 1-9.

[93980] VGR2980 gene encodes VGR2980 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93981] VGR2980 precursor RNA folds spatially, forming VGR2980 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2980 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2980 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93982] VGR2980 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1136 precursor RNA, VGAM1137 precursor RNA and VGAM1138 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93983] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1136

RNA, VGAM1137 RNA and VGAM1138 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93984] VGAM1136 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1136 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1136 host target RNA into VGAM1136 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93985] VGAM1137 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1137 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1137 host target RNA into VGAM1137 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93986] VGAM1138 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1138 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1138 host target RNA into VGAM1138 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93987] It is appreciated that a function of VGR2980 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2980 gene include diagnosis, prevention and treatment of viral infection by Beet Mild Yellowing Virus. Specific functions, and accord-

ingly utilities, of VGR2980 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2980 gene: VGAM1136 host target protein, VGAM1137 host target protein and VGAM1138 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1136, VGAM1137 and VGAM1138.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2981(VGR2981) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93988] VGR2981 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2981 gene was detected is described hereinabove with reference to Figs. 1-9.

[93989] VGR2981 gene encodes VGR2981 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93990] VGR2981 precursor RNA folds spatially, forming VGR2981 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2981 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2981 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[93991] VGR2981 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1139 precursor RNA, VGAM1140 precursor RNA and VGAM1141 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[93992] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1139 RNA, VGAM1140 RNA and VGAM1141 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[93993] VGAM1139 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1139 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1139 host target RNA into VGAM1139 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93994] VGAM1140 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1140 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1140 host target RNA into VGAM1140 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93995] VGAM1141 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1141 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1141 host target RNA into VGAM1141 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[93996] It is appreciated that a function of VGR2981 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2981 gene include diagnosis, prevention and treatment of viral infection by Chayote Mosaic Tymovirus. Specific functions, and accordingly utilities, of VGR2981 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2981 gene: VGAM1139 host target protein, VGAM1140 host target protein and VGAM1141 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1139, VGAM1140 and VGAM1141.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2982(VGR2982) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[93997] VGR2982 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2982 gene was detected is described hereinabove with reference to Figs. 1-9.

[93998] VGR2982 gene encodes VGR2982 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[93999] VGR2982 precursor RNA folds spatially, forming VGR2982 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2982 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2982 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94000] VGR2982 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1142 precursor RNA, VGAM1143 precursor RNA, VGAM1144 precursor RNA and VGAM1145 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94001] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1142 RNA, VGAM1143 RNA, VGAM1144 RNA and VGAM1145 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94002] VGAM1142 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1142 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1142 host target RNA into VGAM1142 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94003] VGAM1143 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1143 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1143 host target RNA into VGAM1143 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94004] VGAM1144 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1144 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1144 host target RNA into VGAM1144 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94005] VGAM1145 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1145 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1145 host target RNA into VGAM1145 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94006] It is appreciated that a function of VGR2982 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2982 gene include diagnosis, prevention and treatment of viral infection by Bamboo Mosaic Virus. Specific functions, and accordingly utilities, of VGR2982 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2982 gene: VGAM1142 host target protein, VGAM1143 host target protein, VGAM1144

host target protein and VGAM1145 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1142, VGAM1143, VGAM1144 and VGAM1145.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2983(VGR2983) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94007] VGR2983 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2983 gene was detected is described hereinabove with reference to Figs. 1-9.

[94008] VGR2983 gene encodes VGR2983 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[94009] VGR2983 precursor RNA folds spatially, forming VGR2983 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2983 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2983 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94010] VGR2983 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1146 precursor RNA and VGAM1147 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94011] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1146 RNA and VGAM1147 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94012] VGAM1146 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1146 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1146 host target RNA into VGAM1146 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94013] VGAM1147 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1147 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1147 host target RNA into VGAM1147 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94014] It is appreciated that a function of VGR2983 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2983 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR2983 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2983 gene: VGAM1146 host target protein and VGAM1147 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1146 and VGAM1147.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2984(VGR2984) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[94015] VGR2984 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2984 gene was detected is described hereinabove with reference to Figs. 1-9.

[94016] VGR2984 gene encodes VGR2984 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94017] VGR2984 precursor RNA folds spatially, forming VGR2984 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2984 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2984 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94018] VGR2984 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1148 precursor RNA, VGAM1149

precursor RNA and VGAM1150 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94019] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1148 RNA, VGAM1149 RNA and VGAM1150 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94020] VGAM1148 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1148 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1148 host target RNA into VGAM1148 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94021] VGAM1149 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1149 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1149 host target RNA into VGAM1149 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94022] VGAM1150 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1150 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1150 host target RNA into

VGAM1150 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94023] It is appreciated that a function of VGR2984 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2984 gene include diagnosis, prevention and treatment of viral infection by Cercopithecine Herpesvirus 7. Specific functions, and accordingly utilities, of VGR2984 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2984 gene: VGAM1148 host target protein, VGAM1149 host target protein and VGAM1150 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1148, VGAM1149 and VGAM1150.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2985(VGR2985) viral gene, which encodes an `operon-like` cluster of novel viral mi-

cro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94024] VGR2985 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2985 gene was detected is described hereinabove with reference to Figs. 1-9.

[94025] VGR2985 gene encodes VGR2985 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94026] VGR2985 precursor RNA folds spatially, forming VGR2985 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2985 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2985 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94027] VGR2985 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1151 precursor RNA, VGAM1152 precursor RNA, VGAM1153 precursor RNA and VGAM1154 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94028] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1151 RNA, VGAM1152 RNA, VGAM1153 RNA and VGAM1154 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94029] VGAM1151 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1151 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1151 host target RNA into VGAM1151 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94030] VGAM1152 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1152 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1152 host target RNA into VGAM1152 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94031] VGAM1153 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1153 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1153 host target RNA into VGAM1153 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94032] VGAM1154 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1154 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1154 host target RNA into VGAM1154 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94033] It is appreciated that a function of VGR2985 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2985 gene include diagnosis, prevention and treatment of viral infection by

Cowpox Virus. Specific functions, and accordingly utilities, of VGR2985 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2985 gene: VGAM1151 host target protein, VGAM1152 host target protein, VGAM1153 host target protein and VGAM1154 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1151, VGAM1152, VGAM1153 and VGAM1154.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2986(VGR2986) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94034] VGR2986 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2986 gene was detected is described hereinabove with reference to Figs.

1-9.

[94035] VGR2986 gene encodes VGR2986 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94036] VGR2986 precursor RNA folds spatially, forming VGR2986 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2986 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2986 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94037] VGR2986 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1155 precursor RNA, VGAM1156 precursor RNA and VGAM1157 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig.

1.

[94038] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1155 RNA, VGAM1156 RNA and VGAM1157 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94039] VGAM1155 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1155 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1155 host target RNA into VGAM1155 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94040] VGAM1156 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1156 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1156 host target RNA into VGAM1156 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94041] VGAM1157 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1157 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1157 host target RNA into VGAM1157 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94042] It is appreciated that a function of VGR2986 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2986 gene include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGR2986 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2986 gene: VGAM1155 host target protein, VGAM1156 host target protein and VGAM1157 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1155, VGAM1156 and VGAM1157.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2987(VGR2987) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94043] VGR2987 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2987 gene was detected is described hereinabove with reference to Figs. 1-9.

[94044] VGR2987 gene encodes VGR2987 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94045] VGR2987 precursor RNA folds spatially, forming VGR2987 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2987 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2987 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94046] VGR2987 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1159 precursor RNA, VGAM1160 precursor RNA and VGAM1161 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94047] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1159 RNA, VGAM1160 RNA and VGAM1161 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94048] VGAM1159 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1159 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1159 host target RNA into VGAM1159 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94049] VGAM1160 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1160 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1160 host target RNA into VGAM1160 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94050] VGAM1161 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1161 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1161 host target RNA into VGAM1161 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94051] It is appreciated that a function of VGR2987 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2987 gene include diagnosis, prevention and treatment of viral infection by Meleagrid Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2987 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2987 gene: VGAM1159 host target protein, VGAM1160 host target protein and VGAM1161 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1159, VGAM1160 and VGAM1161.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2988(VGR2988) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[94052] VGR2988 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2988 gene was detected is described hereinabove with reference to Figs. 1-9.

[94053] VGR2988 gene encodes VGR2988 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94054] VGR2988 precursor RNA folds spatially, forming VGR2988 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2988 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2988 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94055] VGR2988 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1162 precursor RNA, VGAM1163

precursor RNA, VGAM1164 precursor RNA and VGAM1165 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94056] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1162 RNA, VGAM1163 RNA, VGAM1164 RNA and VGAM1165 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94057] VGAM1162 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1162 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1162 host target RNA into VGAM1162 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94058] VGAM1163 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1163 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1163 host target RNA into VGAM1163 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94059] VGAM1164 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1164 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1164 host target RNA into

VGAM1164 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94060] VGAM1165 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1165 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1165 host target RNA into VGAM1165 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94061] It is appreciated that a function of VGR2988 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2988 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR2988 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2988 gene: VGAM1162 host target protein, VGAM1163 host target protein, VGAM1164 host target protein and VGAM1165 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1162, VGAM1163, VGAM1164 and VGAM1165.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2989(VGR2989) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94062] VGR2989 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2989 gene was detected is described hereinabove with reference to Figs. 1-9.

[94063] VGR2989 gene encodes VGR2989 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[94064] VGR2989 precursor RNA folds spatially, forming VGR2989 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2989 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2989 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94065] VGR2989 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1166 precursor RNA and VGAM1167 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94066] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1166

RNA and VGAM1167 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94067] VGAM1166 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1166 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1166 host target RNA into VGAM1166 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94068] VGAM1167 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1167 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1167 host target RNA into VGAM1167 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94069] It is appreciated that a function of VGR2989 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2989 gene include diagnosis, prevention and treatment of viral infection by Cucumber Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGR2989 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2989 gene: VGAM1166 host target protein and VGAM1167 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1166 and VGAM1167.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2990(VGR2990) viral gene, which encodes an `operon-like` cluster of novel viral mi-

cro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94070] VGR2990 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2990 gene was detected is described hereinabove with reference to Figs. 1-9.

[94071] VGR2990 gene encodes VGR2990 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94072] VGR2990 precursor RNA folds spatially, forming VGR2990 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2990 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2990 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94073] VGR2990 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1168 precursor RNA and VGAM1169 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94074] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1168 RNA and VGAM1169 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94075] VGAM1168 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1168 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1168 host target RNA into

VGAM1168 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94076] VGAM1169 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1169 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1169 host target RNA into VGAM1169 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94077] It is appreciated that a function of VGR2990 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2990 gene include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR2990 gene correlate with, and may be deduced from, the identity of the host target genes,

which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2990 gene: VGAM1168 host target protein and VGAM1169 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1168 and VGAM1169.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2991(VGR2991) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94078] VGR2991 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2991 gene was detected is described hereinabove with reference to Figs. 1-9.

[94079] VGR2991 gene encodes VGR2991 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94080] VGR2991 precursor RNA folds spatially, forming VGR2991 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2991 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2991 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94081] VGR2991 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1171 precursor RNA, VGAM1172 precursor RNA and VGAM1173 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94082] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1171

RNA, VGAM1172 RNA and VGAM1173 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94083] VGAM1171 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1171 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1171 host target RNA into VGAM1171 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94084] VGAM1172 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1172 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1172 host target RNA into VGAM1172 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94085] VGAM1173 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1173 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1173 host target RNA into VGAM1173 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94086] It is appreciated that a function of VGR2991 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2991 gene include diagnosis, prevention and treatment of viral infection by Cucumber Fruit Mottle Mosaic Virus. Specific functions,

and accordingly utilities, of VGR2991 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2991 gene: VGAM1171 host target protein, VGAM1172 host target protein and VGAM1173 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1171, VGAM1172 and VGAM1173.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2992(VGR2992) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94087] VGR2992 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2992 gene was detected is described hereinabove with reference to Figs. 1-9.

[94088] VGR2992 gene encodes VGR2992 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94089] VGR2992 precursor RNA folds spatially, forming VGR2992 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2992 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2992 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94090] VGR2992 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1174 precursor RNA, VGAM1175 precursor RNA and VGAM1176 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94091] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1174 RNA, VGAM1175 RNA and VGAM1176 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94092] VGAM1174 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1174 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1174 host target RNA into VGAM1174 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94093] VGAM1175 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1175 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1175 host target RNA into VGAM1175 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94094] VGAM1176 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1176 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1176 host target RNA into VGAM1176 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94095] It is appreciated that a function of VGR2992 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR2992 gene include diagnosis, prevention and treatment of viral infection by Rift Valley Fever Virus. Specific functions, and accordingly utilities, of VGR2992 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2992 gene: VGAM1174 host target protein, VGAM1175 host target protein and VGAM1176 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1174, VGAM1175 and VGAM1176.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2993(VGR2993) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94096] VGR2993 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR2993 gene was detected is described hereinabove with reference to Figs. 1-9.

[94097] VGR2993 gene encodes VGR2993 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94098] VGR2993 precursor RNA folds spatially, forming VGR2993 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2993 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2993 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94099] VGR2993 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1177 precursor RNA, VGAM1178 precursor RNA, VGAM1179 precursor RNA, VGAM1180 precursor RNA and VGAM1181 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR

through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94100] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1177 RNA, VGAM1178 RNA, VGAM1179 RNA, VGAM1180 RNA and VGAM1181 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94101] VGAM1177 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1177 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1177 host target RNA into VGAM1177 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94102] VGAM1178 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1178 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1178 host target RNA into VGAM1178 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94103] VGAM1179 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1179 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1179 host target RNA into VGAM1179 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94104] VGAM1180 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1180 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1180 host target RNA into VGAM1180 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94105] VGAM1181 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1181 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1181 host target RNA into VGAM1181 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94106] It is appreciated that a function of VGR2993 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2993 gene include diagnosis, prevention and treatment of viral infection by Odontoglossum Ringspot Virus. Specific functions, and accordingly utilities, of VGR2993 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2993 gene: VGAM1177 host target protein, VGAM1178 host target protein, VGAM1179 host target protein, VGAM1180 host target protein and VGAM1181 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1177, VGAM1178, VGAM1179, VGAM1180 and VGAM1181.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2994(VGR2994) viral gene, which encodes an

`operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94107] VGR2994 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2994 gene was detected is described hereinabove with reference to Figs. 1-9.

[94108] VGR2994 gene encodes VGR2994 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94109] VGR2994 precursor RNA folds spatially, forming VGR2994 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2994 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2994 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94110] VGR2994 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1183 precursor RNA, VGAM1184 precursor RNA and VGAM1185 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94111] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1183 RNA, VGAM1184 RNA and VGAM1185 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94112] VGAM1183 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1183 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1183 host target RNA into VGAM1183 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94113] VGAM1184 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1184 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1184 host target RNA into VGAM1184 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94114] VGAM1185 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1185 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1185 host target RNA into VGAM1185 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94115] It is appreciated that a function of VGR2994 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2994 gene include diagnosis, prevention and treatment of viral infection by Cactus Virus X. Specific functions, and accordingly utilities, of VGR2994 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2994 gene: VGAM1183 host target protein, VGAM1184 host target protein and VGAM1185 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1183, VGAM1184 and VGAM1185.Fig. 9 further provides a conceptual description of novel bioin-

formatically detected regulatory viral gene, referred to here as Viral Genomic Record 2995(VGR2995) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94116] VGR2995 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2995 gene was detected is described hereinabove with reference to Figs. 1-9.

[94117] VGR2995 gene encodes VGR2995 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94118] VGR2995 precursor RNA folds spatially, forming VGR2995 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2995 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2995 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94119] VGR2995 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1186 precursor RNA, VGAM1187 precursor RNA and VGAM1188 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94120] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1186 RNA, VGAM1187 RNA and VGAM1188 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94121] VGAM1186 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1186 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1186 host target RNA into VGAM1186 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94122] VGAM1187 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1187 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1187 host target RNA into VGAM1187 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94123] VGAM1188 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1188 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1188 host target RNA into VGAM1188 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94124] It is appreciated that a function of VGR2995 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2995 gene include diagnosis, prevention and treatment of viral infection by Human Adenovirus C. Specific functions, and accordingly utilities, of VGR2995 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2995 gene: VGAM1186 host target protein, VGAM1187 host target protein and VGAM1188 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these

host target genes is elaborated hereinabove with reference to VGAM1186, VGAM1187 and VGAM1188.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2996(VGR2996) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94125] VGR2996 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2996 gene was detected is described hereinabove with reference to Figs. 1-9.

[94126] VGR2996 gene encodes VGR2996 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94127] VGR2996 precursor RNA folds spatially, forming VGR2996 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2996 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR2996 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94128] VGR2996 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1189 precursor RNA, VGAM1190 precursor RNA and VGAM1191 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94129] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1189 RNA, VGAM1190 RNA and VGAM1191 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94130] VGAM1189 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1189 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1189 host target RNA into VGAM1189 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94131] VGAM1190 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1190 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1190 host target RNA into VGAM1190 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94132] VGAM1191 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1191 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1191 host target RNA into VGAM1191 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94133] It is appreciated that a function of VGR2996 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2996 gene include diagnosis, prevention and treatment of viral infection by Botrytis Virus F. Specific functions, and accordingly utilities, of VGR2996 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2996 gene: VGAM1189 host target protein, VGAM1190 host target protein and

VGAM1191 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1189, VGAM1190 and VGAM1191.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2997(VGR2997) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94134] VGR2997 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2997 gene was detected is described hereinabove with reference to Figs. 1-9.

[94135] VGR2997 gene encodes VGR2997 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94136] VGR2997 precursor RNA folds spatially, forming VGR2997 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR2997 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2997 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94137] VGR2997 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1192 precursor RNA, VGAM1193 precursor RNA and VGAM1194 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94138] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1192 RNA, VGAM1193 RNA and VGAM1194 RNA, herein schematically represented by VGAM1 RNA through VGAM3

RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94139] VGAM1192 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1192 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1192 host target RNA into VGAM1192 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94140] VGAM1193 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1193 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1193 host target RNA into

VGAM1193 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94141] VGAM1194 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1194 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1194 host target RNA into VGAM1194 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94142] It is appreciated that a function of VGR2997 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2997 gene include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGR2997 gene correlate with, and may be deduced from, the identity of the host target genes, which are in-

hibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2997 gene: VGAM1192 host target protein, VGAM1193 host target protein and VGAM1194 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1192, VGAM1193 and VGAM1194.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2998(VGR2998) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94143] VGR2998 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2998 gene was detected is described hereinabove with reference to Figs. 1-9.

[94144] VGR2998 gene encodes VGR2998 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94145] VGR2998 precursor RNA folds spatially, forming VGR2998 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2998 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2998 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94146] VGR2998 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1195 precursor RNA, VGAM1196 precursor RNA, VGAM1197 precursor RNA and VGAM1198 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94147] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1195

RNA, VGAM1196 RNA, VGAM1197 RNA and VGAM1198 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94148] VGAM1195 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1195 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1195 host target RNA into VGAM1195 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94149] VGAM1196 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1196 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1196 host target RNA into VGAM1196 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94150] VGAM1197 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1197 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1197 host target RNA into VGAM1197 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94151] VGAM1198 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1198 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1198 host target RNA into VGAM1198 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94152] It is appreciated that a function of VGR2998 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2998 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR2998 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2998 gene: VGAM1195 host target protein, VGAM1196 host target protein, VGAM1197 host target protein and VGAM1198 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1195, VGAM1196, VGAM1197 and VGAM1198.Fig. 9 further provides a con-

ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 2999(VGR2999) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94153] VGR2999 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR2999 gene was detected is described hereinabove with reference to Figs. 1-9.

[94154] VGR2999 gene encodes VGR2999 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94155] VGR2999 precursor RNA folds spatially, forming VGR2999 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR2999 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR2999 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94156] VGR2999 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1199 precursor RNA, VGAM1200 precursor RNA, VGAM1201 precursor RNA and VGAM1202 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94157] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1199 RNA, VGAM1200 RNA, VGAM1201 RNA and VGAM1202 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94158] VGAM1199 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1199 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1199 host target RNA into VGAM1199 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94159] VGAM1200 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1200 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1200 host target RNA into VGAM1200 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94160] VGAM1201 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1201 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1201 host target RNA into VGAM1201 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94161] VGAM1202 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1202 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1202 host target RNA into VGAM1202 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94162] It is appreciated that a function of VGR2999 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR2999 gene include diagnosis, prevention and treatment of viral infection by Avian Nephritis Virus. Specific functions, and accordingly utilities, of VGR2999 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR2999 gene: VGAM1199 host target protein, VGAM1200 host target protein, VGAM1201 host target protein and VGAM1202 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1199, VGAM1200, VGAM1201 and VGAM1202.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3000(VGR3000) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94163] VGR3000 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3000 gene was detected is described hereinabove with reference to Figs. 1-9.

[94164] VGR3000 gene encodes VGR3000 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94165] VGR3000 precursor RNA folds spatially, forming VGR3000 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3000 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3000 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94166] VGR3000 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1203 precursor RNA, VGAM1204 precursor RNA and VGAM1205 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR

through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94167] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1203 RNA, VGAM1204 RNA and VGAM1205 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94168] VGAM1203 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1203 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1203 host target RNA into VGAM1203 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94169] VGAM1204 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1204 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1204 host target RNA into VGAM1204 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94170] VGAM1205 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1205 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1205 host target RNA into VGAM1205 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94171] It is appreciated that a function of VGR3000 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3000 gene include diagnosis, prevention and treatment of viral infection by Scallion Virus X. Specific functions, and accordingly utilities, of VGR3000 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3000 gene: VGAM1203 host target protein, VGAM1204 host target protein and VGAM1205 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1203, VGAM1204 and VGAM1205.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3001(VGR3001) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and

utility of which at least one host target gene is known in the art.

[94172] VGR3001 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3001 gene was detected is described hereinabove with reference to Figs. 1-9.

[94173] VGR3001 gene encodes VGR3001 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94174] VGR3001 precursor RNA folds spatially, forming VGR3001 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3001 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3001 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94175] VGR3001 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM

precursor RNAs, VGAM1206 precursor RNA, VGAM1207 precursor RNA, VGAM1208 precursor RNA and VGAM1209 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94176] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1206 RNA, VGAM1207 RNA, VGAM1208 RNA and VGAM1209 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94177] VGAM1206 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1206 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1206 host target RNA into

VGAM1206 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94178] VGAM1207 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1207 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1207 host target RNA into VGAM1207 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94179] VGAM1208 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1208 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1208 host target RNA into VGAM1208 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94180] VGAM1209 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1209 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1209 host target RNA into VGAM1209 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94181] It is appreciated that a function of VGR3001 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3001 gene include diagnosis, prevention and treatment of viral infection by Clover Yellow Mosaic Virus. Specific functions, and accordingly utilities, of VGR3001 gene correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3001 gene: VGAM1206 host target protein, VGAM1207 host target protein, VGAM1208 host target protein and VGAM1209 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1206, VGAM1207, VGAM1208 and VGAM1209.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3002(VGR3002) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94182] VGR3002 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3002 gene was detected is described hereinabove with reference to Figs. 1-9.

[94183] VGR3002 gene encodes VGR3002 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94184] VGR3002 precursor RNA folds spatially, forming VGR3002 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3002 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3002 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94185] VGR3002 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1210 precursor RNA, VGAM1211 precursor RNA and VGAM1212 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94186] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1210 RNA, VGAM1211 RNA and VGAM1212 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94187] VGAM1210 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1210 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1210 host target RNA into VGAM1210 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94188] VGAM1211 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1211 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1211 host target RNA into VGAM1211 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94189] VGAM1212 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1212 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1212 host target RNA into VGAM1212 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94190] It is appreciated that a function of VGR3002 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3002 gene include

diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3002 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3002 gene: VGAM1210 host target protein, VGAM1211 host target protein and VGAM1212 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1210, VGAM1211 and VGAM1212.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3003(VGR3003) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94191] VGR3003 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3003 gene was

detected is described hereinabove with reference to Figs. 1-9.

[94192] VGR3003 gene encodes VGR3003 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94193] VGR3003 precursor RNA folds spatially, forming VGR3003 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3003 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3003 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94194] VGR3003 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1214 precursor RNA, VGAM1215 precursor RNA, VGAM1216 precursor RNA and VGAM1217 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94195] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1214 RNA, VGAM1215 RNA, VGAM1216 RNA and VGAM1217 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94196] VGAM1214 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1214 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1214 host target RNA into VGAM1214 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94197] VGAM1215 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1215 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1215 host target RNA into VGAM1215 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94198] VGAM1216 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1216 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1216 host target RNA into VGAM1216 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94199] VGAM1217 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1217 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1217 host target RNA into VGAM1217 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94200] It is appreciated that a function of VGR3003 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3003 gene include diagnosis, prevention and treatment of viral infection by Tupaia Herpesvirus. Specific functions, and accordingly utilities, of VGR3003 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3003 gene: VGAM1214 host target protein, VGAM1215 host target protein, VGAM1216 host target protein and VGAM1217 host target protein,

herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1214, VGAM1215, VGAM1216 and VGAM1217.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3004(VGR3004) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94201] VGR3004 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3004 gene was detected is described hereinabove with reference to Figs. 1-9.

[94202] VGR3004 gene encodes VGR3004 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94203] VGR3004 precursor RNA folds spatially, forming VGR3004 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3004 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3004 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94204] VGR3004 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1218 precursor RNA and VGAM1219 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94205] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1218 RNA and VGAM1219 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94206] VGAM1218 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1218 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1218 host target RNA into VGAM1218 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94207] VGAM1219 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1219 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1219 host target RNA into VGAM1219 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94208] It is appreciated that a function of VGR3004 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3004 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR3004 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3004 gene: VGAM1218 host target protein and VGAM1219 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1218 and VGAM1219.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3005(VGR3005) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94209] VGR3005 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3005 gene was detected is described hereinabove with reference to Figs. 1-9.

[94210] VGR3005 gene encodes VGR3005 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94211] VGR3005 precursor RNA folds spatially, forming VGR3005 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3005 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3005 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94212] VGR3005 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1220 precursor RNA, VGAM1221 precursor RNA and VGAM1222 precursor RNA, herein

schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94213] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1220 RNA, VGAM1221 RNA and VGAM1222 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94214] VGAM1220 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1220 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1220 host target RNA into VGAM1220 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94215] VGAM1221 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1221 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1221 host target RNA into VGAM1221 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94216] VGAM1222 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1222 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1222 host target RNA into VGAM1222 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94217] It is appreciated that a function of VGR3005 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3005 gene include diagnosis, prevention and treatment of viral infection by Fowl Adenovirus D. Specific functions, and accordingly utilities, of VGR3005 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3005 gene: VGAM1220 host target protein, VGAM1221 host target protein and VGAM1222 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1220, VGAM1221 and VGAM1222.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3006(VGR3006) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates ex-

pression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94218] VGR3006 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3006 gene was detected is described hereinabove with reference to Figs. 1-9.

[94219] VGR3006 gene encodes VGR3006 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94220] VGR3006 precursor RNA folds spatially, forming VGR3006 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3006 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3006 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94221] VGR3006 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1223 precursor RNA and VGAM1224 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94222] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1223 RNA and VGAM1224 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94223] VGAM1223 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1223 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1223 host target RNA into VGAM1223 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94224] VGAM1224 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1224 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1224 host target RNA into VGAM1224 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94225] It is appreciated that a function of VGR3006 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3006 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3006 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR3006 gene: VGAM1223 host target protein and VGAM1224 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1223 and VGAM1224.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3007(VGR3007) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94226] VGR3007 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3007 gene was detected is described hereinabove with reference to Figs. 1-9.

[94227] VGR3007 gene encodes VGR3007 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94228] VGR3007 precursor RNA folds spatially, forming VGR3007

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3007 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3007 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94229] VGR3007 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1226 precursor RNA, VGAM1227 precursor RNA, VGAM1228 precursor RNA and VGAM1229 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94230] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1226 RNA, VGAM1227 RNA, VGAM1228 RNA and VGAM1229

RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94231] VGAM1226 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1226 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1226 host target RNA into VGAM1226 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94232] VGAM1227 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1227 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1227 host target RNA into VGAM1227 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94233] VGAM1228 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1228 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1228 host target RNA into VGAM1228 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94234] VGAM1229 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1229 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1229 host target RNA into VGAM1229 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94235] It is appreciated that a function of VGR3007 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3007 gene include diagnosis, prevention and treatment of viral infection by Tacaribe Virus. Specific functions, and accordingly utilities, of VGR3007 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3007 gene: VGAM1226 host target protein, VGAM1227 host target protein, VGAM1228 host target protein and VGAM1229 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1226, VGAM1227, VGAM1228 and VGAM1229.Fig. 9 further provides a conceptual description of novel bioinformatically detected

regulatory viral gene, referred to here as Viral Genomic Record 3008(VGR3008) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94236] VGR3008 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3008 gene was detected is described hereinabove with reference to Figs. 1-9.

[94237] VGR3008 gene encodes VGR3008 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94238] VGR3008 precursor RNA folds spatially, forming VGR3008 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3008 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3008 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[94239] VGR3008 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1230 precursor RNA, VGAM1231 precursor RNA, VGAM1232 precursor RNA, VGAM1233 precursor RNA and VGAM1234 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94240] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1230 RNA, VGAM1231 RNA, VGAM1232 RNA, VGAM1233 RNA and VGAM1234 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94241] VGAM1230 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1230 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1230 host target RNA into VGAM1230 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94242] VGAM1231 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1231 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1231 host target RNA into VGAM1231 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94243] VGAM1232 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1232 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1232 host target RNA into VGAM1232 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94244] VGAM1233 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1233 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1233 host target RNA into VGAM1233 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94245] VGAM1234 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1234 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1234 host target RNA into VGAM1234 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94246] It is appreciated that a function of VGR3008 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3008 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3008 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3008 gene: VGAM1230 host target protein, VGAM1231 host target protein, VGAM1232 host target protein, VGAM1233 host target protein and VGAM1234 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1230, VGAM1231, VGAM1232, VGAM1233 and VGAM1234.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3009(VGR3009) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94247] VGR3009 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3009 gene was detected is described hereinabove with reference to Figs. 1-9.

[94248] VGR3009 gene encodes VGR3009 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94249] VGR3009 precursor RNA folds spatially, forming VGR3009 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3009 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3009 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94250] VGR3009 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1235 precursor RNA, VGAM1236 precursor RNA, VGAM1237 precursor RNA, VGAM1238 precursor RNA, VGAM1239 precursor RNA and VGAM1240 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94251] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1235 RNA, VGAM1236 RNA, VGAM1237 RNA, VGAM1238 RNA, VGAM1239 RNA and VGAM1240 RNA, herein schemati-

cally represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94252] VGAM1235 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1235 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1235 host target RNA into VGAM1235 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94253] VGAM1236 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1236 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1236 host target RNA into VGAM1236 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94254] VGAM1237 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1237 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1237 host target RNA into VGAM1237 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94255] VGAM1238 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1238 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1238 host target RNA into VGAM1238 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94256] VGAM1239 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1239 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1239 host target RNA into VGAM1239 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94257] VGAM1240 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1240 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1240 host target RNA into VGAM1240 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94258] It is appreciated that a function of VGR3009 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3009 gene include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3009 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3009 gene: VGAM1235 host target protein, VGAM1236 host target protein, VGAM1237 host target protein, VGAM1238 host target protein, VGAM1239 host target protein and VGAM1240 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1235, VGAM1236,

VGAM1237, VGAM1238, VGAM1239 and VGAM1240.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3010(VGR3010) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94259] VGR3010 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3010 gene was detected is described hereinabove with reference to Figs. 1-9.

[94260] VGR3010 gene encodes VGR3010 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94261] VGR3010 precursor RNA folds spatially, forming VGR3010 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3010 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3010 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94262] VGR3010 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1241 precursor RNA and VGAM1242 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94263] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1241 RNA and VGAM1242 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94264] VGAM1241 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1241 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1241 host target RNA into VGAM1241 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94265] VGAM1242 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1242 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1242 host target RNA into VGAM1242 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94266] It is appreciated that a function of VGR3010 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3010 gene include diagnosis, prevention and treatment of viral infection by Gallid Herpesvirus 3. Specific functions, and accordingly utilities, of VGR3010 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3010 gene: VGAM1241 host target protein and VGAM1242 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1241 and VGAM1242.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3011(VGR3011) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94267] VGR3011 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3011 gene was

detected is described hereinabove with reference to Figs. 1-9.

[94268] VGR3011 gene encodes VGR3011 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94269] VGR3011 precursor RNA folds spatially, forming VGR3011 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3011 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3011 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94270] VGR3011 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1243 precursor RNA, VGAM1244 precursor RNA, VGAM1245 precursor RNA and VGAM1246 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94271] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1243 RNA, VGAM1244 RNA, VGAM1245 RNA and VGAM1246 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94272] VGAM1243 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1243 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1243 host target RNA into VGAM1243 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94273] VGAM1244 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1244 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1244 host target RNA into VGAM1244 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94274] VGAM1245 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1245 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1245 host target RNA into VGAM1245 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94275] VGAM1246 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1246 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1246 host target RNA into VGAM1246 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94276] It is appreciated that a function of VGR3011 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3011 gene include diagnosis, prevention and treatment of viral infection by Turkey Adenovirus 3. Specific functions, and accordingly utilities, of VGR3011 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3011 gene: VGAM1243 host target protein, VGAM1244 host target protein, VGAM1245 host target protein and VGAM1246 host target protein,

herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1243, VGAM1244, VGAM1245 and VGAM1246.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3012(VGR3012) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94277] VGR3012 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3012 gene was detected is described hereinabove with reference to Figs. 1-9.

[94278] VGR3012 gene encodes VGR3012 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94279] VGR3012 precursor RNA folds spatially, forming VGR3012 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3012 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3012 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94280] VGR3012 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1247 precursor RNA, VGAM1248 precursor RNA, VGAM1249 precursor RNA, VGAM1250 precursor RNA and VGAM1251 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94281] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1247 RNA, VGAM1248 RNA, VGAM1249 RNA, VGAM1250 RNA and VGAM1251 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94282] VGAM1247 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1247 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1247 host target RNA into VGAM1247 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94283] VGAM1248 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1248 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1248 host target RNA into

VGAM1248 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94284] VGAM1249 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1249 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1249 host target RNA into VGAM1249 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94285] VGAM1250 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1250 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1250 host target RNA into VGAM1250 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94286] VGAM1251 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1251 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1251 host target RNA into VGAM1251 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94287] It is appreciated that a function of VGR3012 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3012 gene include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGR3012 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3012 gene: VGAM1247 host target protein, VGAM1248 host target protein, VGAM1249 host target protein, VGAM1250 host target protein and VGAM1251 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1247, VGAM1248, VGAM1249, VGAM1250 and VGAM1251.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3013(VGR3013) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94288] VGR3013 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3013 gene was detected is described hereinabove with reference to Figs. 1-9.

[94289] VGR3013 gene encodes VGR3013 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94290] VGR3013 precursor RNA folds spatially, forming VGR3013 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3013 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3013 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94291] VGR3013 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1252 precursor RNA, VGAM1253 precursor RNA, VGAM1254 precursor RNA, VGAM1255 precursor RNA and VGAM1256 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig.

1.

[94292] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1252 RNA, VGAM1253 RNA, VGAM1254 RNA, VGAM1255 RNA and VGAM1256 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94293] VGAM1252 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1252 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1252 host target RNA into VGAM1252 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94294] VGAM1253 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1253 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1253 host target RNA into VGAM1253 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94295] VGAM1254 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1254 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1254 host target RNA into VGAM1254 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94296] VGAM1255 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1255 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1255 host target RNA into VGAM1255 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94297] VGAM1256 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1256 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1256 host target RNA into VGAM1256 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94298] It is appreciated that a function of VGR3013 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3013 gene include diagnosis, prevention and treatment of viral infection by Human Adenovirus D. Specific functions, and accordingly utilities, of VGR3013 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3013 gene: VGAM1252 host target protein, VGAM1253 host target protein, VGAM1254 host target protein, VGAM1255 host target protein and VGAM1256 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1252, VGAM1253, VGAM1254, VGAM1255 and VGAM1256.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3014(VGR3014) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[94299] VGR3014 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3014 gene was detected is described hereinabove with reference to Figs. 1-9.

[94300] VGR3014 gene encodes VGR3014 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94301] VGR3014 precursor RNA folds spatially, forming VGR3014 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3014 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3014 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94302] VGR3014 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1257 precursor RNA and

VGAM1258 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94303] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1257 RNA and VGAM1258 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94304] VGAM1257 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1257 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1257 host target RNA into VGAM1257 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94305] VGAM1258 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1258 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1258 host target RNA into VGAM1258 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94306] It is appreciated that a function of VGR3014 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3014 gene include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGR3014 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3014 gene: VGAM1257 host target protein and VGAM1258 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1257 and VGAM1258.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3015(VGR3015) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94307] VGR3015 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3015 gene was detected is described hereinabove with reference to Figs. 1-9.

[94308] VGR3015 gene encodes VGR3015 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94309] VGR3015 precursor RNA folds spatially, forming VGR3015 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3015 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3015 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94310] VGR3015 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1259 precursor RNA, VGAM1260 precursor RNA, VGAM1261 precursor RNA and VGAM1262 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94311] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1259 RNA, VGAM1260 RNA, VGAM1261 RNA and VGAM1262 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corre-

sponding to VGAM RNA of Fig. 1.

[94312] VGAM1259 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1259 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1259 host target RNA into VGAM1259 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94313] VGAM1260 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1260 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1260 host target RNA into VGAM1260 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94314] VGAM1261 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1261 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1261 host target RNA into VGAM1261 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94315] VGAM1262 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1262 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1262 host target RNA into

VGAM1262 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94316] It is appreciated that a function of VGR3015 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3015 gene include diagnosis, prevention and treatment of viral infection by Blackcurrant Reversion Virus. Specific functions, and accordingly utilities, of VGR3015 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3015 gene: VGAM1259 host target protein, VGAM1260 host target protein, VGAM1261 host target protein and VGAM1262 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1259, VGAM1260, VGAM1261 and VGAM1262.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3016(VGR3016) viral gene, which encodes an

`operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94317] VGR3016 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3016 gene was detected is described hereinabove with reference to Figs. 1-9.

[94318] VGR3016 gene encodes VGR3016 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94319] VGR3016 precursor RNA folds spatially, forming VGR3016 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3016 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3016 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94320] VGR3016 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1263 precursor RNA, VGAM1264 precursor RNA, VGAM1265 precursor RNA, VGAM1266 precursor RNA and VGAM1267 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94321] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1263 RNA, VGAM1264 RNA, VGAM1265 RNA, VGAM1266 RNA and VGAM1267 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94322] VGAM1263 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1263 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1263 host target RNA into VGAM1263 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94323] VGAM1264 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1264 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1264 host target RNA into VGAM1264 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94324] VGAM1265 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1265 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1265 host target RNA into VGAM1265 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94325] VGAM1266 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1266 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1266 host target RNA into VGAM1266 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94326] VGAM1267 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1267 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1267 host target RNA into VGAM1267 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94327] It is appreciated that a function of VGR3016 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3016 gene include diagnosis, prevention and treatment of viral infection by Beet Soil-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGR3016 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3016 gene: VGAM1263 host target protein, VGAM1264 host target protein, VGAM1265 host target protein, VGAM1266 host target protein and VGAM1267 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The func-

tion of these host target genes is elaborated hereinabove with reference to VGAM1263, VGAM1264, VGAM1265, VGAM1266 and VGAM1267.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3017(VGR3017) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94328] VGR3017 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3017 gene was detected is described hereinabove with reference to Figs. 1-9.

[94329] VGR3017 gene encodes VGR3017 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94330] VGR3017 precursor RNA folds spatially, forming VGR3017 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3017 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3017 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94331] VGR3017 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1268 precursor RNA, VGAM1269 precursor RNA, VGAM1270 precursor RNA, VGAM1271 precursor RNA and VGAM1272 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94332] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1268 RNA, VGAM1269 RNA, VGAM1270 RNA, VGAM1271 RNA and VGAM1272 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94333] VGAM1268 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1268 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1268 host target RNA into VGAM1268 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94334] VGAM1269 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1269 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1269 host target RNA into VGAM1269 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94335] VGAM1270 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1270 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1270 host target RNA into VGAM1270 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94336] VGAM1271 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1271 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1271 host target RNA into VGAM1271 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94337] VGAM1272 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1272 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1272 host target RNA into VGAM1272 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94338] It is appreciated that a function of VGR3017 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3017 gene include diagnosis, prevention and treatment of viral infection by Grapevine Virus A. Specific functions, and accordingly utilities, of VGR3017 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR3017 gene: VGAM1268 host target protein, VGAM1269 host target protein, VGAM1270 host target protein, VGAM1271 host target protein and VGAM1272 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1268, VGAM1269, VGAM1270, VGAM1271 and VGAM1272.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3018(VGR3018) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94339] VGR3018 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3018 gene was detected is described hereinabove with reference to Figs. 1-9.

[94340] VGR3018 gene encodes VGR3018 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[94341] VGR3018 precursor RNA folds spatially, forming VGR3018 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3018 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3018 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94342] VGR3018 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1273 precursor RNA, VGAM1274 precursor RNA, VGAM1275 precursor RNA and VGAM1276 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94343] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1273 RNA, VGAM1274 RNA, VGAM1275 RNA and VGAM1276 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94344] VGAM1273 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1273 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1273 host target RNA into VGAM1273 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94345] VGAM1274 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1274 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1274 host target RNA into VGAM1274 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94346] VGAM1275 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1275 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1275 host target RNA into VGAM1275 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94347] VGAM1276 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1276 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1276 host target RNA into VGAM1276 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94348] It is appreciated that a function of VGR3018 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3018 gene include diagnosis, prevention and treatment of viral infection by A-2 Plaque Virus. Specific functions, and accordingly utilities, of VGR3018 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3018 gene: VGAM1273 host target protein, VGAM1274 host target protein, VGAM1275 host target protein and VGAM1276 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1273, VGAM1274,

VGAM1275 and VGAM1276.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3019(VGR3019) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94349] VGR3019 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3019 gene was detected is described hereinabove with reference to Figs. 1-9.

[94350] VGR3019 gene encodes VGR3019 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94351] VGR3019 precursor RNA folds spatially, forming VGR3019 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3019 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3019 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94352] VGR3019 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1277 precursor RNA, VGAM1278 precursor RNA, VGAM1279 precursor RNA and VGAM1280 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94353] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1277 RNA, VGAM1278 RNA, VGAM1279 RNA and VGAM1280 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94354] VGAM1277 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1277 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1277 host target RNA into VGAM1277 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94355] VGAM1278 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1278 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1278 host target RNA into VGAM1278 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94356] VGAM1279 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1279 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1279 host target RNA into VGAM1279 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94357] VGAM1280 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1280 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1280 host target RNA into VGAM1280 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94358] It is appreciated that a function of VGR3019 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3019 gene include diagnosis, prevention and treatment of viral infection by Human Enterovirus C. Specific functions, and accordingly utilities, of VGR3019 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3019 gene: VGAM1277 host target protein, VGAM1278 host target protein, VGAM1279 host target protein and VGAM1280 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1277, VGAM1278, VGAM1279 and VGAM1280.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3020(VGR3020) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94359] VGR3020 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3020 gene was detected is described hereinabove with reference to Figs. 1-9.

[94360] VGR3020 gene encodes VGR3020 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94361] VGR3020 precursor RNA folds spatially, forming VGR3020 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3020 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3020 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94362] VGR3020 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1281 precursor RNA, VGAM1282 precursor RNA, VGAM1283 precursor RNA, VGAM1284

precursor RNA, VGAM1285 precursor RNA, VGAM1286 precursor RNA and VGAM1287 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94363] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1281 RNA, VGAM1282 RNA, VGAM1283 RNA, VGAM1284 RNA, VGAM1285 RNA, VGAM1286 RNA and VGAM1287 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94364] VGAM1281 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1281 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1281 host target RNA into VGAM1281 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94365] VGAM1282 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1282 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1282 host target RNA into VGAM1282 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94366] VGAM1283 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1283 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1283 host target RNA into VGAM1283 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94367] VGAM1284 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1284 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1284 host target RNA into VGAM1284 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94368] VGAM1285 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1285 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1285 host target RNA into VGAM1285 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94369] VGAM1286 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1286 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1286 host target RNA into VGAM1286 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94370] VGAM1287 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1287 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1287 host target RNA into VGAM1287 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94371] It is appreciated that a function of VGR3020 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3020 gene include diagnosis, prevention and treatment of viral infection by Beet Virus Q. Specific functions, and accordingly utilities, of VGR3020 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3020 gene: VGAM1281 host target protein, VGAM1282 host target protein, VGAM1283 host target protein, VGAM1284 host target protein, VGAM1285 host target protein, VGAM1286 host target protein and VGAM1287 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these

host target genes is elaborated hereinabove with reference to VGAM1281, VGAM1282, VGAM1283, VGAM1284, VGAM1285, VGAM1286 and VGAM1287.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3021(VGR3021) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94372] VGR3021 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3021 gene was detected is described hereinabove with reference to Figs. 1-9.

[94373] VGR3021 gene encodes VGR3021 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94374] VGR3021 precursor RNA folds spatially, forming VGR3021 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3021 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3021 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94375] VGR3021 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1288 precursor RNA and VGAM1289 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94376] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1288 RNA and VGAM1289 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94377] VGAM1288 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1288 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1288 host target RNA into VGAM1288 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94378] VGAM1289 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1289 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1289 host target RNA into VGAM1289 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94379] It is appreciated that a function of VGR3021 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3021 gene include diagnosis, prevention and treatment of viral infection by Saimiriine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3021 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3021 gene: VGAM1288 host target protein and VGAM1289 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1288 and VGAM1289.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3022(VGR3022) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94380] VGR3022 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3022 gene was detected is described hereinabove with reference to Figs. 1-9.

[94381] VGR3022 gene encodes VGR3022 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94382] VGR3022 precursor RNA folds spatially, forming VGR3022 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3022 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3022 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94383] VGR3022 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1291 precursor RNA, VGAM1292 precursor RNA and VGAM1293 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94384] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1291 RNA, VGAM1292 RNA and VGAM1293 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94385] VGAM1291 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1291 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1291 host target RNA into VGAM1291 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94386] VGAM1292 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1292 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1292 host target RNA into VGAM1292 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94387] VGAM1293 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1293 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1293 host target RNA into VGAM1293 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94388] It is appreciated that a function of VGR3022 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3022 gene include diagnosis, prevention and treatment of viral infection by Swinepox Virus. Specific functions, and accordingly utilities, of VGR3022 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3022 gene: VGAM1291 host target protein, VGAM1292 host target protein and VGAM1293 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1291, VGAM1292 and VGAM1293.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3023(VGR3023) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[94389] VGR3023 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3023 gene was detected is described hereinabove with reference to Figs. 1-9.

[94390] VGR3023 gene encodes VGR3023 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94391] VGR3023 precursor RNA folds spatially, forming VGR3023 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3023 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3023 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94392] VGR3023 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1294 precursor RNA, VGAM1295

precursor RNA and VGAM1296 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94393] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1294 RNA, VGAM1295 RNA and VGAM1296 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94394] VGAM1294 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1294 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1294 host target RNA into VGAM1294 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94395] VGAM1295 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1295 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1295 host target RNA into VGAM1295 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94396] VGAM1296 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1296 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1296 host target RNA into

VGAM1296 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94397] It is appreciated that a function of VGR3023 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3023 gene include diagnosis, prevention and treatment of viral infection by Vaccinia Virus. Specific functions, and accordingly utilities, of VGR3023 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3023 gene: VGAM1294 host target protein, VGAM1295 host target protein and VGAM1296 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1294, VGAM1295 and VGAM1296.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3024(VGR3024) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes,

each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94398] VGR3024 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3024 gene was detected is described hereinabove with reference to Figs. 1-9.

[94399] VGR3024 gene encodes VGR3024 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94400] VGR3024 precursor RNA folds spatially, forming VGR3024 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3024 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3024 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94401] VGR3024 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1297 precursor RNA, VGAM1298 precursor RNA, VGAM1299 precursor RNA, VGAM1300 precursor RNA and VGAM1301 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94402] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1297 RNA, VGAM1298 RNA, VGAM1299 RNA, VGAM1300 RNA and VGAM1301 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94403] VGAM1297 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1297 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1297 host target RNA into VGAM1297 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94404] VGAM1298 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1298 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1298 host target RNA into VGAM1298 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94405] VGAM1299 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1299 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1299 host target RNA into VGAM1299 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94406] VGAM1300 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1300 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1300 host target RNA into VGAM1300 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94407] VGAM1301 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1301 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1301 host target RNA into VGAM1301 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94408] It is appreciated that a function of VGR3024 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3024 gene include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGR3024 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3024 gene: VGAM1297 host target protein, VGAM1298 host target protein, VGAM1299 host target protein, VGAM1300 host target protein and VGAM1301 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with refer-

ence to VGAM1297, VGAM1298, VGAM1299, VGAM1300 and VGAM1301.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3025(VGR3025) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94409] VGR3025 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3025 gene was detected is described hereinabove with reference to Figs. 1-9.

[94410] VGR3025 gene encodes VGR3025 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94411] VGR3025 precursor RNA folds spatially, forming VGR3025 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3025 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3025 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94412] VGR3025 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1302 precursor RNA, VGAM1303 precursor RNA and VGAM1304 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94413] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1302 RNA, VGAM1303 RNA and VGAM1304 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94414] VGAM1302 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1302 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1302 host target RNA into VGAM1302 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94415] VGAM1303 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1303 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1303 host target RNA into VGAM1303 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94416] VGAM1304 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1304 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1304 host target RNA into VGAM1304 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94417] It is appreciated that a function of VGR3025 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3025 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGR3025 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3025 gene: VGAM1302 host target protein, VGAM1303 host target protein and VGAM1304 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1302, VGAM1303 and VGAM1304.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3026(VGR3026) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94418] VGR3026 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3026 gene was detected is described hereinabove with reference to Figs. 1-9.

[94419] VGR3026 gene encodes VGR3026 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94420] VGR3026 precursor RNA folds spatially, forming VGR3026 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3026 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3026 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94421] VGR3026 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1305 precursor RNA, VGAM1306 precursor RNA, VGAM1307 precursor RNA and VGAM1308 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94422] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1305 RNA, VGAM1306 RNA, VGAM1307 RNA and VGAM1308 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corre-

sponding to VGAM RNA of Fig. 1.

[94423] VGAM1305 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1305 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1305 host target RNA into VGAM1305 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94424] VGAM1306 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1306 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1306 host target RNA into VGAM1306 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94425] VGAM1307 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1307 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1307 host target RNA into VGAM1307 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94426] VGAM1308 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1308 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1308 host target RNA into

VGAM1308 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94427] It is appreciated that a function of VGR3026 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3026 gene include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus SAT 2 (FMDV-SAT2). Specific functions, and accordingly utilities, of VGR3026 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3026 gene: VGAM1305 host target protein, VGAM1306 host target protein, VGAM1307 host target protein and VGAM1308 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1305, VGAM1306, VGAM1307 and VGAM1308.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3027(VGR3027) viral gene, which en-

codes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94428] VGR3027 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3027 gene was detected is described hereinabove with reference to Figs. 1-9.

[94429] VGR3027 gene encodes VGR3027 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94430] VGR3027 precursor RNA folds spatially, forming VGR3027 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3027 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3027 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94431] VGR3027 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1309 precursor RNA and VGAM1310 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94432] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1309 RNA and VGAM1310 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94433] VGAM1309 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1309 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1309 host target RNA into

VGAM1309 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94434] VGAM1310 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1310 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1310 host target RNA into VGAM1310 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94435] It is appreciated that a function of VGR3027 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3027 gene include diagnosis, prevention and treatment of viral infection by Human Adenovirus D. Specific functions, and accordingly utilities, of VGR3027 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3027 gene: VGAM1309 host target protein and VGAM1310 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1309 and VGAM1310.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3028(VGR3028) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94436] VGR3028 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3028 gene was detected is described hereinabove with reference to Figs. 1-9.

[94437] VGR3028 gene encodes VGR3028 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94438] VGR3028 precursor RNA folds spatially, forming VGR3028 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3028 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3028 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94439] VGR3028 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1311 precursor RNA, VGAM1312 precursor RNA, VGAM1313 precursor RNA, VGAM1314 precursor RNA, VGAM1315 precursor RNA and VGAM1316 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94440] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1311 RNA, VGAM1312 RNA, VGAM1313 RNA, VGAM1314 RNA, VGAM1315 RNA and VGAM1316 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94441] VGAM1311 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1311 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1311 host target RNA into VGAM1311 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94442] VGAM1312 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1312 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1312 host target RNA into VGAM1312 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94443] VGAM1313 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1313 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1313 host target RNA into VGAM1313 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94444] VGAM1314 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1314 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1314 host target RNA into VGAM1314 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94445] VGAM1315 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1315 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1315 host target RNA into VGAM1315 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94446] VGAM1316 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1316 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1316 host target RNA into VGAM1316 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94447] It is appreciated that a function of VGR3028 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3028 gene include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus C. Specific functions, and accordingly utilities, of VGR3028 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3028 gene: VGAM1311 host target protein, VGAM1312 host target protein, VGAM1313 host target protein, VGAM1314 host target protein, VGAM1315 host target protein and VGAM1316 host target protein, herein schematically represented by

VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1311, VGAM1312, VGAM1313, VGAM1314, VGAM1315 and VGAM1316.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3029(VGR3029) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94448] VGR3029 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3029 gene was detected is described hereinabove with reference to Figs. 1-9.

[94449] VGR3029 gene encodes VGR3029 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94450] VGR3029 precursor RNA folds spatially, forming VGR3029 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3029 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3029 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94451] VGR3029 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1317 precursor RNA, VGAM1318 precursor RNA and VGAM1319 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94452] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1317 RNA, VGAM1318 RNA and VGAM1319 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM

RNA of Fig. 1.

[94453] VGAM1317 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1317 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1317 host target RNA into VGAM1317 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94454] VGAM1318 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1318 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1318 host target RNA into VGAM1318 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94455] VGAM1319 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1319 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1319 host target RNA into VGAM1319 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94456] It is appreciated that a function of VGR3029 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3029 gene include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus O. Specific functions, and accordingly utilities, of VGR3029 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR3029 gene: VGAM1317 host target protein, VGAM1318 host target protein and VGAM1319 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1317, VGAM1318 and VGAM1319.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3030(VGR3030) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94457] VGR3030 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3030 gene was detected is described hereinabove with reference to Figs. 1-9.

[94458] VGR3030 gene encodes VGR3030 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94459] VGR3030 precursor RNA folds spatially, forming VGR3030 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3030 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3030 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94460] VGR3030 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1320 precursor RNA and VGAM1321 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94461] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1320 RNA and VGAM1321 RNA, herein schematically repre-

sented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94462] VGAM1320 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1320 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1320 host target RNA into VGAM1320 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94463] VGAM1321 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1321 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1321 host target RNA into

VGAM1321 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94464] It is appreciated that a function of VGR3030 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3030 gene include diagnosis, prevention and treatment of viral infection by Melanoplus Sanguinipes Entomopoxvirus. Specific functions, and accordingly utilities, of VGR3030 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3030 gene: VGAM1320 host target protein and VGAM1321 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1320 and VGAM1321.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3031(VGR3031) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes,

each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94465] VGR3031 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3031 gene was detected is described hereinabove with reference to Figs. 1-9.

[94466] VGR3031 gene encodes VGR3031 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94467] VGR3031 precursor RNA folds spatially, forming VGR3031 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3031 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3031 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94468] VGR3031 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1322 precursor RNA, VGAM1323 precursor RNA, VGAM1324 precursor RNA and VGAM1325 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94469] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1322 RNA, VGAM1323 RNA, VGAM1324 RNA and VGAM1325 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94470] VGAM1322 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1322 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1322 host target RNA into VGAM1322 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94471] VGAM1323 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1323 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1323 host target RNA into VGAM1323 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94472] VGAM1324 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1324 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1324 host target RNA into VGAM1324 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94473] VGAM1325 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1325 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1325 host target RNA into VGAM1325 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94474] It is appreciated that a function of VGR3031 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3031 gene include diagnosis, prevention and treatment of viral infection by Garlic Latent Virus. Specific functions, and accordingly

utilities, of VGR3031 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3031 gene: VGAM1322 host target protein, VGAM1323 host target protein, VGAM1324 host target protein and VGAM1325 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1322, VGAM1323, VGAM1324 and VGAM1325.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3032(VGR3032) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94475] VGR3032 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3032 gene was detected is described hereinabove with reference to Figs. 1-9.

[94476] VGR3032 gene encodes VGR3032 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94477] VGR3032 precursor RNA folds spatially, forming VGR3032 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3032 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3032 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94478] VGR3032 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1326 precursor RNA, VGAM1327 precursor RNA and VGAM1328 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94479] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1326 RNA, VGAM1327 RNA and VGAM1328 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94480] VGAM1326 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1326 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1326 host target RNA into VGAM1326 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94481] VGAM1327 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1327 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1327 host target RNA into VGAM1327 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94482] VGAM1328 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1328 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1328 host target RNA into VGAM1328 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94483] It is appreciated that a function of VGR3032 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3032 gene include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGR3032 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3032 gene: VGAM1326 host target protein, VGAM1327 host target protein and VGAM1328 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1326, VGAM1327 and VGAM1328.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3033(VGR3033) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94484] VGR3033 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3033 gene was detected is described hereinabove with reference to Figs. 1-9.

[94485] VGR3033 gene encodes VGR3033 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94486] VGR3033 precursor RNA folds spatially, forming VGR3033 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3033 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3033 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94487] VGR3033 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1330 precursor RNA, VGAM1331 precursor RNA, VGAM1332 precursor RNA, VGAM1333 precursor RNA, VGAM1334 precursor RNA and VGAM1335 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94488] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1330 RNA, VGAM1331 RNA, VGAM1332 RNA, VGAM1333 RNA, VGAM1334 RNA and VGAM1335 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94489] VGAM1330 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1330 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1330 host target RNA into VGAM1330 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94490] VGAM1331 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1331 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1331 host target RNA into VGAM1331 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94491] VGAM1332 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1332 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1332 host target RNA into VGAM1332 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94492] VGAM1333 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1333 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1333 host target RNA into VGAM1333 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94493] VGAM1334 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1334 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1334 host target RNA into

VGAM1334 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94494] VGAM1335 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1335 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1335 host target RNA into VGAM1335 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94495] It is appreciated that a function of VGR3033 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3033 gene include diagnosis, prevention and treatment of viral infection by Human Adenovirus A. Specific functions, and accordingly utilities, of VGR3033 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3033 gene: VGAM1330 host target protein, VGAM1331 host target protein, VGAM1332 host target protein, VGAM1333 host target protein, VGAM1334 host target protein and VGAM1335 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1330, VGAM1331, VGAM1332, VGAM1333, VGAM1334 and VGAM1335.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3034(VGR3034) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94496] VGR3034 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3034 gene was detected is described hereinabove with reference to Figs. 1-9.

[94497] VGR3034 gene encodes VGR3034 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94498] VGR3034 precursor RNA folds spatially, forming VGR3034 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3034 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3034 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94499] VGR3034 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1336 precursor RNA and VGAM1337 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94500] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1336 RNA and VGAM1337 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94501] VGAM1336 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1336 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1336 host target RNA into VGAM1336 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94502] VGAM1337 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1337 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1337 host target RNA into VGAM1337 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94503] It is appreciated that a function of VGR3034 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3034 gene include diagnosis, prevention and treatment of viral infection by Sheeppox Virus. Specific functions, and accordingly utilities, of VGR3034 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3034 gene: VGAM1336 host target protein and VGAM1337 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1336 and VGAM1337.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here

as Viral Genomic Record 3035(VGR3035) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94504] VGR3035 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3035 gene was detected is described hereinabove with reference to Figs. 1-9.

[94505] VGR3035 gene encodes VGR3035 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94506] VGR3035 precursor RNA folds spatially, forming VGR3035 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3035 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3035 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[94507] VGR3035 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1340 precursor RNA, VGAM1341 precursor RNA, VGAM1342 precursor RNA and VGAM1343 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94508] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1340 RNA, VGAM1341 RNA, VGAM1342 RNA and VGAM1343 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94509] VGAM1340 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1340 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1340 host target RNA into VGAM1340 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94510] VGAM1341 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1341 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1341 host target RNA into VGAM1341 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94511] VGAM1342 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1342 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1342 host target RNA into VGAM1342 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94512] VGAM1343 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1343 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1343 host target RNA into VGAM1343 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94513] It is appreciated that a function of VGR3035 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3035 gene include diagnosis, prevention and treatment of viral infection by Garlic Virus A. Specific functions, and accordingly utilities, of VGR3035 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3035 gene: VGAM1340 host target protein, VGAM1341 host target protein, VGAM1342 host target protein and VGAM1343 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1340, VGAM1341, VGAM1342 and VGAM1343.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3036(VGR3036) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94514] VGR3036 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3036 gene was detected is described hereinabove with reference to Figs. 1-9.

[94515] VGR3036 gene encodes VGR3036 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94516] VGR3036 precursor RNA folds spatially, forming VGR3036 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3036 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3036 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94517] VGR3036 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1346 precursor RNA, VGAM1347 precursor RNA, VGAM1348 precursor RNA, VGAM1349 precursor RNA, VGAM1350 precursor RNA, VGAM1351 precursor RNA, VGAM1352 precursor RNA and VGAM1353

precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94518] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1346 RNA, VGAM1347 RNA, VGAM1348 RNA, VGAM1349 RNA, VGAM1350 RNA, VGAM1351 RNA, VGAM1352 RNA and VGAM1353 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94519] VGAM1346 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1346 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1346 host target RNA into VGAM1346 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94520] VGAM1347 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1347 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1347 host target RNA into VGAM1347 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94521] VGAM1348 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1348 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1348 host target RNA into

VGAM1348 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94522] VGAM1349 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1349 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1349 host target RNA into VGAM1349 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94523] VGAM1350 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1350 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1350 host target RNA into VGAM1350 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94524] VGAM1351 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1351 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1351 host target RNA into VGAM1351 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94525] VGAM1352 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1352 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1352 host target RNA into VGAM1352 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94526] VGAM1353 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1353 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1353 host target RNA into VGAM1353 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94527] It is appreciated that a function of VGR3036 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3036 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utili-

ties, of VGR3036 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3036 gene: VGAM1346 host target protein, VGAM1347 host target protein, VGAM1348 host target protein, VGAM1349 host target protein, VGAM1350 host target protein, VGAM1351 host target protein, VGAM1352 host target protein and VGAM1353 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1346, VGAM1347, VGAM1348, VGAM1349, VGAM1350, VGAM1351, VGAM1352 and VGAM1353.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3037(VGR3037) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94528] VGR3037 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3037 gene was detected is described hereinabove with reference to Figs. 1-9.

[94529] VGR3037 gene encodes VGR3037 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94530] VGR3037 precursor RNA folds spatially, forming VGR3037 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3037 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3037 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94531] VGR3037 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1354 precursor RNA, VGAM1355 precursor RNA, VGAM1356 precursor RNA, VGAM1357 precursor RNA, VGAM1358 precursor RNA, VGAM1359 precursor RNA, VGAM1360 precursor RNA and VGAM1361

precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94532] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1354 RNA, VGAM1355 RNA, VGAM1356 RNA, VGAM1357 RNA, VGAM1358 RNA, VGAM1359 RNA, VGAM1360 RNA and VGAM1361 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94533] VGAM1354 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1354 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1354 host target RNA into VGAM1354 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94534] VGAM1355 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1355 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1355 host target RNA into VGAM1355 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94535] VGAM1356 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1356 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1356 host target RNA into

VGAM1356 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94536] VGAM1357 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1357 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1357 host target RNA into VGAM1357 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94537] VGAM1358 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1358 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1358 host target RNA into VGAM1358 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94538] VGAM1359 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1359 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1359 host target RNA into VGAM1359 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94539] VGAM1360 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1360 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1360 host target RNA into VGAM1360 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94540] VGAM1361 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1361 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1361 host target RNA into VGAM1361 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94541] It is appreciated that a function of VGR3037 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3037 gene include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utili-

ties, of VGR3037 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3037 gene: VGAM1354 host target protein, VGAM1355 host target protein, VGAM1356 host target protein, VGAM1357 host target protein, VGAM1358 host target protein, VGAM1359 host target protein, VGAM1360 host target protein and VGAM1361 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1354, VGAM1355, VGAM1356, VGAM1357, VGAM1358, VGAM1359, VGAM1360 and VGAM1361.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3038(VGR3038) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94542] VGR3038 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3038 gene was detected is described hereinabove with reference to Figs. 1-9.

[94543] VGR3038 gene encodes VGR3038 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94544] VGR3038 precursor RNA folds spatially, forming VGR3038 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3038 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3038 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94545] VGR3038 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1362 precursor RNA, VGAM1363 precursor RNA, VGAM1364 precursor RNA and VGAM1365 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94546] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1362 RNA, VGAM1363 RNA, VGAM1364 RNA and VGAM1365 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94547] VGAM1362 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1362 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1362 host target RNA into VGAM1362 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94548] VGAM1363 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1363 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1363 host target RNA into VGAM1363 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94549] VGAM1364 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1364 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1364 host target RNA into VGAM1364 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94550] VGAM1365 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1365 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1365 host target RNA into VGAM1365 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94551] It is appreciated that a function of VGR3038 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3038 gene include diagnosis, prevention and treatment of viral infection by Duck Adenovirus 1. Specific functions, and accordingly utilities, of VGR3038 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3038 gene: VGAM1362 host target protein, VGAM1363 host target protein, VGAM1364

host target protein and VGAM1365 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1362, VGAM1363, VGAM1364 and VGAM1365.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3039(VGR3039) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94552] VGR3039 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3039 gene was detected is described hereinabove with reference to Figs. 1-9.

[94553] VGR3039 gene encodes VGR3039 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[94554] VGR3039 precursor RNA folds spatially, forming VGR3039 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3039 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3039 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94555] VGR3039 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1366 precursor RNA, VGAM1367 precursor RNA, VGAM1368 precursor RNA, VGAM1369 precursor RNA, VGAM1370 precursor RNA and VGAM1371 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94556] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1366 RNA, VGAM1367 RNA, VGAM1368 RNA, VGAM1369 RNA,

VGAM1370 RNA and VGAM1371 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94557] VGAM1366 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1366 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1366 host target RNA into VGAM1366 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94558] VGAM1367 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1367 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1367 host target RNA into VGAM1367 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94559] VGAM1368 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1368 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1368 host target RNA into VGAM1368 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94560] VGAM1369 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1369 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1369 host target RNA into VGAM1369 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94561] VGAM1370 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1370 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1370 host target RNA into VGAM1370 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94562] VGAM1371 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1371 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1371 host target RNA into VGAM1371 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94563] It is appreciated that a function of VGR3039 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3039 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 6. Specific functions, and accordingly utilities, of VGR3039 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3039 gene: VGAM1366 host target protein, VGAM1367 host target protein, VGAM1368 host target protein, VGAM1369 host target protein, VGAM1370 host target protein and VGAM1371 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated

hereinabove with reference to VGAM1366, VGAM1367, VGAM1368, VGAM1369, VGAM1370 and VGAM1371.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3040(VGR3040) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94564] VGR3040 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3040 gene was detected is described hereinabove with reference to Figs. 1-9.

[94565] VGR3040 gene encodes VGR3040 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94566] VGR3040 precursor RNA folds spatially, forming VGR3040 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3040 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3040 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94567] VGR3040 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1372 precursor RNA, VGAM1373 precursor RNA, VGAM1374 precursor RNA, VGAM1375 precursor RNA, VGAM1376 precursor RNA and VGAM1377 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94568] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1372 RNA, VGAM1373 RNA, VGAM1374 RNA, VGAM1375 RNA, VGAM1376 RNA and VGAM1377 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 1.

[94569] VGAM1372 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1372 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1372 host target RNA into VGAM1372 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94570] VGAM1373 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1373 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1373 host target RNA into VGAM1373 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94571] VGAM1374 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1374 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1374 host target RNA into VGAM1374 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94572] VGAM1375 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1375 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1375 host target RNA into

VGAM1375 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94573] VGAM1376 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1376 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1376 host target RNA into VGAM1376 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94574] VGAM1377 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1377 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1377 host target RNA into VGAM1377 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94575] It is appreciated that a function of VGR3040 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3040 gene include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR3040 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3040 gene: VGAM1372 host target protein, VGAM1373 host target protein, VGAM1374 host target protein, VGAM1375 host target protein, VGAM1376 host target protein and VGAM1377 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1372, VGAM1373, VGAM1374, VGAM1375, VGAM1376 and VGAM1377.Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3041(VGR3041) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94576] VGR3041 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3041 gene was detected is described hereinabove with reference to Figs. 1-9.

[94577] VGR3041 gene encodes VGR3041 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94578] VGR3041 precursor RNA folds spatially, forming VGR3041 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3041 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3041 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94579] VGR3041 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1378 precursor RNA and VGAM1379 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94580] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1378 RNA and VGAM1379 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94581] VGAM1378 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1378 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1378 host target RNA into VGAM1378 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94582] VGAM1379 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1379 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1379 host target RNA into VGAM1379 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94583] It is appreciated that a function of VGR3041 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3041 gene include diagnosis, prevention and treatment of viral infection by

Human Herpesvirus 1. Specific functions, and accordingly utilities, of VGR3041 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3041 gene: VGAM1378 host target protein and VGAM1379 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1378 and VGAM1379.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3042(VGR3042) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94584] VGR3042 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3042 gene was detected is described hereinabove with reference to Figs. 1-9.

[94585] VGR3042 gene encodes VGR3042 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94586] VGR3042 precursor RNA folds spatially, forming VGR3042 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3042 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3042 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94587] VGR3042 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1380 precursor RNA, VGAM1381 precursor RNA, VGAM1382 precursor RNA, VGAM1383 precursor RNA, VGAM1384 precursor RNA, VGAM1385 precursor RNA, VGAM1386 precursor RNA and VGAM1387 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94588] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1380 RNA, VGAM1381 RNA, VGAM1382 RNA, VGAM1383 RNA, VGAM1384 RNA, VGAM1385 RNA, VGAM1386 RNA and VGAM1387 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94589] VGAM1380 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1380 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1380 host target RNA into VGAM1380 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94590] VGAM1381 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1381 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1381 host target RNA into VGAM1381 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94591] VGAM1382 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1382 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1382 host target RNA into VGAM1382 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94592] VGAM1383 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1383 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1383 host target RNA into VGAM1383 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94593] VGAM1384 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1384 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1384 host target RNA into VGAM1384 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94594] VGAM1385 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1385 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1385 host target RNA into VGAM1385 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94595] VGAM1386 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1386 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1386 host target RNA into VGAM1386 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94596] VGAM1387 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1387 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1387 host target RNA into VGAM1387 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94597] It is appreciated that a function of VGR3042 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3042 gene include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGR3042 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR3042 gene: VGAM1380 host target protein, VGAM1381 host target protein, VGAM1382 host target protein, VGAM1383 host target protein, VGAM1384 host target protein, VGAM1385 host target protein, VGAM1386 host target protein and VGAM1387 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1380, VGAM1381, VGAM1382, VGAM1383, VGAM1384, VGAM1385, VGAM1386 and VGAM1387.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3043(VGR3043) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94598] VGR3043 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3043 gene was detected is described hereinabove with reference to Figs. 1-9.

[94599] VGR3043 gene encodes VGR3043 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94600] VGR3043 precursor RNA folds spatially, forming VGR3043 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3043 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3043 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94601] VGR3043 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1388 precursor RNA, VGAM1389 precursor RNA and VGAM1390 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94602] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1388 RNA, VGAM1389 RNA and VGAM1390 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94603] VGAM1388 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1388 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1388 host target RNA into VGAM1388 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94604] VGAM1389 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1389 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1389 host target RNA into VGAM1389 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94605] VGAM1390 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1390 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1390 host target RNA into VGAM1390 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94606] It is appreciated that a function of VGR3043 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3043 gene include diagnosis, prevention and treatment of viral infection by Cercopithecine Herpesvirus 7. Specific functions, and accordingly utilities, of VGR3043 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3043 gene: VGAM1388 host target protein, VGAM1389 host target protein and VGAM1390 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1388, VGAM1389 and VGAM1390.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3044(VGR3044) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94607] VGR3044 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3044 gene was detected is described hereinabove with reference to Figs. 1-9.

[94608] VGR3044 gene encodes VGR3044 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94609] VGR3044 precursor RNA folds spatially, forming VGR3044 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3044 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3044 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94610] VGR3044 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1391 precursor RNA, VGAM1392 precursor RNA, VGAM1393 precursor RNA and VGAM1394 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94611] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1391 RNA, VGAM1392 RNA, VGAM1393 RNA and VGAM1394 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94612] VGAM1391 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1391 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1391 host target RNA into VGAM1391 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94613] VGAM1392 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1392 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1392 host target RNA into VGAM1392 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94614] VGAM1393 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1393 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1393 host target RNA into VGAM1393 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94615] VGAM1394 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1394 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1394 host target RNA into VGAM1394 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94616] It is appreciated that a function of VGR3044 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3044 gene include diagnosis, prevention and treatment of viral infection by Wheat Streak Mosaic Virus. Specific functions, and accordingly utilities, of VGR3044 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3044 gene: VGAM1391 host target protein, VGAM1392 host target protein, VGAM1393

host target protein and VGAM1394 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1391, VGAM1392, VGAM1393 and VGAM1394.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3045(VGR3045) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94617] VGR3045 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3045 gene was detected is described hereinabove with reference to Figs. 1-9.

[94618] VGR3045 gene encodes VGR3045 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[94619] VGR3045 precursor RNA folds spatially, forming VGR3045 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3045 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3045 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94620] VGR3045 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1395 precursor RNA, VGAM1396 precursor RNA and VGAM1397 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94621] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1395 RNA, VGAM1396 RNA and VGAM1397 RNA, herein schematically represented by VGAM1 RNA through VGAM3

RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94622] VGAM1395 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1395 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1395 host target RNA into VGAM1395 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94623] VGAM1396 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1396 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1396 host target RNA into

VGAM1396 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94624] VGAM1397 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1397 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1397 host target RNA into VGAM1397 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94625] It is appreciated that a function of VGR3045 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3045 gene include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGR3045 gene correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3045 gene: VGAM1395 host target protein, VGAM1396 host target protein and VGAM1397 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1395, VGAM1396 and VGAM1397.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3046(VGR3046) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94626] VGR3046 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3046 gene was detected is described hereinabove with reference to Figs. 1-9.

[94627] VGR3046 gene encodes VGR3046 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[94628] VGR3046 precursor RNA folds spatially, forming VGR3046 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3046 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3046 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94629] VGR3046 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1398 precursor RNA, VGAM1399 precursor RNA, VGAM1400 precursor RNA, VGAM1401 precursor RNA, VGAM1402 precursor RNA, VGAM1403 precursor RNA and VGAM1404 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94630] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1398 RNA, VGAM1399 RNA, VGAM1400 RNA, VGAM1401 RNA, VGAM1402 RNA, VGAM1403 RNA and VGAM1404 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94631] VGAM1398 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1398 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1398 host target RNA into VGAM1398 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94632] VGAM1399 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1399 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1399 host target RNA into VGAM1399 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94633] VGAM1400 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1400 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1400 host target RNA into VGAM1400 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94634] VGAM1401 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1401 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1401 host target RNA into VGAM1401 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94635] VGAM1402 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1402 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1402 host target RNA into VGAM1402 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94636] VGAM1403 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1403 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1403 host target RNA into VGAM1403 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94637] VGAM1404 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1404 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1404 host target RNA into VGAM1404 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94638] It is appreciated that a function of VGR3046 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3046 gene include diagnosis, prevention and treatment of viral infection by Perina Nuda Picorna-like Virus. Specific functions, and accordingly utilities, of VGR3046 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3046 gene: VGAM1398 host target protein, VGAM1399 host target protein, VGAM1400 host target protein, VGAM1401 host target protein, VGAM1402 host target protein, VGAM1403 host target protein and VGAM1404 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1398, VGAM1399, VGAM1400, VGAM1401, VGAM1402, VGAM1403 and VGAM1404.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3047(VGR3047) viral gene, which encodes an `operon-like` cluster of novel vi-

ral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94639] VGR3047 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3047 gene was detected is described hereinabove with reference to Figs. 1-9.

[94640] VGR3047 gene encodes VGR3047 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94641] VGR3047 precursor RNA folds spatially, forming VGR3047 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3047 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3047 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94642] VGR3047 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1405 precursor RNA and VGAM1406 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94643] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1405 RNA and VGAM1406 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94644] VGAM1405 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1405 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1405 host target RNA into

VGAM1405 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94645] VGAM1406 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1406 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1406 host target RNA into VGAM1406 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94646] It is appreciated that a function of VGR3047 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3047 gene include diagnosis, prevention and treatment of viral infection by Perina Nuda Picorna-like Virus. Specific functions, and accordingly utilities, of VGR3047 gene correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3047 gene: VGAM1405 host target protein and VGAM1406 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1405 and VGAM1406.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3048(VGR3048) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94647] VGR3048 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3048 gene was detected is described hereinabove with reference to Figs. 1-9.

[94648] VGR3048 gene encodes VGR3048 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94649] VGR3048 precursor RNA folds spatially, forming VGR3048 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3048 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3048 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94650] VGR3048 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1407 precursor RNA, VGAM1408 precursor RNA, VGAM1409 precursor RNA, VGAM1410 precursor RNA and VGAM1411 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94651] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1407 RNA, VGAM1408 RNA, VGAM1409 RNA, VGAM1410 RNA and VGAM1411 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94652] VGAM1407 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1407 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1407 host target RNA into VGAM1407 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94653] VGAM1408 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1408 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1408 host target RNA into VGAM1408 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94654] VGAM1409 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1409 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1409 host target RNA into VGAM1409 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94655] VGAM1410 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1410 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1410 host target RNA into VGAM1410 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94656] VGAM1411 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1411 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1411 host target RNA into VGAM1411 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94657] It is appreciated that a function of VGR3048 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3048 gene include

diagnosis, prevention and treatment of viral infection by Acute Bee Paralysis Virus. Specific functions, and accordingly utilities, of VGR3048 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3048 gene: VGAM1407 host target protein, VGAM1408 host target protein, VGAM1409 host target protein, VGAM1410 host target protein and VGAM1411 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1407, VGAM1408, VGAM1409, VGAM1410 and VGAM1411.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3049(VGR3049) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94658] VGR3049 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3049 gene was detected is described hereinabove with reference to Figs. 1-9.

[94659] VGR3049 gene encodes VGR3049 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94660] VGR3049 precursor RNA folds spatially, forming VGR3049 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3049 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3049 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94661] VGR3049 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1412 precursor RNA, VGAM1413 precursor RNA, VGAM1414 precursor RNA and VGAM1415 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94662] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1412 RNA, VGAM1413 RNA, VGAM1414 RNA and VGAM1415 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94663] VGAM1412 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1412 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1412 host target RNA into VGAM1412 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94664] VGAM1413 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1413 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1413 host target RNA into VGAM1413 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94665] VGAM1414 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1414 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1414 host target RNA into VGAM1414 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94666] VGAM1415 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1415 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1415 host target RNA into VGAM1415 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94667] It is appreciated that a function of VGR3049 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3049 gene include diagnosis, prevention and treatment of viral infection by Bean Yellow Mosaic Virus. Specific functions, and accordingly utilities, of VGR3049 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3049 gene: VGAM1412 host target protein, VGAM1413 host target protein, VGAM1414

host target protein and VGAM1415 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1412, VGAM1413, VGAM1414 and VGAM1415.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3050(VGR3050) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94668] VGR3050 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3050 gene was detected is described hereinabove with reference to Figs. 1-9.

[94669] VGR3050 gene encodes VGR3050 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[94670] VGR3050 precursor RNA folds spatially, forming VGR3050 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3050 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3050 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94671] VGR3050 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1416 precursor RNA, VGAM1417 precursor RNA, VGAM1418 precursor RNA and VGAM1419 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94672] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1416 RNA, VGAM1417 RNA, VGAM1418 RNA and VGAM1419 RNA, herein schematically represented by VGAM1 RNA

through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94673] VGAM1416 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1416 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1416 host target RNA into VGAM1416 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94674] VGAM1417 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1417 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1417 host target RNA into

VGAM1417 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94675] VGAM1418 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1418 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1418 host target RNA into VGAM1418 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94676] VGAM1419 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1419 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1419 host target RNA into VGAM1419 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94677] It is appreciated that a function of VGR3050 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3050 gene include diagnosis, prevention and treatment of viral infection by Ryegrass Mosaic Virus. Specific functions, and accordingly utilities, of VGR3050 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3050 gene: VGAM1416 host target protein, VGAM1417 host target protein, VGAM1418 host target protein and VGAM1419 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1416, VGAM1417, VGAM1418 and VGAM1419.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic

Record 3051(VGR3051) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94678] VGR3051 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3051 gene was detected is described hereinabove with reference to Figs. 1-9.

[94679] VGR3051 gene encodes VGR3051 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94680] VGR3051 precursor RNA folds spatially, forming VGR3051 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3051 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3051 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[94681] VGR3051 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1420 precursor RNA, VGAM1421 precursor RNA, VGAM1422 precursor RNA and VGAM1423 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94682] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1420 RNA, VGAM1421 RNA, VGAM1422 RNA and VGAM1423 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94683] VGAM1420 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1420 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1420 host target RNA into VGAM1420 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94684] VGAM1421 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1421 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1421 host target RNA into VGAM1421 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94685] VGAM1422 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1422 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1422 host target RNA into VGAM1422 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94686] VGAM1423 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1423 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1423 host target RNA into VGAM1423 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94687] It is appreciated that a function of VGR3051 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3051 gene include

diagnosis, prevention and treatment of viral infection by Hepatitis GB Virus A. Specific functions, and accordingly utilities, of VGR3051 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3051 gene: VGAM1420 host target protein, VGAM1421 host target protein, VGAM1422 host target protein and VGAM1423 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1420, VGAM1421, VGAM1422 and VGAM1423.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3052(VGR3052) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94688] VGR3052 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3052 gene was

detected is described hereinabove with reference to Figs. 1-9.

[94689] VGR3052 gene encodes VGR3052 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94690] VGR3052 precursor RNA folds spatially, forming VGR3052 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3052 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3052 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94691] VGR3052 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1424 precursor RNA, VGAM1425 precursor RNA, VGAM1426 precursor RNA, VGAM1427 precursor RNA, VGAM1428 precursor RNA, VGAM1429 precursor RNA and VGAM1430 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR

through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94692] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1424 RNA, VGAM1425 RNA, VGAM1426 RNA, VGAM1427 RNA, VGAM1428 RNA, VGAM1429 RNA and VGAM1430 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94693] VGAM1424 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1424 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1424 host target RNA into VGAM1424 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94694] VGAM1425 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1425 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1425 host target RNA into VGAM1425 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94695] VGAM1426 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1426 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1426 host target RNA into VGAM1426 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94696] VGAM1427 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1427 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1427 host target RNA into VGAM1427 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94697] VGAM1428 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1428 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1428 host target RNA into

VGAM1428 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94698] VGAM1429 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1429 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1429 host target RNA into VGAM1429 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94699] VGAM1430 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1430 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1430 host target RNA into VGAM1430 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94700] It is appreciated that a function of VGR3052 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3052 gene include diagnosis, prevention and treatment of viral infection by Clover Yellow Vein Virus. Specific functions, and accordingly utilities, of VGR3052 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3052 gene: VGAM1424 host target protein, VGAM1425 host target protein, VGAM1426 host target protein, VGAM1427 host target protein, VGAM1428 host target protein, VGAM1429 host target protein and VGAM1430 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1424, VGAM1425, VGAM1426, VGAM1427, VGAM1428, VGAM1429 and VGAM1430.Fig.

9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3053(VGR3053) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94701] VGR3053 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3053 gene was detected is described hereinabove with reference to Figs. 1-9.

[94702] VGR3053 gene encodes VGR3053 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94703] VGR3053 precursor RNA folds spatially, forming VGR3053 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3053 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3053 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94704] VGR3053 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1431 precursor RNA, VGAM1432 precursor RNA, VGAM1433 precursor RNA, VGAM1434 precursor RNA, VGAM1435 precursor RNA, VGAM1436 precursor RNA and VGAM1437 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94705] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1431 RNA, VGAM1432 RNA, VGAM1433 RNA, VGAM1434 RNA, VGAM1435 RNA, VGAM1436 RNA and VGAM1437 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94706] VGAM1431 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1431 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1431 host target RNA into VGAM1431 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94707] VGAM1432 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1432 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1432 host target RNA into VGAM1432 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94708] VGAM1433 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1433 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1433 host target RNA into VGAM1433 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94709] VGAM1434 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1434 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1434 host target RNA into VGAM1434 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94710] VGAM1435 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1435 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1435 host target RNA into VGAM1435 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94711] VGAM1436 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1436 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1436 host target RNA into

VGAM1436 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94712] VGAM1437 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1437 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1437 host target RNA into VGAM1437 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94713] It is appreciated that a function of VGR3053 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3053 gene include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGR3053 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3053 gene: VGAM1431 host target protein, VGAM1432 host target protein, VGAM1433 host target protein, VGAM1434 host target protein, VGAM1435 host target protein, VGAM1436 host target protein and VGAM1437 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1431, VGAM1432, VGAM1433, VGAM1434, VGAM1435, VGAM1436 and VGAM1437.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3054(VGR3054) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94714] VGR3054 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3054 gene was detected is described hereinabove with reference to Figs.

1-9.

[94715] VGR3054 gene encodes VGR3054 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94716] VGR3054 precursor RNA folds spatially, forming VGR3054 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3054 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3054 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94717] VGR3054 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1438 precursor RNA, VGAM1439 precursor RNA, VGAM1440 precursor RNA, VGAM1441 precursor RNA and VGAM1442 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment,

corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94718] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1438 RNA, VGAM1439 RNA, VGAM1440 RNA, VGAM1441 RNA and VGAM1442 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94719] VGAM1438 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1438 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1438 host target RNA into VGAM1438 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94720] VGAM1439 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1439 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1439 host target RNA into VGAM1439 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94721] VGAM1440 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1440 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1440 host target RNA into VGAM1440 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94722] VGAM1441 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1441 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1441 host target RNA into VGAM1441 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94723] VGAM1442 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1442 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1442 host target RNA into VGAM1442 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94724] It is appreciated that a function of VGR3054 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3054 gene include diagnosis, prevention and treatment of viral infection by Bean Common Mosaic Necrosis Virus. Specific functions, and accordingly utilities, of VGR3054 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3054 gene: VGAM1438 host target protein, VGAM1439 host target protein, VGAM1440 host target protein, VGAM1441 host target protein and VGAM1442 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1438, VGAM1439, VGAM1440, VGAM1441 and VGAM1442.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3055(VGR3055) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one

host target gene, the function and utility of which at least one host target gene is known in the art.

[94725] VGR3055 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3055 gene was detected is described hereinabove with reference to Figs. 1-9.

[94726] VGR3055 gene encodes VGR3055 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94727] VGR3055 precursor RNA folds spatially, forming VGR3055 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3055 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3055 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94728] VGR3055 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM

precursor RNAs, VGAM1443 precursor RNA, VGAM1444 precursor RNA, VGAM1445 precursor RNA, VGAM1446 precursor RNA, VGAM1447 precursor RNA and VGAM1448 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94729] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1443 RNA, VGAM1444 RNA, VGAM1445 RNA, VGAM1446 RNA, VGAM1447 RNA and VGAM1448 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94730] VGAM1443 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1443 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1443 host target RNA into VGAM1443 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94731] VGAM1444 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1444 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1444 host target RNA into VGAM1444 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94732] VGAM1445 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1445 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1445 host target RNA into VGAM1445 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94733] VGAM1446 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1446 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1446 host target RNA into VGAM1446 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94734] VGAM1447 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1447 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1447 host target RNA into VGAM1447 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94735] VGAM1448 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1448 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1448 host target RNA into VGAM1448 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94736] It is appreciated that a function of VGR3055 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3055 gene include

diagnosis, prevention and treatment of viral infection by Pepper Mottle Virus. Specific functions, and accordingly utilities, of VGR3055 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3055 gene: VGAM1443 host target protein, VGAM1444 host target protein, VGAM1445 host target protein, VGAM1446 host target protein, VGAM1447 host target protein and VGAM1448 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1443, VGAM1444, VGAM1445, VGAM1446, VGAM1447 and VGAM1448.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3056(VGR3056) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94737] VGR3056 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3056 gene was detected is described hereinabove with reference to Figs. 1-9.

[94738] VGR3056 gene encodes VGR3056 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94739] VGR3056 precursor RNA folds spatially, forming VGR3056 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3056 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3056 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94740] VGR3056 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1449 precursor RNA, VGAM1450 precursor RNA, VGAM1451 precursor RNA, VGAM1452 precursor RNA, VGAM1453 precursor RNA, VGAM1454

precursor RNA, VGAM1455 precursor RNA and VGAM1456 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94741] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1449 RNA, VGAM1450 RNA, VGAM1451 RNA, VGAM1452 RNA, VGAM1453 RNA, VGAM1454 RNA, VGAM1455 RNA and VGAM1456 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94742] VGAM1449 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1449 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1449 host target RNA into

VGAM1449 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94743] VGAM1450 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1450 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1450 host target RNA into VGAM1450 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94744] VGAM1451 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1451 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1451 host target RNA into VGAM1451 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94745] VGAM1452 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1452 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1452 host target RNA into VGAM1452 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94746] VGAM1453 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1453 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1453 host target RNA into VGAM1453 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94747] VGAM1454 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1454 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1454 host target RNA into VGAM1454 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94748] VGAM1455 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1455 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1455 host target RNA into VGAM1455 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94749] VGAM1456 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1456 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1456 host target RNA into VGAM1456 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94750] It is appreciated that a function of VGR3056 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3056 gene include diagnosis, prevention and treatment of viral infection by

Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3056 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3056 gene: VGAM1449 host target protein, VGAM1450 host target protein, VGAM1451 host target protein, VGAM1452 host target protein, VGAM1453 host target protein, VGAM1454 host target protein, VGAM1455 host target protein and VGAM1456 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1449, VGAM1450, VGAM1451, VGAM1452, VGAM1453, VGAM1454, VGAM1455 and VGAM1456.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3057(VGR3057) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94751] VGR3057 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3057 gene was detected is described hereinabove with reference to Figs. 1-9.

[94752] VGR3057 gene encodes VGR3057 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94753] VGR3057 precursor RNA folds spatially, forming VGR3057 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3057 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3057 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94754] VGR3057 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1457 precursor RNA, VGAM1458 precursor RNA, VGAM1459 precursor RNA, VGAM1460 precursor RNA, VGAM1461 precursor RNA, VGAM1462

precursor RNA, VGAM1463 precursor RNA and VGAM1464 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94755] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1457 RNA, VGAM1458 RNA, VGAM1459 RNA, VGAM1460 RNA, VGAM1461 RNA, VGAM1462 RNA, VGAM1463 RNA and VGAM1464 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94756] VGAM1457 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1457 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1457 host target RNA into

VGAM1457 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94757] VGAM1458 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1458 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1458 host target RNA into VGAM1458 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94758] VGAM1459 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1459 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1459 host target RNA into VGAM1459 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94759] VGAM1460 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1460 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1460 host target RNA into VGAM1460 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94760] VGAM1461 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1461 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1461 host target RNA into VGAM1461 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94761] VGAM1462 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1462 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1462 host target RNA into VGAM1462 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94762] VGAM1463 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1463 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1463 host target RNA into VGAM1463 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94763] VGAM1464 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1464 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1464 host target RNA into VGAM1464 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94764] It is appreciated that a function of VGR3057 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3057 gene include diagnosis, prevention and treatment of viral infection by

Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3057 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3057 gene: VGAM1457 host target protein, VGAM1458 host target protein, VGAM1459 host target protein, VGAM1460 host target protein, VGAM1461 host target protein, VGAM1462 host target protein, VGAM1463 host target protein and VGAM1464 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1457, VGAM1458, VGAM1459, VGAM1460, VGAM1461, VGAM1462, VGAM1463 and VGAM1464.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3058(VGR3058) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94765] VGR3058 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3058 gene was detected is described hereinabove with reference to Figs. 1-9.

[94766] VGR3058 gene encodes VGR3058 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94767] VGR3058 precursor RNA folds spatially, forming VGR3058 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3058 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3058 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94768] VGR3058 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1465 precursor RNA, VGAM1466 precursor RNA and VGAM1467 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR

through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94769] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1465 RNA, VGAM1466 RNA and VGAM1467 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94770] VGAM1465 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1465 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1465 host target RNA into VGAM1465 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94771] VGAM1466 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1466 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1466 host target RNA into VGAM1466 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94772] VGAM1467 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1467 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1467 host target RNA into VGAM1467 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94773] It is appreciated that a function of VGR3058 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3058 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3058 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3058 gene: VGAM1465 host target protein, VGAM1466 host target protein and VGAM1467 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1465, VGAM1466 and VGAM1467.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3059(VGR3059) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and

utility of which at least one host target gene is known in the art.

[94774] VGR3059 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3059 gene was detected is described hereinabove with reference to Figs. 1-9.

[94775] VGR3059 gene encodes VGR3059 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94776] VGR3059 precursor RNA folds spatially, forming VGR3059 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3059 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3059 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94777] VGR3059 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM1468 precursor RNA and VGAM1469 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94778] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1468 RNA and VGAM1469 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94779] VGAM1468 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1468 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1468 host target RNA into VGAM1468 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94780] VGAM1469 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1469 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1469 host target RNA into VGAM1469 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94781] It is appreciated that a function of VGR3059 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3059 gene include diagnosis, prevention and treatment of viral infection by Infectious Flacherie Virus. Specific functions, and accordingly utilities, of VGR3059 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3059 gene: VGAM1468 host

target protein and VGAM1469 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1468 and VGAM1469.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3060(VGR3060) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94782] VGR3060 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3060 gene was detected is described hereinabove with reference to Figs. 1-9.

[94783] VGR3060 gene encodes VGR3060 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94784] VGR3060 precursor RNA folds spatially, forming VGR3060 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3060 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3060 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94785] VGR3060 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1470 precursor RNA, VGAM1471 precursor RNA, VGAM1472 precursor RNA, VGAM1473 precursor RNA, VGAM1474 precursor RNA, VGAM1475 precursor RNA, VGAM1476 precursor RNA and VGAM1477 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94786] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1470 RNA, VGAM1471 RNA, VGAM1472 RNA, VGAM1473 RNA, VGAM1474 RNA, VGAM1475 RNA, VGAM1476 RNA and VGAM1477 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94787] VGAM1470 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1470 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1470 host target RNA into VGAM1470 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94788] VGAM1471 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1471 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1471 host target RNA into VGAM1471 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94789] VGAM1472 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1472 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1472 host target RNA into VGAM1472 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94790] VGAM1473 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1473 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1473 host target RNA into VGAM1473 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94791] VGAM1474 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1474 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1474 host target RNA into VGAM1474 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94792] VGAM1475 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1475 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1475 host target RNA into VGAM1475 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94793] VGAM1476 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1476 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1476 host target RNA into VGAM1476 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94794] VGAM1477 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1477 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1477 host target RNA into VGAM1477 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94795] It is appreciated that a function of VGR3060 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3060 gene include diagnosis, prevention and treatment of viral infection by Cocksfoot Streak Virus (CSV). Specific functions, and accordingly utilities, of VGR3060 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR3060 gene: VGAM1470 host target protein, VGAM1471 host target protein, VGAM1472 host target protein, VGAM1473 host target protein, VGAM1474 host target protein, VGAM1475 host target protein, VGAM1476 host target protein and VGAM1477 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1470, VGAM1471, VGAM1472, VGAM1473, VGAM1474, VGAM1475, VGAM1476 and VGAM1477.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3061(VGR3061) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94796] VGR3061 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3061 gene was detected is described hereinabove with reference to Figs.

1-9.

[94797] VGR3061 gene encodes VGR3061 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94798] VGR3061 precursor RNA folds spatially, forming VGR3061 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3061 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3061 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94799] VGR3061 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1478 precursor RNA, VGAM1479 precursor RNA, VGAM1480 precursor RNA, VGAM1481 precursor RNA, VGAM1482 precursor RNA and VGAM1483 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94800] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1478 RNA, VGAM1479 RNA, VGAM1480 RNA, VGAM1481 RNA, VGAM1482 RNA and VGAM1483 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94801] VGAM1478 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1478 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1478 host target RNA into VGAM1478 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94802] VGAM1479 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1479 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1479 host target RNA into VGAM1479 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94803] VGAM1480 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1480 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1480 host target RNA into VGAM1480 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94804] VGAM1481 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1481 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1481 host target RNA into VGAM1481 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94805] VGAM1482 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1482 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1482 host target RNA into VGAM1482 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94806] VGAM1483 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1483 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1483 host target RNA into VGAM1483 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94807] It is appreciated that a function of VGR3061 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3061 gene include diagnosis, prevention and treatment of viral infection by Brome Streak Mosaic Virus. Specific functions, and accordingly utilities, of VGR3061 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3061 gene: VGAM1478

host target protein, VGAM1479 host target protein, VGAM1480 host target protein, VGAM1481 host target protein, VGAM1482 host target protein and VGAM1483 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1478, VGAM1479, VGAM1480, VGAM1481, VGAM1482 and VGAM1483.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3062(VGR3062) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94808] VGR3062 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3062 gene was detected is described hereinabove with reference to Figs. 1-9.

[94809] VGR3062 gene encodes VGR3062 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[94810] VGR3062 precursor RNA folds spatially, forming VGR3062 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3062 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3062 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94811] VGR3062 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1484 precursor RNA, VGAM1485 precursor RNA, VGAM1486 precursor RNA and VGAM1487 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94812] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1484 RNA, VGAM1485 RNA, VGAM1486 RNA and VGAM1487 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94813] VGAM1484 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1484 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1484 host target RNA into VGAM1484 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94814] VGAM1485 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1485 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1485 host target RNA into VGAM1485 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94815] VGAM1486 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1486 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1486 host target RNA into VGAM1486 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94816] VGAM1487 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1487 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1487 host target RNA into VGAM1487 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94817] It is appreciated that a function of VGR3062 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3062 gene include diagnosis, prevention and treatment of viral infection by Gallid Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3062 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3062 gene: VGAM1484 host target protein, VGAM1485 host target protein, VGAM1486 host target protein and VGAM1487 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1484, VGAM1485,

VGAM1486 and VGAM1487.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3063(VGR3063) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94818] VGR3063 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3063 gene was detected is described hereinabove with reference to Figs. 1-9.

[94819] VGR3063 gene encodes VGR3063 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94820] VGR3063 precursor RNA folds spatially, forming VGR3063 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3063 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3063 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94821] VGR3063 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1488 precursor RNA, VGAM1489 precursor RNA, VGAM1490 precursor RNA and VGAM1491 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94822] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1488 RNA, VGAM1489 RNA, VGAM1490 RNA and VGAM1491 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94823] VGAM1488 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1488 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1488 host target RNA into VGAM1488 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94824] VGAM1489 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1489 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1489 host target RNA into VGAM1489 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94825] VGAM1490 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1490 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1490 host target RNA into VGAM1490 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94826] VGAM1491 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1491 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1491 host target RNA into VGAM1491 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94827] It is appreciated that a function of VGR3063 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3063 gene include diagnosis, prevention and treatment of viral infection by Plum Pox Virus. Specific functions, and accordingly utilities, of VGR3063 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3063 gene: VGAM1488 host target protein, VGAM1489 host target protein, VGAM1490 host target protein and VGAM1491 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1488, VGAM1489, VGAM1490 and VGAM1491.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3064(VGR3064) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94828] VGR3064 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3064 gene was detected is described hereinabove with reference to Figs. 1-9.

[94829] VGR3064 gene encodes VGR3064 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94830] VGR3064 precursor RNA folds spatially, forming VGR3064 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3064 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3064 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94831] VGR3064 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1492 precursor RNA, VGAM1493 precursor RNA, VGAM1494 precursor RNA and VGAM1495

precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94832] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1492 RNA, VGAM1493 RNA, VGAM1494 RNA and VGAM1495 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94833] VGAM1492 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1492 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1492 host target RNA into VGAM1492 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94834] VGAM1493 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1493 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1493 host target RNA into VGAM1493 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94835] VGAM1494 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1494 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1494 host target RNA into VGAM1494 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94836] VGAM1495 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1495 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1495 host target RNA into VGAM1495 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94837] It is appreciated that a function of VGR3064 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3064 gene include diagnosis, prevention and treatment of viral infection by Johnsongrass Mosaic Virus. Specific functions, and accordingly utilities, of VGR3064 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR3064 gene: VGAM1492 host target protein, VGAM1493 host target protein, VGAM1494 host target protein and VGAM1495 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1492, VGAM1493, VGAM1494 and VGAM1495.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3065(VGR3065) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94838] VGR3065 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3065 gene was detected is described hereinabove with reference to Figs. 1-9.

[94839] VGR3065 gene encodes VGR3065 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94840] VGR3065 precursor RNA folds spatially, forming VGR3065 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3065 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3065 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94841] VGR3065 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1496 precursor RNA, VGAM1497 precursor RNA, VGAM1498 precursor RNA and VGAM1499 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94842] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1496

RNA, VGAM1497 RNA, VGAM1498 RNA and VGAM1499 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94843] VGAM1496 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1496 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1496 host target RNA into VGAM1496 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94844] VGAM1497 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1497 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1497 host target RNA into VGAM1497 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94845] VGAM1498 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1498 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1498 host target RNA into VGAM1498 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94846] VGAM1499 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1499 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1499 host target RNA into VGAM1499 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94847] It is appreciated that a function of VGR3065 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3065 gene include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR3065 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3065 gene: VGAM1496 host target protein, VGAM1497 host target protein, VGAM1498 host target protein and VGAM1499 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1496, VGAM1497, VGAM1498 and VGAM1499.Fig. 9 further provides a con-

ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3066(VGR3066) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94848] VGR3066 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3066 gene was detected is described hereinabove with reference to Figs. 1-9.

[94849] VGR3066 gene encodes VGR3066 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94850] VGR3066 precursor RNA folds spatially, forming VGR3066 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3066 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3066 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94851] VGR3066 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1500 precursor RNA, VGAM1501 precursor RNA, VGAM1502 precursor RNA, VGAM1503 precursor RNA, VGAM1504 precursor RNA, VGAM1505 precursor RNA, VGAM1506 precursor RNA and VGAM1507 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94852] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1500 RNA, VGAM1501 RNA, VGAM1502 RNA, VGAM1503 RNA, VGAM1504 RNA, VGAM1505 RNA, VGAM1506 RNA and VGAM1507 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94853] VGAM1500 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1500 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1500 host target RNA into VGAM1500 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94854] VGAM1501 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1501 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1501 host target RNA into VGAM1501 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94855] VGAM1502 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1502 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1502 host target RNA into VGAM1502 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94856] VGAM1503 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1503 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1503 host target RNA into VGAM1503 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94857] VGAM1504 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1504 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1504 host target RNA into VGAM1504 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94858] VGAM1505 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1505 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1505 host target RNA into VGAM1505 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94859] VGAM1506 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1506 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1506 host target RNA into VGAM1506 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94860] VGAM1507 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1507 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1507 host target RNA into

VGAM1507 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94861] It is appreciated that a function of VGR3066 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3066 gene include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGR3066 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3066 gene: VGAM1500 host target protein, VGAM1501 host target protein, VGAM1502 host target protein, VGAM1503 host target protein, VGAM1504 host target protein, VGAM1505 host target protein, VGAM1506 host target protein and VGAM1507 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1500, VGAM1501, VGAM1502, VGAM1503, VGAM1504, VGAM1505, VGAM1506 and VGAM1507.Fig.

9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3067(VGR3067) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94862] VGR3067 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3067 gene was detected is described hereinabove with reference to Figs. 1-9.

[94863] VGR3067 gene encodes VGR3067 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94864] VGR3067 precursor RNA folds spatially, forming VGR3067 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3067 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3067 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94865] VGR3067 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1508 precursor RNA, VGAM1509 precursor RNA, VGAM1510 precursor RNA and VGAM1511 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94866] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1508 RNA, VGAM1509 RNA, VGAM1510 RNA and VGAM1511 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94867] VGAM1508 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1508 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1508 host target RNA into VGAM1508 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94868] VGAM1509 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1509 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1509 host target RNA into VGAM1509 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94869] VGAM1510 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1510 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1510 host target RNA into VGAM1510 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94870] VGAM1511 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1511 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1511 host target RNA into VGAM1511 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94871] It is appreciated that a function of VGR3067 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3067 gene include diagnosis, prevention and treatment of viral infection by Potato Virus V. Specific functions, and accordingly utilities, of VGR3067 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3067 gene: VGAM1508 host target protein, VGAM1509 host target protein, VGAM1510 host target protein and VGAM1511 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1508, VGAM1509, VGAM1510 and VGAM1511.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3068(VGR3068) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94872] VGR3068 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3068 gene was detected is described hereinabove with reference to Figs. 1-9.

[94873] VGR3068 gene encodes VGR3068 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94874] VGR3068 precursor RNA folds spatially, forming VGR3068 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3068 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3068 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94875] VGR3068 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1512 precursor RNA, VGAM1513 precursor RNA, VGAM1514 precursor RNA, VGAM1515

precursor RNA and VGAM1516 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94876] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1512 RNA, VGAM1513 RNA, VGAM1514 RNA, VGAM1515 RNA and VGAM1516 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94877] VGAM1512 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1512 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1512 host target RNA into VGAM1512 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94878] VGAM1513 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1513 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1513 host target RNA into VGAM1513 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94879] VGAM1514 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1514 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1514 host target RNA into

VGAM1514 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94880] VGAM1515 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1515 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1515 host target RNA into VGAM1515 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94881] VGAM1516 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1516 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1516 host target RNA into VGAM1516 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94882] It is appreciated that a function of VGR3068 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3068 gene include diagnosis, prevention and treatment of viral infection by Parsnip Yellow Fleck Virus. Specific functions, and accordingly utilities, of VGR3068 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3068 gene: VGAM1512 host target protein, VGAM1513 host target protein, VGAM1514 host target protein, VGAM1515 host target protein and VGAM1516 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1512, VGAM1513, VGAM1514, VGAM1515 and VGAM1516.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory vi-

ral gene, referred to here as Viral Genomic Record 3069(VGR3069) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94883] VGR3069 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3069 gene was detected is described hereinabove with reference to Figs. 1-9.

[94884] VGR3069 gene encodes VGR3069 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94885] VGR3069 precursor RNA folds spatially, forming VGR3069 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3069 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3069 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[94886] VGR3069 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1517 precursor RNA, VGAM1518 precursor RNA and VGAM1519 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94887] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1517 RNA, VGAM1518 RNA and VGAM1519 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94888] VGAM1517 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1517 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1517 host target RNA into VGAM1517 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94889] VGAM1518 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1518 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1518 host target RNA into VGAM1518 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94890] VGAM1519 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1519 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1519 host target RNA into VGAM1519 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94891] It is appreciated that a function of VGR3069 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3069 gene include diagnosis, prevention and treatment of viral infection by Pea Seed-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGR3069 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3069 gene: VGAM1517 host target protein, VGAM1518 host target protein and VGAM1519 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with refer-

ence to VGAM1517, VGAM1518 and VGAM1519.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3070(VGR3070) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94892] VGR3070 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3070 gene was detected is described hereinabove with reference to Figs. 1-9.

[94893] VGR3070 gene encodes VGR3070 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94894] VGR3070 precursor RNA folds spatially, forming VGR3070 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3070 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3070 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94895] VGR3070 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1520 precursor RNA, VGAM1521 precursor RNA, VGAM1522 precursor RNA, VGAM1523 precursor RNA, VGAM1524 precursor RNA, VGAM1525 precursor RNA, VGAM1526 precursor RNA and VGAM1527 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94896] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1520 RNA, VGAM1521 RNA, VGAM1522 RNA, VGAM1523 RNA, VGAM1524 RNA, VGAM1525 RNA, VGAM1526 RNA and VGAM1527 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[94897] VGAM1520 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1520 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1520 host target RNA into VGAM1520 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94898] VGAM1521 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1521 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1521 host target RNA into VGAM1521 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94899] VGAM1522 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1522 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1522 host target RNA into VGAM1522 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94900] VGAM1523 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1523 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1523 host target RNA into

VGAM1523 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94901] VGAM1524 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1524 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1524 host target RNA into VGAM1524 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94902] VGAM1525 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1525 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1525 host target RNA into VGAM1525 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94903] VGAM1526 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1526 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1526 host target RNA into VGAM1526 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94904] VGAM1527 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1527 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1527 host target RNA into VGAM1527 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94905] It is appreciated that a function of VGR3070 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3070 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR3070 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3070 gene: VGAM1520 host target protein, VGAM1521 host target protein, VGAM1522 host target protein, VGAM1523 host target protein, VGAM1524 host target protein, VGAM1525 host target protein, VGAM1526 host target protein and VGAM1527 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1520,

VGAM1521, VGAM1522, VGAM1523, VGAM1524, VGAM1525, VGAM1526 and VGAM1527.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3071(VGR3071) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94906] VGR3071 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3071 gene was detected is described hereinabove with reference to Figs. 1-9.

[94907] VGR3071 gene encodes VGR3071 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94908] VGR3071 precursor RNA folds spatially, forming VGR3071 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3071 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3071 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94909] VGR3071 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1528 precursor RNA, VGAM1529 precursor RNA, VGAM1530 precursor RNA and VGAM1531 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94910] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1528 RNA, VGAM1529 RNA, VGAM1530 RNA and VGAM1531 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94911] VGAM1528 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1528 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1528 host target RNA into VGAM1528 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94912] VGAM1529 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1529 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1529 host target RNA into VGAM1529 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94913] VGAM1530 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1530 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1530 host target RNA into VGAM1530 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94914] VGAM1531 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1531 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1531 host target RNA into VGAM1531 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94915] It is appreciated that a function of VGR3071 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3071 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR3071 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3071 gene: VGAM1528 host target protein, VGAM1529 host target protein, VGAM1530 host target protein and VGAM1531 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1528, VGAM1529, VGAM1530 and VGAM1531.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3072(VGR3072) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[94916] VGR3072 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3072 gene was detected is described hereinabove with reference to Figs. 1-9.

[94917] VGR3072 gene encodes VGR3072 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94918] VGR3072 precursor RNA folds spatially, forming VGR3072 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3072 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3072 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94919] VGR3072 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1532 precursor RNA, VGAM1533

precursor RNA, VGAM1534 precursor RNA, VGAM1535 precursor RNA, VGAM1536 precursor RNA and VGAM1537 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94920] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1532 RNA, VGAM1533 RNA, VGAM1534 RNA, VGAM1535 RNA, VGAM1536 RNA and VGAM1537 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94921] VGAM1532 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1532 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1532 host target RNA into VGAM1532 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94922] VGAM1533 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1533 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1533 host target RNA into VGAM1533 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94923] VGAM1534 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1534 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1534 host target RNA into VGAM1534 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94924] VGAM1535 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1535 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1535 host target RNA into VGAM1535 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94925] VGAM1536 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1536 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1536 host target RNA into VGAM1536 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94926] VGAM1537 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1537 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1537 host target RNA into VGAM1537 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94927] It is appreciated that a function of VGR3072 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3072 gene include diagnosis, prevention and treatment of viral infection by

Cowpox Virus. Specific functions, and accordingly utilities, of VGR3072 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3072 gene: VGAM1532 host target protein, VGAM1533 host target protein, VGAM1534 host target protein, VGAM1535 host target protein, VGAM1536 host target protein and VGAM1537 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1532, VGAM1533, VGAM1534, VGAM1535, VGAM1536 and VGAM1537.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3073(VGR3073) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94928] VGR3073 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3073 gene was

detected is described hereinabove with reference to Figs. 1-9.

[94929] VGR3073 gene encodes VGR3073 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94930] VGR3073 precursor RNA folds spatially, forming VGR3073 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3073 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3073 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94931] VGR3073 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1538 precursor RNA, VGAM1539 precursor RNA, VGAM1540 precursor RNA and VGAM1541 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94932] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1538 RNA, VGAM1539 RNA, VGAM1540 RNA and VGAM1541 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94933] VGAM1538 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1538 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1538 host target RNA into VGAM1538 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94934] VGAM1539 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1539 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1539 host target RNA into VGAM1539 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94935] VGAM1540 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1540 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1540 host target RNA into VGAM1540 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94936] VGAM1541 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1541 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1541 host target RNA into VGAM1541 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94937] It is appreciated that a function of VGR3073 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3073 gene include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGR3073 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3073 gene: VGAM1538 host target protein, VGAM1539 host target protein, VGAM1540 host target protein and VGAM1541 host target protein,

herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1538, VGAM1539, VGAM1540 and VGAM1541.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3074(VGR3074) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94938] VGR3074 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3074 gene was detected is described hereinabove with reference to Figs. 1-9.

[94939] VGR3074 gene encodes VGR3074 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94940] VGR3074 precursor RNA folds spatially, forming VGR3074 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3074 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3074 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94941] VGR3074 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1542 precursor RNA, VGAM1543 precursor RNA, VGAM1544 precursor RNA, VGAM1545 precursor RNA, VGAM1546 precursor RNA and VGAM1547 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94942] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1542 RNA, VGAM1543 RNA, VGAM1544 RNA, VGAM1545 RNA, VGAM1546 RNA and VGAM1547 RNA, herein schemati-

cally represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94943] VGAM1542 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1542 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1542 host target RNA into VGAM1542 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94944] VGAM1543 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1543 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1543 host target RNA into VGAM1543 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94945] VGAM1544 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1544 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1544 host target RNA into VGAM1544 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94946] VGAM1545 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1545 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1545 host target RNA into VGAM1545 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94947] VGAM1546 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1546 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1546 host target RNA into VGAM1546 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94948] VGAM1547 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1547 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1547 host target RNA into VGAM1547 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94949] It is appreciated that a function of VGR3074 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3074 gene include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGR3074 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3074 gene: VGAM1542 host target protein, VGAM1543 host target protein, VGAM1544 host target protein, VGAM1545 host target protein, VGAM1546 host target protein and VGAM1547 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1542, VGAM1543, VGAM1544,

VGAM1545, VGAM1546 and VGAM1547.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3075(VGR3075) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94950] VGR3075 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3075 gene was detected is described hereinabove with reference to Figs. 1-9.

[94951] VGR3075 gene encodes VGR3075 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94952] VGR3075 precursor RNA folds spatially, forming VGR3075 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3075 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3075 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94953] VGR3075 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1548 precursor RNA, VGAM1549 precursor RNA, VGAM1550 precursor RNA, VGAM1551 precursor RNA, VGAM1552 precursor RNA, VGAM1553 precursor RNA, VGAM1554 precursor RNA and VGAM1555 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94954] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1548 RNA, VGAM1549 RNA, VGAM1550 RNA, VGAM1551 RNA, VGAM1552 RNA, VGAM1553 RNA, VGAM1554 RNA and VGAM1555 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94955] VGAM1548 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1548 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1548 host target RNA into VGAM1548 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94956] VGAM1549 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1549 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1549 host target RNA into VGAM1549 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94957] VGAM1550 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1550 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1550 host target RNA into VGAM1550 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94958] VGAM1551 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1551 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1551 host target RNA into VGAM1551 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94959] VGAM1552 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1552 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1552 host target RNA into VGAM1552 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94960] VGAM1553 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1553 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1553 host target RNA into

VGAM1553 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94961] VGAM1554 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1554 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1554 host target RNA into VGAM1554 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94962] VGAM1555 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1555 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1555 host target RNA into VGAM1555 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94963] It is appreciated that a function of VGR3075 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3075 gene include diagnosis, prevention and treatment of viral infection by Macaca Mulatta Rhadinovirus. Specific functions, and accordingly utilities, of VGR3075 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3075 gene: VGAM1548 host target protein, VGAM1549 host target protein, VGAM1550 host target protein, VGAM1551 host target protein, VGAM1552 host target protein, VGAM1553 host target protein, VGAM1554 host target protein and VGAM1555 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1548, VGAM1549, VGAM1550, VGAM1551,

VGAM1552, VGAM1553, VGAM1554 and VGAM1555.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3076(VGR3076) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94964] VGR3076 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3076 gene was detected is described hereinabove with reference to Figs. 1-9.

[94965] VGR3076 gene encodes VGR3076 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94966] VGR3076 precursor RNA folds spatially, forming VGR3076 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3076 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3076 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94967] VGR3076 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1556 precursor RNA and VGAM1557 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94968] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1556 RNA and VGAM1557 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94969] VGAM1556 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1556 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1556 host target RNA into VGAM1556 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94970] VGAM1557 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1557 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1557 host target RNA into VGAM1557 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94971] It is appreciated that a function of VGR3076 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3076 gene include diagnosis, prevention and treatment of viral infection by Macaca Mulatta Rhadinovirus. Specific functions, and accordingly utilities, of VGR3076 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3076 gene: VGAM1556 host target protein and VGAM1557 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1556 and VGAM1557.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3077(VGR3077) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94972] VGR3077 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3077 gene was

detected is described hereinabove with reference to Figs. 1-9.

[94973] VGR3077 gene encodes VGR3077 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94974] VGR3077 precursor RNA folds spatially, forming VGR3077 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3077 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3077 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94975] VGR3077 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1558 precursor RNA, VGAM1559 precursor RNA, VGAM1560 precursor RNA, VGAM1561 precursor RNA, VGAM1562 precursor RNA and VGAM1563 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94976] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1558 RNA, VGAM1559 RNA, VGAM1560 RNA, VGAM1561 RNA, VGAM1562 RNA and VGAM1563 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94977] VGAM1558 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1558 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1558 host target RNA into VGAM1558 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94978] VGAM1559 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1559 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1559 host target RNA into VGAM1559 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94979] VGAM1560 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1560 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1560 host target RNA into VGAM1560 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94980] VGAM1561 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1561 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1561 host target RNA into VGAM1561 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94981] VGAM1562 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1562 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1562 host target RNA into VGAM1562 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94982] VGAM1563 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1563 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1563 host target RNA into VGAM1563 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94983] It is appreciated that a function of VGR3077 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3077 gene include diagnosis, prevention and treatment of viral infection by Bean Common Mosaic Virus. Specific functions, and accordingly utilities, of VGR3077 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR3077 gene: VGAM1558 host target protein, VGAM1559 host target protein, VGAM1560 host target protein, VGAM1561 host target protein, VGAM1562 host target protein and VGAM1563 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1558, VGAM1559, VGAM1560, VGAM1561, VGAM1562 and VGAM1563.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3078(VGR3078) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94984] VGR3078 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3078 gene was detected is described hereinabove with reference to Figs. 1-9.

[94985] VGR3078 gene encodes VGR3078 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94986] VGR3078 precursor RNA folds spatially, forming VGR3078 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3078 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3078 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94987] VGR3078 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1564 precursor RNA, VGAM1565 precursor RNA and VGAM1566 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94988] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1564 RNA, VGAM1565 RNA and VGAM1566 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94989] VGAM1564 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1564 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1564 host target RNA into VGAM1564 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94990] VGAM1565 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1565 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1565 host target RNA into VGAM1565 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94991] VGAM1566 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1566 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1566 host target RNA into VGAM1566 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94992] It is appreciated that a function of VGR3078 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3078 gene include

diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGR3078 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3078 gene: VGAM1564 host target protein, VGAM1565 host target protein and VGAM1566 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1564, VGAM1565 and VGAM1566.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3079(VGR3079) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[94993] VGR3079 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3079 gene was

detected is described hereinabove with reference to Figs. 1-9.

[94994] VGR3079 gene encodes VGR3079 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[94995] VGR3079 precursor RNA folds spatially, forming VGR3079 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3079 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3079 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[94996] VGR3079 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1567 precursor RNA, VGAM1568 precursor RNA, VGAM1569 precursor RNA and VGAM1570 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[94997] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1567 RNA, VGAM1568 RNA, VGAM1569 RNA and VGAM1570 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[94998] VGAM1567 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1567 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1567 host target RNA into VGAM1567 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[94999] VGAM1568 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1568 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1568 host target RNA into VGAM1568 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95000] VGAM1569 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1569 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1569 host target RNA into VGAM1569 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95001] VGAM1570 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1570 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1570 host target RNA into VGAM1570 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95002] It is appreciated that a function of VGR3079 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3079 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGR3079 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3079 gene: VGAM1567 host target protein, VGAM1568 host target protein, VGAM1569 host target protein and VGAM1570 host target protein,

herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1567, VGAM1568, VGAM1569 and VGAM1570.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3080(VGR3080) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95003] VGR3080 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3080 gene was detected is described hereinabove with reference to Figs. 1-9.

[95004] VGR3080 gene encodes VGR3080 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95005] VGR3080 precursor RNA folds spatially, forming VGR3080 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3080 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3080 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95006] VGR3080 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1571 precursor RNA, VGAM1572 precursor RNA, VGAM1573 precursor RNA, VGAM1574 precursor RNA, VGAM1575 precursor RNA, VGAM1576 precursor RNA, VGAM1577 precursor RNA and VGAM1578 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95007] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1571 RNA, VGAM1572 RNA, VGAM1573 RNA, VGAM1574 RNA,

VGAM1575 RNA, VGAM1576 RNA, VGAM1577 RNA and VGAM1578 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95008] VGAM1571 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1571 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1571 host target RNA into VGAM1571 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95009] VGAM1572 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1572 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1572 host target RNA into VGAM1572 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95010] VGAM1573 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1573 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1573 host target RNA into VGAM1573 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95011] VGAM1574 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1574 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1574 host target RNA into VGAM1574 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95012] VGAM1575 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1575 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1575 host target RNA into VGAM1575 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95013] VGAM1576 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1576 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1576 host target RNA into VGAM1576 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95014] VGAM1577 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1577 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1577 host target RNA into VGAM1577 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95015] VGAM1578 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1578 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1578 host target RNA into VGAM1578 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95016] It is appreciated that a function of VGR3080 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3080 gene include diagnosis, prevention and treatment of viral infection by Rhopalosiphum Padi Virus. Specific functions, and accordingly utilities, of VGR3080 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3080 gene: VGAM1571 host target protein, VGAM1572 host target protein, VGAM1573 host target protein, VGAM1574 host target protein, VGAM1575 host target protein, VGAM1576 host target protein, VGAM1577 host target protein and VGAM1578 host target protein, herein schematically represented by

VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1571, VGAM1572, VGAM1573, VGAM1574, VGAM1575, VGAM1576, VGAM1577 and VGAM1578.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3081(VGR3081) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95017] VGR3081 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3081 gene was detected is described hereinabove with reference to Figs. 1-9.

[95018] VGR3081 gene encodes VGR3081 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95019] VGR3081 precursor RNA folds spatially, forming VGR3081 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3081 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3081 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95020] VGR3081 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1579 precursor RNA and VGAM1580 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95021] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1579 RNA and VGAM1580 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95022] VGAM1579 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1579 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1579 host target RNA into VGAM1579 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95023] VGAM1580 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1580 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1580 host target RNA into VGAM1580 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95024] It is appreciated that a function of VGR3081 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3081 gene include diagnosis, prevention and treatment of viral infection by Rhopalosiphum Padi Virus. Specific functions, and accordingly utilities, of VGR3081 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3081 gene: VGAM1579 host target protein and VGAM1580 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1579 and VGAM1580.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3082(VGR3082) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95025] VGR3082 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3082 gene was detected is described hereinabove with reference to Figs. 1-9.

[95026] VGR3082 gene encodes VGR3082 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95027] VGR3082 precursor RNA folds spatially, forming VGR3082 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3082 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3082 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95028] VGR3082 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1581 precursor RNA, VGAM1582 precursor RNA, VGAM1583 precursor RNA, VGAM1584

precursor RNA, VGAM1585 precursor RNA, VGAM1586 precursor RNA, VGAM1587 precursor RNA and VGAM1588 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95029] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1581 RNA, VGAM1582 RNA, VGAM1583 RNA, VGAM1584 RNA, VGAM1585 RNA, VGAM1586 RNA, VGAM1587 RNA and VGAM1588 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95030] VGAM1581 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1581 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1581 host target RNA into VGAM1581 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95031] VGAM1582 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1582 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1582 host target RNA into VGAM1582 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95032] VGAM1583 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1583 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1583 host target RNA into VGAM1583 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95033] VGAM1584 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1584 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1584 host target RNA into VGAM1584 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95034] VGAM1585 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1585 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1585 host target RNA into VGAM1585 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95035] VGAM1586 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1586 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1586 host target RNA into VGAM1586 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95036] VGAM1587 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1587 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1587 host target RNA into VGAM1587 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95037] VGAM1588 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1588 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1588 host target RNA into VGAM1588 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95038] It is appreciated that a function of VGR3082 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3082 gene include

diagnosis, prevention and treatment of viral infection by Saimiriine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3082 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3082 gene: VGAM1581 host target protein, VGAM1582 host target protein, VGAM1583 host target protein, VGAM1584 host target protein, VGAM1585 host target protein, VGAM1586 host target protein, VGAM1587 host target protein and VGAM1588 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1581, VGAM1582, VGAM1583, VGAM1584, VGAM1585, VGAM1586, VGAM1587 and VGAM1588.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3083(VGR3083) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95039] VGR3083 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3083 gene was detected is described hereinabove with reference to Figs. 1-9.

[95040] VGR3083 gene encodes VGR3083 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95041] VGR3083 precursor RNA folds spatially, forming VGR3083 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3083 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3083 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95042] VGR3083 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1589 precursor RNA, VGAM1590 precursor RNA, VGAM1591 precursor RNA, VGAM1592

precursor RNA and VGAM1593 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95043] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1589 RNA, VGAM1590 RNA, VGAM1591 RNA, VGAM1592 RNA and VGAM1593 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95044] VGAM1589 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1589 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1589 host target RNA into VGAM1589 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95045] VGAM1590 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1590 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1590 host target RNA into VGAM1590 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95046] VGAM1591 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1591 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1591 host target RNA into

VGAM1591 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95047] VGAM1592 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1592 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1592 host target RNA into VGAM1592 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95048] VGAM1593 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1593 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1593 host target RNA into VGAM1593 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95049] It is appreciated that a function of VGR3083 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3083 gene include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGR3083 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3083 gene: VGAM1589 host target protein, VGAM1590 host target protein, VGAM1591 host target protein, VGAM1592 host target protein and VGAM1593 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1589, VGAM1590, VGAM1591, VGAM1592 and VGAM1593.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory vi-

ral gene, referred to here as Viral Genomic Record 3084(VGR3084) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95050] VGR3084 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3084 gene was detected is described hereinabove with reference to Figs. 1-9.

[95051] VGR3084 gene encodes VGR3084 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95052] VGR3084 precursor RNA folds spatially, forming VGR3084 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3084 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3084 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[95053] VGR3084 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1594 precursor RNA, VGAM1595 precursor RNA, VGAM1596 precursor RNA and VGAM1597 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95054] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1594 RNA, VGAM1595 RNA, VGAM1596 RNA and VGAM1597 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95055] VGAM1594 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1594 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1594 host target RNA into VGAM1594 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95056] VGAM1595 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1595 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1595 host target RNA into VGAM1595 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95057] VGAM1596 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1596 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1596 host target RNA into VGAM1596 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95058] VGAM1597 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1597 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1597 host target RNA into VGAM1597 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95059] It is appreciated that a function of VGR3084 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3084 gene include diagnosis, prevention and treatment of viral infection by Leek Yellow Stripe Potyvirus. Specific functions, and accordingly utilities, of VGR3084 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3084 gene: VGAM1594 host target protein, VGAM1595 host target protein, VGAM1596 host target protein and VGAM1597 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1594, VGAM1595, VGAM1596 and VGAM1597.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3085(VGR3085) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95060] VGR3085 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3085 gene was detected is described hereinabove with reference to Figs. 1-9.

[95061] VGR3085 gene encodes VGR3085 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95062] VGR3085 precursor RNA folds spatially, forming VGR3085 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3085 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3085 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95063] VGR3085 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1598 precursor RNA, VGAM1599 precursor RNA, VGAM1600 precursor RNA, VGAM1601 precursor RNA and VGAM1602 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR

through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95064] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1598 RNA, VGAM1599 RNA, VGAM1600 RNA, VGAM1601 RNA and VGAM1602 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95065] VGAM1598 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1598 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1598 host target RNA into VGAM1598 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95066] VGAM1599 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1599 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1599 host target RNA into VGAM1599 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95067] VGAM1600 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1600 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1600 host target RNA into VGAM1600 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95068] VGAM1601 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1601 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1601 host target RNA into VGAM1601 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95069] VGAM1602 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1602 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1602 host target RNA into VGAM1602 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95070] It is appreciated that a function of VGR3085 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3085 gene include diagnosis, prevention and treatment of viral infection by Human Adenovirus E. Specific functions, and accordingly utilities, of VGR3085 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3085 gene: VGAM1598 host target protein, VGAM1599 host target protein, VGAM1600 host target protein, VGAM1601 host target protein and VGAM1602 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1598, VGAM1599, VGAM1600, VGAM1601 and VGAM1602.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3086(VGR3086) viral gene, which encodes an

`operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95071] VGR3086 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3086 gene was detected is described hereinabove with reference to Figs. 1-9.

[95072] VGR3086 gene encodes VGR3086 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95073] VGR3086 precursor RNA folds spatially, forming VGR3086 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3086 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3086 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95074] VGR3086 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1603 precursor RNA, VGAM1604 precursor RNA, VGAM1605 precursor RNA, VGAM1606 precursor RNA, VGAM1607 precursor RNA and VGAM1608 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95075] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1603 RNA, VGAM1604 RNA, VGAM1605 RNA, VGAM1606 RNA, VGAM1607 RNA and VGAM1608 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95076] VGAM1603 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1603 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1603 host target RNA into VGAM1603 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95077] VGAM1604 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1604 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1604 host target RNA into VGAM1604 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95078] VGAM1605 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1605 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1605 host target RNA into VGAM1605 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95079] VGAM1606 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1606 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1606 host target RNA into VGAM1606 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95080] VGAM1607 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1607 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1607 host target RNA into VGAM1607 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95081] VGAM1608 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1608 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1608 host target RNA into VGAM1608 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95082] It is appreciated that a function of VGR3086 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3086 gene include diagnosis, prevention and treatment of viral infection by Taura Syndrome Virus. Specific functions, and accordingly utilities, of VGR3086 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3086 gene: VGAM1603 host target protein, VGAM1604 host target protein, VGAM1605 host target protein, VGAM1606 host target protein, VGAM1607 host target protein and VGAM1608 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1603, VGAM1604, VGAM1605, VGAM1606, VGAM1607 and VGAM1608.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3087(VGR3087) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[95083] VGR3087 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3087 gene was detected is described hereinabove with reference to Figs. 1-9.

[95084] VGR3087 gene encodes VGR3087 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95085] VGR3087 precursor RNA folds spatially, forming VGR3087 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3087 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3087 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95086] VGR3087 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1609 precursor RNA, VGAM1610

precursor RNA, VGAM1611 precursor RNA, VGAM1612 precursor RNA, VGAM1613 precursor RNA, VGAM1614 precursor RNA, VGAM1615 precursor RNA and VGAM1616 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95087] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1609 RNA, VGAM1610 RNA, VGAM1611 RNA, VGAM1612 RNA, VGAM1613 RNA, VGAM1614 RNA, VGAM1615 RNA and VGAM1616 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95088] VGAM1609 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1609 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1609 host target RNA into VGAM1609 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95089] VGAM1610 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1610 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1610 host target RNA into VGAM1610 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95090] VGAM1611 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1611 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1611 host target RNA into VGAM1611 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95091] VGAM1612 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1612 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1612 host target RNA into VGAM1612 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95092] VGAM1613 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1613 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1613 host target RNA into VGAM1613 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95093] VGAM1614 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1614 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1614 host target RNA into VGAM1614 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95094] VGAM1615 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1615 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1615 host target RNA into VGAM1615 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95095] VGAM1616 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1616 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1616 host target RNA into VGAM1616 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95096] It is appreciated that a function of VGR3087 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3087 gene include diagnosis, prevention and treatment of viral infection by Chimpanzee Cytomegalovirus. Specific functions, and accordingly utilities, of VGR3087 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3087 gene: VGAM1609 host target protein, VGAM1610 host target protein, VGAM1611 host target protein, VGAM1612 host target protein, VGAM1613 host target protein, VGAM1614 host target protein, VGAM1615 host target protein and VGAM1616 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1609, VGAM1610, VGAM1611, VGAM1612, VGAM1613, VGAM1614, VGAM1615 and VGAM1616.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3088(VGR3088) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[95097] VGR3088 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3088 gene was detected is described hereinabove with reference to Figs. 1-9.

[95098] VGR3088 gene encodes VGR3088 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95099] VGR3088 precursor RNA folds spatially, forming VGR3088 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3088 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3088 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95100] VGR3088 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM

precursor RNAs, VGAM1617 precursor RNA, VGAM1618 precursor RNA, VGAM1619 precursor RNA, VGAM1620 precursor RNA and VGAM1621 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95101] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1617 RNA, VGAM1618 RNA, VGAM1619 RNA, VGAM1620 RNA and VGAM1621 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95102] VGAM1617 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1617 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1617 host target RNA into VGAM1617 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95103] VGAM1618 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1618 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1618 host target RNA into VGAM1618 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95104] VGAM1619 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1619 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1619 host target RNA into VGAM1619 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95105] VGAM1620 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1620 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1620 host target RNA into VGAM1620 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95106] VGAM1621 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1621 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1621 host target RNA into VGAM1621 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95107] It is appreciated that a function of VGR3088 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3088 gene include diagnosis, prevention and treatment of viral infection by Fowl Adenovirus D. Specific functions, and accordingly utilities, of VGR3088 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3088 gene: VGAM1617 host target protein, VGAM1618 host target protein, VGAM1619 host target protein, VGAM1620 host target protein and VGAM1621 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1617, VGAM1618, VGAM1619, VGAM1620

and VGAM1621.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3089(VGR3089) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95108] VGR3089 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3089 gene was detected is described hereinabove with reference to Figs. 1-9.

[95109] VGR3089 gene encodes VGR3089 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95110] VGR3089 precursor RNA folds spatially, forming VGR3089 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3089 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3089 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95111] VGR3089 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1622 precursor RNA, VGAM1623 precursor RNA, VGAM1624 precursor RNA, VGAM1625 precursor RNA, VGAM1626 precursor RNA, VGAM1627 precursor RNA, VGAM1628 precursor RNA and VGAM1629 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95112] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1622 RNA, VGAM1623 RNA, VGAM1624 RNA, VGAM1625 RNA, VGAM1626 RNA, VGAM1627 RNA, VGAM1628 RNA and VGAM1629 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95113] VGAM1622 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1622 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1622 host target RNA into VGAM1622 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95114] VGAM1623 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1623 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1623 host target RNA into VGAM1623 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95115] VGAM1624 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1624 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1624 host target RNA into VGAM1624 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95116] VGAM1625 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1625 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1625 host target RNA into VGAM1625 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95117] VGAM1626 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1626 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1626 host target RNA into VGAM1626 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95118] VGAM1627 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1627 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1627 host target RNA into

VGAM1627 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95119] VGAM1628 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1628 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1628 host target RNA into VGAM1628 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95120] VGAM1629 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1629 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1629 host target RNA into VGAM1629 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95121] It is appreciated that a function of VGR3089 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3089 gene include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3089 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3089 gene: VGAM1622 host target protein, VGAM1623 host target protein, VGAM1624 host target protein, VGAM1625 host target protein, VGAM1626 host target protein, VGAM1627 host target protein, VGAM1628 host target protein and VGAM1629 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1622, VGAM1623, VGAM1624, VGAM1625, VGAM1626,

VGAM1627, VGAM1628 and VGAM1629.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3090(VGR3090) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95122] VGR3090 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3090 gene was detected is described hereinabove with reference to Figs. 1-9.

[95123] VGR3090 gene encodes VGR3090 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95124] VGR3090 precursor RNA folds spatially, forming VGR3090 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3090 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3090 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95125] VGR3090 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1630 precursor RNA, VGAM1631 precursor RNA, VGAM1632 precursor RNA, VGAM1633 precursor RNA and VGAM1634 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95126] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1630 RNA, VGAM1631 RNA, VGAM1632 RNA, VGAM1633 RNA and VGAM1634 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95127] VGAM1630 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1630 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1630 host target RNA into VGAM1630 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95128] VGAM1631 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1631 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1631 host target RNA into VGAM1631 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95129] VGAM1632 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1632 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1632 host target RNA into VGAM1632 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95130] VGAM1633 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1633 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1633 host target RNA into VGAM1633 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95131] VGAM1634 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1634 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1634 host target RNA into VGAM1634 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95132] It is appreciated that a function of VGR3090 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3090 gene include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3090 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3090 gene: VGAM1630 host target protein, VGAM1631 host target protein, VGAM1632

host target protein, VGAM1633 host target protein and VGAM1634 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1630, VGAM1631, VGAM1632, VGAM1633 and VGAM1634.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3091(VGR3091) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95133] VGR3091 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3091 gene was detected is described hereinabove with reference to Figs. 1-9.

[95134] VGR3091 gene encodes VGR3091 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95135] VGR3091 precursor RNA folds spatially, forming VGR3091

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3091 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3091 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95136] VGR3091 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1635 precursor RNA, VGAM1636 precursor RNA, VGAM1637 precursor RNA, VGAM1638 precursor RNA, VGAM1639 precursor RNA and VGAM1640 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95137] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1635

RNA, VGAM1636 RNA, VGAM1637 RNA, VGAM1638 RNA, VGAM1639 RNA and VGAM1640 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95138] VGAM1635 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1635 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1635 host target RNA into VGAM1635 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95139] VGAM1636 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1636 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1636 host target RNA into VGAM1636 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95140] VGAM1637 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1637 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1637 host target RNA into VGAM1637 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95141] VGAM1638 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1638 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1638 host target RNA into VGAM1638 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95142] VGAM1639 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1639 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1639 host target RNA into VGAM1639 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95143] VGAM1640 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1640 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1640 host target RNA into VGAM1640 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95144] It is appreciated that a function of VGR3091 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3091 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 8. Specific functions, and accordingly utilities, of VGR3091 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3091 gene: VGAM1635 host target protein, VGAM1636 host target protein, VGAM1637 host target protein, VGAM1638 host target protein, VGAM1639 host target protein and VGAM1640 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN.

The function of these host target genes is elaborated hereinabove with reference to VGAM1635, VGAM1636, VGAM1637, VGAM1638, VGAM1639 and VGAM1640.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3092(VGR3092) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95145] VGR3092 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3092 gene was detected is described hereinabove with reference to Figs. 1-9.

[95146] VGR3092 gene encodes VGR3092 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95147] VGR3092 precursor RNA folds spatially, forming VGR3092 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3092 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3092 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95148] VGR3092 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1641 precursor RNA, VGAM1642 precursor RNA and VGAM1643 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95149] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1641 RNA, VGAM1642 RNA and VGAM1643 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95150] VGAM1641 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1641 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1641 host target RNA into VGAM1641 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95151] VGAM1642 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1642 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1642 host target RNA into VGAM1642 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95152] VGAM1643 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1643 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1643 host target RNA into VGAM1643 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95153] It is appreciated that a function of VGR3092 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3092 gene include diagnosis, prevention and treatment of viral infection by Cell Fusing Agent Virus. Specific functions, and accordingly utilities, of VGR3092 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3092 gene: VGAM1641 host

target protein, VGAM1642 host target protein and VGAM1643 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1641, VGAM1642 and VGAM1643.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3093(VGR3093) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95154] VGR3093 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3093 gene was detected is described hereinabove with reference to Figs. 1-9.

[95155] VGR3093 gene encodes VGR3093 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95156] VGR3093 precursor RNA folds spatially, forming VGR3093

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3093 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3093 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95157] VGR3093 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1644 precursor RNA, VGAM1645 precursor RNA and VGAM1646 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95158] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1644 RNA, VGAM1645 RNA and VGAM1646 RNA, herein

schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95159] VGAM1644 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1644 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1644 host target RNA into VGAM1644 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95160] VGAM1645 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1645 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1645 host target RNA into VGAM1645 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95161] VGAM1646 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1646 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1646 host target RNA into VGAM1646 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95162] It is appreciated that a function of VGR3093 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3093 gene include diagnosis, prevention and treatment of viral infection by Dengue Virus. Specific functions, and accordingly utilities, of VGR3093 gene correlate with, and may be deduced

from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3093 gene: VGAM1644 host target protein, VGAM1645 host target protein and VGAM1646 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1644, VGAM1645 and VGAM1646.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3094(VGR3094) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95163] VGR3094 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3094 gene was detected is described hereinabove with reference to Figs. 1-9.

[95164] VGR3094 gene encodes VGR3094 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[95165] VGR3094 precursor RNA folds spatially, forming VGR3094 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3094 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3094 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95166] VGR3094 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1647 precursor RNA, VGAM1648 precursor RNA, VGAM1649 precursor RNA, VGAM1650 precursor RNA and VGAM1651 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95167] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1647 RNA, VGAM1648 RNA, VGAM1649 RNA, VGAM1650 RNA and VGAM1651 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95168] VGAM1647 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1647 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1647 host target RNA into VGAM1647 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95169] VGAM1648 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1648 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1648 host target RNA into VGAM1648 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95170] VGAM1649 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1649 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1649 host target RNA into VGAM1649 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95171] VGAM1650 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1650 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1650 host target RNA into VGAM1650 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95172] VGAM1651 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1651 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1651 host target RNA into VGAM1651 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95173] It is appreciated that a function of VGR3094 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3094 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 8. Specific functions, and accordingly utilities, of VGR3094 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3094 gene: VGAM1647 host target protein, VGAM1648 host target protein, VGAM1649 host target protein, VGAM1650 host target protein and VGAM1651 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1647, VGAM1648, VGAM1649, VGAM1650 and VGAM1651.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3095(VGR3095) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95174] VGR3095 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3095 gene was detected is described hereinabove with reference to Figs. 1-9.

[95175] VGR3095 gene encodes VGR3095 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95176] VGR3095 precursor RNA folds spatially, forming VGR3095 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3095 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3095 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95177] VGR3095 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1652 precursor RNA, VGAM1653 precursor RNA, VGAM1654 precursor RNA and VGAM1655 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95178] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1652 RNA, VGAM1653 RNA, VGAM1654 RNA and VGAM1655 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95179] VGAM1652 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1652 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1652 host target RNA into VGAM1652 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95180] VGAM1653 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1653 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1653 host target RNA into VGAM1653 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95181] VGAM1654 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1654 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1654 host target RNA into VGAM1654 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95182] VGAM1655 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1655 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1655 host target RNA into VGAM1655 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95183] It is appreciated that a function of VGR3095 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3095 gene include diagnosis, prevention and treatment of viral infection by Yellow Fever Virus. Specific functions, and accordingly utilities, of VGR3095 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3095 gene: VGAM1652 host

target protein, VGAM1653 host target protein, VGAM1654 host target protein and VGAM1655 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1652, VGAM1653, VGAM1654 and VGAM1655.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3096(VGR3096) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95184] VGR3096 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3096 gene was detected is described hereinabove with reference to Figs. 1-9.

[95185] VGR3096 gene encodes VGR3096 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[95186] VGR3096 precursor RNA folds spatially, forming VGR3096

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3096 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3096 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95187] VGR3096 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1656 precursor RNA, VGAM1657 precursor RNA, VGAM1658 precursor RNA, VGAM1659 precursor RNA and VGAM1660 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95188] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1656

RNA, VGAM1657 RNA, VGAM1658 RNA, VGAM1659 RNA and VGAM1660 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95189] VGAM1656 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1656 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1656 host target RNA into VGAM1656 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95190] VGAM1657 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1657 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1657 host target RNA into VGAM1657 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95191] VGAM1658 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1658 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1658 host target RNA into VGAM1658 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95192] VGAM1659 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1659 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1659 host target RNA into VGAM1659 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95193] VGAM1660 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1660 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1660 host target RNA into VGAM1660 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95194] It is appreciated that a function of VGR3096 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3096 gene include diagnosis, prevention and treatment of viral infection by

Molluscum Contagiosum Virus. Specific functions, and accordingly utilities, of VGR3096 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3096 gene: VGAM1656 host target protein, VGAM1657 host target protein, VGAM1658 host target protein, VGAM1659 host target protein and VGAM1660 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1656, VGAM1657, VGAM1658, VGAM1659 and VGAM1660.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3097(VGR3097) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95195] VGR3097 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3097 gene was

detected is described hereinabove with reference to Figs. 1-9.

[95196] VGR3097 gene encodes VGR3097 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95197] VGR3097 precursor RNA folds spatially, forming VGR3097 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3097 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3097 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95198] VGR3097 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1661 precursor RNA, VGAM1662 precursor RNA, VGAM1663 precursor RNA and VGAM1664 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95199] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1661 RNA, VGAM1662 RNA, VGAM1663 RNA and VGAM1664 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95200] VGAM1661 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1661 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1661 host target RNA into VGAM1661 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95201] VGAM1662 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1662 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1662 host target RNA into VGAM1662 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95202] VGAM1663 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1663 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1663 host target RNA into VGAM1663 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95203] VGAM1664 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1664 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1664 host target RNA into VGAM1664 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95204] It is appreciated that a function of VGR3097 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3097 gene include diagnosis, prevention and treatment of viral infection by Cercopithecine Herpesvirus 7. Specific functions, and accordingly utilities, of VGR3097 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3097 gene: VGAM1661 host target protein, VGAM1662 host target protein, VGAM1663 host target protein and VGAM1664 host target

protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1661, VGAM1662, VGAM1663 and VGAM1664.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3098(VGR3098) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95205] VGR3098 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3098 gene was detected is described hereinabove with reference to Figs. 1-9.

[95206] VGR3098 gene encodes VGR3098 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95207] VGR3098 precursor RNA folds spatially, forming VGR3098 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3098 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3098 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95208] VGR3098 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1665 precursor RNA, VGAM1666 precursor RNA and VGAM1667 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95209] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1665 RNA, VGAM1666 RNA and VGAM1667 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM

RNA of Fig. 1.

[95210] VGAM1665 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1665 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1665 host target RNA into VGAM1665 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95211] VGAM1666 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1666 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1666 host target RNA into VGAM1666 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95212] VGAM1667 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1667 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1667 host target RNA into VGAM1667 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95213] It is appreciated that a function of VGR3098 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3098 gene include diagnosis, prevention and treatment of viral infection by Infectious Spleen and Kidney Necrosis Virus. Specific functions, and accordingly utilities, of VGR3098 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs

comprised in the `operon-like` cluster of VGR3098 gene: VGAM1665 host target protein, VGAM1666 host target protein and VGAM1667 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1665, VGAM1666 and VGAM1667.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3099(VGR3099) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95214] VGR3099 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3099 gene was detected is described hereinabove with reference to Figs. 1-9.

[95215] VGR3099 gene encodes VGR3099 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95216] VGR3099 precursor RNA folds spatially, forming VGR3099 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3099 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3099 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95217] VGR3099 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1668 precursor RNA, VGAM1669 precursor RNA, VGAM1670 precursor RNA and VGAM1671 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95218] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1668

RNA, VGAM1669 RNA, VGAM1670 RNA and VGAM1671 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95219] VGAM1668 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1668 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1668 host target RNA into VGAM1668 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95220] VGAM1669 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1669 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1669 host target RNA into VGAM1669 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95221] VGAM1670 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1670 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1670 host target RNA into VGAM1670 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95222] VGAM1671 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1671 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1671 host target RNA into VGAM1671 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95223] It is appreciated that a function of VGR3099 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3099 gene include diagnosis, prevention and treatment of viral infection by Human Adenovirus D. Specific functions, and accordingly utilities, of VGR3099 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3099 gene: VGAM1668 host target protein, VGAM1669 host target protein, VGAM1670 host target protein and VGAM1671 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1668, VGAM1669, VGAM1670 and VGAM1671.Fig. 9 further provides a con-

ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3100(VGR3100) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95224] VGR3100 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3100 gene was detected is described hereinabove with reference to Figs. 1-9.

[95225] VGR3100 gene encodes VGR3100 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95226] VGR3100 precursor RNA folds spatially, forming VGR3100 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3100 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3100 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95227] VGR3100 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1672 precursor RNA, VGAM1673 precursor RNA and VGAM1674 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95228] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1672 RNA, VGAM1673 RNA and VGAM1674 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95229] VGAM1672 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1672 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1672 host target RNA into VGAM1672 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95230] VGAM1673 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1673 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1673 host target RNA into VGAM1673 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95231] VGAM1674 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1674 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1674 host target RNA into VGAM1674 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95232] It is appreciated that a function of VGR3100 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3100 gene include diagnosis, prevention and treatment of viral infection by Tick-borne Encephalitis Virus. Specific functions, and accordingly utilities, of VGR3100 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3100 gene: VGAM1672 host target protein, VGAM1673 host target protein and VGAM1674 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these

host target genes is elaborated hereinabove with reference to VGAM1672, VGAM1673 and VGAM1674.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3101(VGR3101) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95233] VGR3101 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3101 gene was detected is described hereinabove with reference to Figs. 1-9.

[95234] VGR3101 gene encodes VGR3101 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95235] VGR3101 precursor RNA folds spatially, forming VGR3101 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3101 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3101 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95236] VGR3101 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1675 precursor RNA, VGAM1676 precursor RNA, VGAM1677 precursor RNA, VGAM1678 precursor RNA, VGAM1679 precursor RNA and VGAM1680 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95237] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1675 RNA, VGAM1676 RNA, VGAM1677 RNA, VGAM1678 RNA, VGAM1679 RNA and VGAM1680 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 1.

[95238] VGAM1675 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1675 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1675 host target RNA into VGAM1675 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95239] VGAM1676 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1676 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1676 host target RNA into VGAM1676 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95240] VGAM1677 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1677 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1677 host target RNA into VGAM1677 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95241] VGAM1678 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1678 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1678 host target RNA into

VGAM1678 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95242] VGAM1679 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1679 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1679 host target RNA into VGAM1679 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95243] VGAM1680 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1680 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1680 host target RNA into VGAM1680 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95244] It is appreciated that a function of VGR3101 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3101 gene include diagnosis, prevention and treatment of viral infection by Viral Hemorrhagic Septicemia Virus. Specific functions, and accordingly utilities, of VGR3101 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3101 gene: VGAM1675 host target protein, VGAM1676 host target protein, VGAM1677 host target protein, VGAM1678 host target protein, VGAM1679 host target protein and VGAM1680 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1675, VGAM1676, VGAM1677, VGAM1678, VGAM1679 and VGAM1680.Fig. 9 further provides a conceptual descrip-

tion of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3102(VGR3102) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95245] VGR3102 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3102 gene was detected is described hereinabove with reference to Figs. 1-9.

[95246] VGR3102 gene encodes VGR3102 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95247] VGR3102 precursor RNA folds spatially, forming VGR3102 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3102 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3102 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95248] VGR3102 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1681 precursor RNA, VGAM1682 precursor RNA, VGAM1683 precursor RNA, VGAM1684 precursor RNA, VGAM1685 precursor RNA and VGAM1686 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95249] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1681 RNA, VGAM1682 RNA, VGAM1683 RNA, VGAM1684 RNA, VGAM1685 RNA and VGAM1686 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95250] VGAM1681 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1681 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1681 host target RNA into VGAM1681 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95251] VGAM1682 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1682 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1682 host target RNA into VGAM1682 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95252] VGAM1683 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1683 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1683 host target RNA into VGAM1683 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95253] VGAM1684 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1684 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1684 host target RNA into VGAM1684 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95254] VGAM1685 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1685 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1685 host target RNA into VGAM1685 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95255] VGAM1686 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1686 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1686 host target RNA into VGAM1686 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95256] It is appreciated that a function of VGR3102 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3102 gene include diagnosis, prevention and treatment of viral infection by Vesicular Stomatitis Indiana Virus. Specific functions, and accordingly utilities, of VGR3102 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3102 gene: VGAM1681 host target protein, VGAM1682 host target protein, VGAM1683 host target protein, VGAM1684 host target protein, VGAM1685 host target protein and VGAM1686 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1681, VGAM1682, VGAM1683, VGAM1684, VGAM1685 and VGAM1686.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3103(VGR3103) viral gene, which encodes an

`operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95257] VGR3103 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3103 gene was detected is described hereinabove with reference to Figs. 1-9.

[95258] VGR3103 gene encodes VGR3103 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95259] VGR3103 precursor RNA folds spatially, forming VGR3103 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3103 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3103 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95260] VGR3103 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1687 precursor RNA, VGAM1688 precursor RNA and VGAM1689 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95261] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1687 RNA, VGAM1688 RNA and VGAM1689 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95262] VGAM1687 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1687 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1687 host target RNA into VGAM1687 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95263] VGAM1688 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1688 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1688 host target RNA into VGAM1688 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95264] VGAM1689 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1689 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1689 host target RNA into VGAM1689 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95265] It is appreciated that a function of VGR3103 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3103 gene include diagnosis, prevention and treatment of viral infection by Chimpanzee Cytomegalovirus. Specific functions, and accordingly utilities, of VGR3103 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3103 gene: VGAM1687 host target protein, VGAM1688 host target protein and VGAM1689 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1687, VGAM1688 and VGAM1689.Fig. 9 further provides a conceptual description of novel bioin-

formatically detected regulatory viral gene, referred to here as Viral Genomic Record 3104(VGR3104) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95266] VGR3104 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3104 gene was detected is described hereinabove with reference to Figs. 1-9.

[95267] VGR3104 gene encodes VGR3104 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95268] VGR3104 precursor RNA folds spatially, forming VGR3104 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3104 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3104 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95269] VGR3104 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1690 precursor RNA, VGAM1691 precursor RNA, VGAM1692 precursor RNA, VGAM1693 precursor RNA, VGAM1694 precursor RNA, VGAM1695 precursor RNA, VGAM1696 precursor RNA and VGAM1697 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95270] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1690 RNA, VGAM1691 RNA, VGAM1692 RNA, VGAM1693 RNA, VGAM1694 RNA, VGAM1695 RNA, VGAM1696 RNA and VGAM1697 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95271] VGAM1690 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1690 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1690 host target RNA into VGAM1690 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95272] VGAM1691 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1691 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1691 host target RNA into VGAM1691 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95273] VGAM1692 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1692 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1692 host target RNA into VGAM1692 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95274] VGAM1693 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1693 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1693 host target RNA into VGAM1693 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95275] VGAM1694 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1694 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1694 host target RNA into VGAM1694 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95276] VGAM1695 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1695 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1695 host target RNA into VGAM1695 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95277] VGAM1696 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1696 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1696 host target RNA into VGAM1696 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95278] VGAM1697 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1697 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1697 host target RNA into

VGAM1697 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95279] It is appreciated that a function of VGR3104 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3104 gene include diagnosis, prevention and treatment of viral infection by Ectocarpus Siliculosus Virus. Specific functions, and accordingly utilities, of VGR3104 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3104 gene: VGAM1690 host target protein, VGAM1691 host target protein, VGAM1692 host target protein, VGAM1693 host target protein, VGAM1694 host target protein, VGAM1695 host target protein, VGAM1696 host target protein and VGAM1697 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1690, VGAM1691, VGAM1692, VGAM1693, VGAM1694, VGAM1695, VGAM1696 and VGAM1697.Fig.

9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3105(VGR3105) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95280] VGR3105 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3105 gene was detected is described hereinabove with reference to Figs. 1-9.

[95281] VGR3105 gene encodes VGR3105 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95282] VGR3105 precursor RNA folds spatially, forming VGR3105 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3105 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3105 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95283] VGR3105 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1698 precursor RNA, VGAM1699 precursor RNA, VGAM1700 precursor RNA, VGAM1701 precursor RNA, VGAM1702 precursor RNA, VGAM1703 precursor RNA, VGAM1704 precursor RNA and VGAM1705 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95284] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1698 RNA, VGAM1699 RNA, VGAM1700 RNA, VGAM1701 RNA, VGAM1702 RNA, VGAM1703 RNA, VGAM1704 RNA and VGAM1705 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95285] VGAM1698 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1698 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1698 host target RNA into VGAM1698 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95286] VGAM1699 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1699 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1699 host target RNA into VGAM1699 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95287] VGAM1700 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1700 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1700 host target RNA into VGAM1700 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95288] VGAM1701 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1701 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1701 host target RNA into VGAM1701 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95289] VGAM1702 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1702 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1702 host target RNA into VGAM1702 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95290] VGAM1703 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1703 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1703 host target RNA into

VGAM1703 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95291] VGAM1704 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1704 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1704 host target RNA into VGAM1704 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95292] VGAM1705 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1705 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1705 host target RNA into VGAM1705 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95293] It is appreciated that a function of VGR3105 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3105 gene include diagnosis, prevention and treatment of viral infection by Ectocarpus Siliculosus Virus. Specific functions, and accordingly utilities, of VGR3105 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3105 gene: VGAM1698 host target protein, VGAM1699 host target protein, VGAM1700 host target protein, VGAM1701 host target protein, VGAM1702 host target protein, VGAM1703 host target protein, VGAM1704 host target protein and VGAM1705 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1698, VGAM1699, VGAM1700, VGAM1701,

VGAM1702, VGAM1703, VGAM1704 and VGAM1705.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3106(VGR3106) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95294] VGR3106 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3106 gene was detected is described hereinabove with reference to Figs. 1-9.

[95295] VGR3106 gene encodes VGR3106 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95296] VGR3106 precursor RNA folds spatially, forming VGR3106 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3106 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3106 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95297] VGR3106 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1706 precursor RNA and VGAM1707 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95298] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1706 RNA and VGAM1707 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95299] VGAM1706 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1706 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1706 host target RNA into VGAM1706 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95300] VGAM1707 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1707 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1707 host target RNA into VGAM1707 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95301] It is appreciated that a function of VGR3106 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3106 gene include diagnosis, prevention and treatment of viral infection by Ectocarpus Siliculosus Virus. Specific functions, and accordingly utilities, of VGR3106 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3106 gene: VGAM1706 host target protein and VGAM1707 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1706 and VGAM1707.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3107(VGR3107) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95302] VGR3107 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3107 gene was

detected is described hereinabove with reference to Figs. 1-9.

[95303] VGR3107 gene encodes VGR3107 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95304] VGR3107 precursor RNA folds spatially, forming VGR3107 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3107 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3107 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95305] VGR3107 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1709 precursor RNA, VGAM1710 precursor RNA and VGAM1711 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment,

corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95306] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1709 RNA, VGAM1710 RNA and VGAM1711 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95307] VGAM1709 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1709 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1709 host target RNA into VGAM1709 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95308] VGAM1710 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1710 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1710 host target RNA into VGAM1710 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95309] VGAM1711 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1711 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1711 host target RNA into VGAM1711 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95310] It is appreciated that a function of VGR3107 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3107 gene include diagnosis, prevention and treatment of viral infection by Semliki Forest Virus. Specific functions, and accordingly utilities, of VGR3107 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3107 gene: VGAM1709 host target protein, VGAM1710 host target protein and VGAM1711 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1709, VGAM1710 and VGAM1711.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3108(VGR3108) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95311] VGR3108 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3108 gene was detected is described hereinabove with reference to Figs. 1-9.

[95312] VGR3108 gene encodes VGR3108 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95313] VGR3108 precursor RNA folds spatially, forming VGR3108 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3108 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3108 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95314] VGR3108 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1712 precursor RNA, VGAM1713 precursor RNA, VGAM1714 precursor RNA, VGAM1715

precursor RNA and VGAM1716 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95315] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1712 RNA, VGAM1713 RNA, VGAM1714 RNA, VGAM1715 RNA and VGAM1716 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95316] VGAM1712 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1712 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1712 host target RNA into VGAM1712 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95317] VGAM1713 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1713 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1713 host target RNA into VGAM1713 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95318] VGAM1714 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1714 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1714 host target RNA into

VGAM1714 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95319] VGAM1715 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1715 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1715 host target RNA into VGAM1715 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95320] VGAM1716 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1716 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1716 host target RNA into VGAM1716 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95321] It is appreciated that a function of VGR3108 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3108 gene include diagnosis, prevention and treatment of viral infection by Sindbis Virus. Specific functions, and accordingly utilities, of VGR3108 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3108 gene: VGAM1712 host target protein, VGAM1713 host target protein, VGAM1714 host target protein, VGAM1715 host target protein and VGAM1716 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1712, VGAM1713, VGAM1714, VGAM1715 and VGAM1716.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred

to here as Viral Genomic Record 3109(VGR3109) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95322] VGR3109 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3109 gene was detected is described hereinabove with reference to Figs. 1-9.

[95323] VGR3109 gene encodes VGR3109 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95324] VGR3109 precursor RNA folds spatially, forming VGR3109 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3109 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3109 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[95325] VGR3109 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1717 precursor RNA and VGAM1718 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95326] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1717 RNA and VGAM1718 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95327] VGAM1717 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1717 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1717 host target RNA into VGAM1717 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95328] VGAM1718 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1718 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1718 host target RNA into VGAM1718 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95329] It is appreciated that a function of VGR3109 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3109 gene include diagnosis, prevention and treatment of viral infection by Molluscum Contagiosum Virus. Specific functions, and ac-

cordingly utilities, of VGR3109 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3109 gene: VGAM1717 host target protein and VGAM1718 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1717 and VGAM1718.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3110(VGR3110) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95330] VGR3110 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3110 gene was detected is described hereinabove with reference to Figs. 1-9.

[95331] VGR3110 gene encodes VGR3110 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95332] VGR3110 precursor RNA folds spatially, forming VGR3110 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3110 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3110 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95333] VGR3110 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1719 precursor RNA and VGAM1720 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95334] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM1719 RNA and VGAM1720 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95335] VGAM1719 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1719 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1719 host target RNA into VGAM1719 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95336] VGAM1720 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1720 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1720 host target RNA into VGAM1720 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95337] It is appreciated that a function of VGR3110 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3110 gene include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGR3110 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3110 gene: VGAM1719 host target protein and VGAM1720 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1719 and VGAM1720.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3111(VGR3111) viral gene, which

encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95338] VGR3111 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3111 gene was detected is described hereinabove with reference to Figs. 1-9.

[95339] VGR3111 gene encodes VGR3111 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95340] VGR3111 precursor RNA folds spatially, forming VGR3111 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3111 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3111 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[95341] VGR3111 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1721 precursor RNA, VGAM1722 precursor RNA and VGAM1723 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95342] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1721 RNA, VGAM1722 RNA and VGAM1723 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95343] VGAM1721 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1721 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1721 host target RNA into VGAM1721 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95344] VGAM1722 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1722 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1722 host target RNA into VGAM1722 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95345] VGAM1723 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1723 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1723 host target RNA into VGAM1723 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95346] It is appreciated that a function of VGR3111 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3111 gene include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGR3111 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3111 gene: VGAM1721 host target protein, VGAM1722 host target protein and VGAM1723 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1721, VGAM1722 and VGAM1723.Fig. 9

further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3112(VGR3112) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95347] VGR3112 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3112 gene was detected is described hereinabove with reference to Figs. 1-9.

[95348] VGR3112 gene encodes VGR3112 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95349] VGR3112 precursor RNA folds spatially, forming VGR3112 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3112 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3112 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95350] VGR3112 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1724 precursor RNA, VGAM1725 precursor RNA, VGAM1726 precursor RNA, VGAM1727 precursor RNA, VGAM1728 precursor RNA, VGAM1729 precursor RNA and VGAM1730 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95351] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1724 RNA, VGAM1725 RNA, VGAM1726 RNA, VGAM1727 RNA, VGAM1728 RNA, VGAM1729 RNA and VGAM1730 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95352] VGAM1724 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1724 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1724 host target RNA into VGAM1724 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95353] VGAM1725 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1725 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1725 host target RNA into VGAM1725 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95354] VGAM1726 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1726 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1726 host target RNA into VGAM1726 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95355] VGAM1727 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1727 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1727 host target RNA into VGAM1727 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95356] VGAM1728 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1728 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1728 host target RNA into VGAM1728 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95357] VGAM1729 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1729 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1729 host target RNA into

VGAM1729 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95358] VGAM1730 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1730 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1730 host target RNA into VGAM1730 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95359] It is appreciated that a function of VGR3112 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3112 gene include diagnosis, prevention and treatment of viral infection by Rabies Virus. Specific functions, and accordingly utilities, of VGR3112 gene correlate with, and may be deduced from, the identity of the host target genes, which are in-

hibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3112 gene: VGAM1724 host target protein, VGAM1725 host target protein, VGAM1726 host target protein, VGAM1727 host target protein, VGAM1728 host target protein, VGAM1729 host target protein and VGAM1730 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1724, VGAM1725, VGAM1726, VGAM1727, VGAM1728, VGAM1729 and VGAM1730.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3113(VGR3113) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95360] VGR3113 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3113 gene was detected is described hereinabove with reference to Figs. 1-9.

[95361] VGR3113 gene encodes VGR3113 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95362] VGR3113 precursor RNA folds spatially, forming VGR3113 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3113 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3113 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95363] VGR3113 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1731 precursor RNA and VGAM1732 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95364] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1731 RNA and VGAM1732 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95365] VGAM1731 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1731 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1731 host target RNA into VGAM1731 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95366] VGAM1732 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1732 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1732 host target RNA into VGAM1732 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95367] It is appreciated that a function of VGR3113 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3113 gene include diagnosis, prevention and treatment of viral infection by Rabies Virus. Specific functions, and accordingly utilities, of VGR3113 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3113 gene: VGAM1731 host target protein and VGAM1732 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1731 and VGAM1732.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Ge-

nomic Record 3114(VGR3114) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95368] VGR3114 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3114 gene was detected is described hereinabove with reference to Figs. 1-9.

[95369] VGR3114 gene encodes VGR3114 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95370] VGR3114 precursor RNA folds spatially, forming VGR3114 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3114 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3114 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[95371] VGR3114 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1733 precursor RNA, VGAM1734 precursor RNA, VGAM1735 precursor RNA, VGAM1736 precursor RNA, VGAM1737 precursor RNA, VGAM1738 precursor RNA, VGAM1739 precursor RNA and VGAM1740 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95372] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1733 RNA, VGAM1734 RNA, VGAM1735 RNA, VGAM1736 RNA, VGAM1737 RNA, VGAM1738 RNA, VGAM1739 RNA and VGAM1740 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95373] VGAM1733 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1733 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1733 host target RNA into VGAM1733 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95374] VGAM1734 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1734 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1734 host target RNA into VGAM1734 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95375] VGAM1735 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1735 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1735 host target RNA into VGAM1735 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95376] VGAM1736 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1736 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1736 host target RNA into VGAM1736 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95377] VGAM1737 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1737 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1737 host target RNA into VGAM1737 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95378] VGAM1738 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1738 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1738 host target RNA into VGAM1738 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95379] VGAM1739 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1739 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1739 host target RNA into VGAM1739 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95380] VGAM1740 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1740 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1740 host target RNA into VGAM1740 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95381] It is appreciated that a function of VGR3114 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3114 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 3. Specific functions, and accordingly utilities, of VGR3114 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3114 gene: VGAM1733 host target protein, VGAM1734 host target protein, VGAM1735 host target protein, VGAM1736 host target protein, VGAM1737 host target protein, VGAM1738 host target protein, VGAM1739 host target protein and VGAM1740 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1733, VGAM1734, VGAM1735, VGAM1736, VGAM1737, VGAM1738, VGAM1739 and VGAM1740.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Vi-

ral Genomic Record 3115(VGR3115) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95382] VGR3115 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3115 gene was detected is described hereinabove with reference to Figs. 1-9.

[95383] VGR3115 gene encodes VGR3115 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95384] VGR3115 precursor RNA folds spatially, forming VGR3115 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3115 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3115 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[95385] VGR3115 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1741 precursor RNA, VGAM1742 precursor RNA, VGAM1743 precursor RNA, VGAM1744 precursor RNA, VGAM1745 precursor RNA and VGAM1746 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95386] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1741 RNA, VGAM1742 RNA, VGAM1743 RNA, VGAM1744 RNA, VGAM1745 RNA and VGAM1746 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95387] VGAM1741 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1741 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1741 host target RNA into VGAM1741 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95388] VGAM1742 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1742 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1742 host target RNA into VGAM1742 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95389] VGAM1743 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1743 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1743 host target RNA into VGAM1743 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95390] VGAM1744 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1744 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1744 host target RNA into VGAM1744 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95391] VGAM1745 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1745 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1745 host target RNA into VGAM1745 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95392] VGAM1746 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1746 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1746 host target RNA into VGAM1746 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95393] It is appreciated that a function of VGR3115 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3115 gene include diagnosis, prevention and treatment of viral infection by Cercopithecine Herpesvirus 7. Specific functions, and accordingly utilities, of VGR3115 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3115 gene: VGAM1741 host target protein, VGAM1742 host target protein, VGAM1743 host target protein, VGAM1744 host target protein, VGAM1745 host target protein and VGAM1746 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1741, VGAM1742, VGAM1743, VGAM1744, VGAM1745 and VGAM1746.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3116(VGR3116) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one

host target gene, the function and utility of which at least one host target gene is known in the art.

[95394] VGR3116 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3116 gene was detected is described hereinabove with reference to Figs. 1-9.

[95395] VGR3116 gene encodes VGR3116 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95396] VGR3116 precursor RNA folds spatially, forming VGR3116 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3116 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3116 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95397] VGR3116 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM

precursor RNAs, VGAM1747 precursor RNA, VGAM1748 precursor RNA, VGAM1749 precursor RNA, VGAM1750 precursor RNA, VGAM1751 precursor RNA, VGAM1752 precursor RNA, VGAM1753 precursor RNA and VGAM1754 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95398] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1747 RNA, VGAM1748 RNA, VGAM1749 RNA, VGAM1750 RNA, VGAM1751 RNA, VGAM1752 RNA, VGAM1753 RNA and VGAM1754 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95399] VGAM1747 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1747 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1747 host target RNA into VGAM1747 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95400] VGAM1748 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1748 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1748 host target RNA into VGAM1748 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95401] VGAM1749 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1749 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1749 host target RNA into VGAM1749 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95402] VGAM1750 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1750 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1750 host target RNA into VGAM1750 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95403] VGAM1751 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1751 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1751 host target RNA into VGAM1751 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95404] VGAM1752 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1752 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1752 host target RNA into VGAM1752 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95405] VGAM1753 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1753 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1753 host target RNA into VGAM1753 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95406] VGAM1754 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1754 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1754 host target RNA into VGAM1754 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95407] It is appreciated that a function of VGR3116 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3116 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3116 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3116 gene: VGAM1747 host target protein, VGAM1748 host target protein, VGAM1749 host target protein, VGAM1750 host target protein, VGAM1751 host target protein, VGAM1752 host target protein, VGAM1753 host target protein and VGAM1754 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1747, VGAM1748, VGAM1749, VGAM1750, VGAM1751, VGAM1752, VGAM1753 and VGAM1754.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3117(VGR3117) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of

at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95408] VGR3117 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3117 gene was detected is described hereinabove with reference to Figs. 1-9.

[95409] VGR3117 gene encodes VGR3117 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95410] VGR3117 precursor RNA folds spatially, forming VGR3117 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3117 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3117 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95411] VGR3117 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM

precursor RNAs, VGAM1755 precursor RNA, VGAM1756 precursor RNA, VGAM1757 precursor RNA and VGAM1758 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95412] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1755 RNA, VGAM1756 RNA, VGAM1757 RNA and VGAM1758 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95413] VGAM1755 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1755 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1755 host target RNA into

VGAM1755 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95414] VGAM1756 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1756 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1756 host target RNA into VGAM1756 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95415] VGAM1757 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1757 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1757 host target RNA into VGAM1757 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95416] VGAM1758 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1758 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1758 host target RNA into VGAM1758 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95417] It is appreciated that a function of VGR3117 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3117 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3117 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3117 gene: VGAM1755 host target protein, VGAM1756 host target protein, VGAM1757 host target protein and VGAM1758 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1755, VGAM1756, VGAM1757 and VGAM1758.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3118(VGR3118) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95418] VGR3118 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3118 gene was detected is described hereinabove with reference to Figs. 1-9.

[95419] VGR3118 gene encodes VGR3118 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95420] VGR3118 precursor RNA folds spatially, forming VGR3118 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3118 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3118 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95421] VGR3118 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1759 precursor RNA, VGAM1760 precursor RNA, VGAM1761 precursor RNA, VGAM1762 precursor RNA, VGAM1763 precursor RNA, VGAM1764 precursor RNA, VGAM1765 precursor RNA and VGAM1766 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM

FOLDED PRECURSOR RNA of Fig. 1.

[95422] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1759 RNA, VGAM1760 RNA, VGAM1761 RNA, VGAM1762 RNA, VGAM1763 RNA, VGAM1764 RNA, VGAM1765 RNA and VGAM1766 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95423] VGAM1759 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1759 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1759 host target RNA into VGAM1759 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95424] VGAM1760 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1760 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1760 host target RNA into VGAM1760 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95425] VGAM1761 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1761 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1761 host target RNA into VGAM1761 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95426] VGAM1762 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1762 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1762 host target RNA into VGAM1762 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95427] VGAM1763 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1763 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1763 host target RNA into VGAM1763 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95428] VGAM1764 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1764 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1764 host target RNA into VGAM1764 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95429] VGAM1765 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1765 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1765 host target RNA into VGAM1765 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95430] VGAM1766 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1766 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1766 host target RNA into VGAM1766 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95431] It is appreciated that a function of VGR3118 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3118 gene include diagnosis, prevention and treatment of viral infection by Bovine Viral Diarrhea Virus Genotype 2 (BVDV-2). Specific functions, and accordingly utilities, of VGR3118 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3118 gene:

VGAM1759 host target protein, VGAM1760 host target protein, VGAM1761 host target protein, VGAM1762 host target protein, VGAM1763 host target protein, VGAM1764 host target protein, VGAM1765 host target protein and VGAM1766 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1759, VGAM1760, VGAM1761, VGAM1762, VGAM1763, VGAM1764, VGAM1765 and VGAM1766.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3119(VGR3119) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95432] VGR3119 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3119 gene was detected is described hereinabove with reference to Figs. 1-9.

[95433] VGR3119 gene encodes VGR3119 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95434] VGR3119 precursor RNA folds spatially, forming VGR3119 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3119 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3119 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95435] VGR3119 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM1767 precursor RNA, VGAM1768 precursor RNA, VGAM1769 precursor RNA and VGAM1770 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95436] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1767 RNA, VGAM1768 RNA, VGAM1769 RNA and VGAM1770 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95437] VGAM1767 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1767 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1767 host target RNA into VGAM1767 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95438] VGAM1768 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1768 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1768 host target RNA into VGAM1768 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95439] VGAM1769 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1769 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1769 host target RNA into VGAM1769 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95440] VGAM1770 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1770 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1770 host target RNA into VGAM1770 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95441] It is appreciated that a function of VGR3119 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3119 gene include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGR3119 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3119 gene: VGAM1767 host target protein, VGAM1768 host target protein, VGAM1769 host target protein and VGAM1770 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The

function of these host target genes is elaborated herein-above with reference to VGAM1767, VGAM1768, VGAM1769 and VGAM1770.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3120(VGR3120) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95442] VGR3120 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3120 gene was detected is described hereinabove with reference to Figs. 1-9.

[95443] VGR3120 gene encodes VGR3120 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95444] VGR3120 precursor RNA folds spatially, forming VGR3120 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3120 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3120 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95445] VGR3120 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1771 precursor RNA and VGAM1772 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95446] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1771 RNA and VGAM1772 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95447] VGAM1771 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1771 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1771 host target RNA into VGAM1771 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95448] VGAM1772 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1772 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1772 host target RNA into VGAM1772 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95449] It is appreciated that a function of VGR3120 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3120 gene include diagnosis, prevention and treatment of viral infection by Pestivirus Type 1. Specific functions, and accordingly utilities, of VGR3120 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3120 gene: VGAM1771 host target protein and VGAM1772 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1771 and VGAM1772.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3121(VGR3121) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95450] VGR3121 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3121 gene was detected is described hereinabove with reference to Figs. 1-9.

[95451] VGR3121 gene encodes VGR3121 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95452] VGR3121 precursor RNA folds spatially, forming VGR3121 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3121 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3121 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95453] VGR3121 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1773 precursor RNA, VGAM1774 precursor RNA, VGAM1775 precursor RNA, VGAM1776 precursor RNA, VGAM1777 precursor RNA, VGAM1778 precursor RNA, VGAM1779 precursor RNA and VGAM1780

precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95454] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1773 RNA, VGAM1774 RNA, VGAM1775 RNA, VGAM1776 RNA, VGAM1777 RNA, VGAM1778 RNA, VGAM1779 RNA and VGAM1780 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95455] VGAM1773 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1773 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1773 host target RNA into VGAM1773 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95456] VGAM1774 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1774 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1774 host target RNA into VGAM1774 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95457] VGAM1775 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1775 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1775 host target RNA into

VGAM1775 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95458] VGAM1776 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1776 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1776 host target RNA into VGAM1776 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95459] VGAM1777 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1777 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1777 host target RNA into VGAM1777 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95460] VGAM1778 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1778 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1778 host target RNA into VGAM1778 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95461] VGAM1779 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1779 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1779 host target RNA into VGAM1779 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95462] VGAM1780 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1780 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1780 host target RNA into VGAM1780 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95463] It is appreciated that a function of VGR3121 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3121 gene include diagnosis, prevention and treatment of viral infection by Cryphonectria Hypovirus 1. Specific functions, and ac-

cordingly utilities, of VGR3121 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3121 gene: VGAM1773 host target protein, VGAM1774 host target protein, VGAM1775 host target protein, VGAM1776 host target protein, VGAM1777 host target protein, VGAM1778 host target protein, VGAM1779 host target protein and VGAM1780 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1773, VGAM1774, VGAM1775, VGAM1776, VGAM1777, VGAM1778, VGAM1779 and VGAM1780.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3122(VGR3122) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95464] VGR3122 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3122 gene was detected is described hereinabove with reference to Figs. 1-9.

[95465] VGR3122 gene encodes VGR3122 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95466] VGR3122 precursor RNA folds spatially, forming VGR3122 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3122 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3122 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95467] VGR3122 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1781 precursor RNA and VGAM1782 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3

FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95468] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1781 RNA and VGAM1782 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95469] VGAM1781 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1781 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1781 host target RNA into VGAM1781 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95470] VGAM1782 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1782 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1782 host target RNA into VGAM1782 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95471] It is appreciated that a function of VGR3122 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3122 gene include diagnosis, prevention and treatment of viral infection by Cryphonectria Hypovirus 1. Specific functions, and accordingly utilities, of VGR3122 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3122 gene: VGAM1781 host target protein and VGAM1782 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The

function of these host target genes is elaborated herein-above with reference to VGAM1781 and VGAM1782.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3123(VGR3123) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95472] VGR3123 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3123 gene was detected is described hereinabove with reference to Figs. 1-9.

[95473] VGR3123 gene encodes VGR3123 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95474] VGR3123 precursor RNA folds spatially, forming VGR3123 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3123 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3123 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95475] VGR3123 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1783 precursor RNA, VGAM1784 precursor RNA, VGAM1785 precursor RNA, VGAM1786 precursor RNA, VGAM1787 precursor RNA, VGAM1788 precursor RNA and VGAM1789 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95476] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1783 RNA, VGAM1784 RNA, VGAM1785 RNA, VGAM1786 RNA, VGAM1787 RNA, VGAM1788 RNA and VGAM1789 RNA, herein schematically represented by VGAM1 RNA through

VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95477] VGAM1783 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1783 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1783 host target RNA into VGAM1783 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95478] VGAM1784 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1784 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1784 host target RNA into

VGAM1784 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95479] VGAM1785 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1785 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1785 host target RNA into VGAM1785 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95480] VGAM1786 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1786 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1786 host target RNA into VGAM1786 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95481] VGAM1787 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1787 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1787 host target RNA into VGAM1787 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95482] VGAM1788 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1788 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1788 host target RNA into VGAM1788 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95483] VGAM1789 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1789 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1789 host target RNA into VGAM1789 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95484] It is appreciated that a function of VGR3123 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3123 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utili-

ties, of VGR3123 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3123 gene: VGAM1783 host target protein, VGAM1784 host target protein, VGAM1785 host target protein, VGAM1786 host target protein, VGAM1787 host target protein, VGAM1788 host target protein and VGAM1789 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1783, VGAM1784, VGAM1785, VGAM1786, VGAM1787, VGAM1788 and VGAM1789.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3124(VGR3124) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95485] VGR3124 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3124 gene was detected is described hereinabove with reference to Figs. 1-9.

[95486] VGR3124 gene encodes VGR3124 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95487] VGR3124 precursor RNA folds spatially, forming VGR3124 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3124 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3124 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95488] VGR3124 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1790 precursor RNA, VGAM1791 precursor RNA, VGAM1792 precursor RNA, VGAM1793 precursor RNA, VGAM1794 precursor RNA, VGAM1795 precursor RNA and VGAM1796 precursor RNA, herein

schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95489] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1790 RNA, VGAM1791 RNA, VGAM1792 RNA, VGAM1793 RNA, VGAM1794 RNA, VGAM1795 RNA and VGAM1796 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95490] VGAM1790 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1790 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1790 host target RNA into VGAM1790 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95491] VGAM1791 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1791 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1791 host target RNA into VGAM1791 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95492] VGAM1792 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1792 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1792 host target RNA into

VGAM1792 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95493] VGAM1793 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1793 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1793 host target RNA into VGAM1793 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95494] VGAM1794 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1794 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1794 host target RNA into VGAM1794 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95495] VGAM1795 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1795 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1795 host target RNA into VGAM1795 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95496] VGAM1796 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1796 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1796 host target RNA into VGAM1796 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95497] It is appreciated that a function of VGR3124 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3124 gene include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR3124 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3124 gene: VGAM1790 host target protein, VGAM1791 host target protein, VGAM1792 host target protein, VGAM1793 host target protein, VGAM1794 host target protein, VGAM1795 host target protein and VGAM1796 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1790, VGAM1791, VGAM1792,

VGAM1793, VGAM1794, VGAM1795 and VGAM1796.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3125(VGR3125) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95498] VGR3125 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3125 gene was detected is described hereinabove with reference to Figs. 1-9.

[95499] VGR3125 gene encodes VGR3125 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95500] VGR3125 precursor RNA folds spatially, forming VGR3125 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3125 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3125 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95501] VGR3125 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1797 precursor RNA and VGAM1798 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95502] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1797 RNA and VGAM1798 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95503] VGAM1797 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1797 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1797 host target RNA into VGAM1797 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95504] VGAM1798 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1798 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1798 host target RNA into VGAM1798 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95505] It is appreciated that a function of VGR3125 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3125 gene include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR3125 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3125 gene: VGAM1797 host target protein and VGAM1798 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1797 and VGAM1798.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3126(VGR3126) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95506] VGR3126 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3126 gene was

detected is described hereinabove with reference to Figs. 1-9.

[95507] VGR3126 gene encodes VGR3126 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95508] VGR3126 precursor RNA folds spatially, forming VGR3126 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3126 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3126 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95509] VGR3126 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1799 precursor RNA, VGAM1800 precursor RNA, VGAM1801 precursor RNA, VGAM1802 precursor RNA, VGAM1803 precursor RNA, VGAM1804 precursor RNA, VGAM1805 precursor RNA and VGAM1806 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95510] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1799 RNA, VGAM1800 RNA, VGAM1801 RNA, VGAM1802 RNA, VGAM1803 RNA, VGAM1804 RNA, VGAM1805 RNA and VGAM1806 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95511] VGAM1799 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1799 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1799 host target RNA into VGAM1799 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95512] VGAM1800 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1800 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1800 host target RNA into VGAM1800 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95513] VGAM1801 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1801 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1801 host target RNA into VGAM1801 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95514] VGAM1802 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1802 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1802 host target RNA into VGAM1802 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95515] VGAM1803 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1803 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1803 host target RNA into

VGAM1803 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95516] VGAM1804 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1804 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1804 host target RNA into VGAM1804 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95517] VGAM1805 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1805 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1805 host target RNA into VGAM1805 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95518] VGAM1806 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1806 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1806 host target RNA into VGAM1806 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95519] It is appreciated that a function of VGR3126 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3126 gene include diagnosis, prevention and treatment of viral infection by Tupaia Herpesvirus. Specific functions, and accordingly utilities, of VGR3126 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3126 gene: VGAM1799 host target protein, VGAM1800 host target protein, VGAM1801 host target protein, VGAM1802 host target protein, VGAM1803 host target protein, VGAM1804 host target protein, VGAM1805 host target protein and VGAM1806 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1799, VGAM1800, VGAM1801, VGAM1802, VGAM1803, VGAM1804, VGAM1805 and VGAM1806.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3127(VGR3127) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95520] VGR3127 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3127 gene was

detected is described hereinabove with reference to Figs. 1-9.

[95521] VGR3127 gene encodes VGR3127 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95522] VGR3127 precursor RNA folds spatially, forming VGR3127 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3127 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3127 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95523] VGR3127 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1807 precursor RNA, VGAM1808 precursor RNA and VGAM1809 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment,

corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95524] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1807 RNA, VGAM1808 RNA and VGAM1809 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95525] VGAM1807 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1807 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1807 host target RNA into VGAM1807 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95526] VGAM1808 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1808 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1808 host target RNA into VGAM1808 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95527] VGAM1809 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1809 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1809 host target RNA into VGAM1809 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95528] It is appreciated that a function of VGR3127 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3127 gene include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR3127 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3127 gene: VGAM1807 host target protein, VGAM1808 host target protein and VGAM1809 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1807, VGAM1808 and VGAM1809.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3128(VGR3128) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95529] VGR3128 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3128 gene was detected is described hereinabove with reference to Figs. 1-9.

[95530] VGR3128 gene encodes VGR3128 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95531] VGR3128 precursor RNA folds spatially, forming VGR3128 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3128 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3128 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95532] VGR3128 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1810 precursor RNA, VGAM1811 precursor RNA, VGAM1812 precursor RNA, VGAM1813

precursor RNA, VGAM1814 precursor RNA and VGAM1815 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95533] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1810 RNA, VGAM1811 RNA, VGAM1812 RNA, VGAM1813 RNA, VGAM1814 RNA and VGAM1815 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95534] VGAM1810 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1810 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1810 host target RNA into

VGAM1810 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95535] VGAM1811 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1811 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1811 host target RNA into VGAM1811 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95536] VGAM1812 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1812 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1812 host target RNA into VGAM1812 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95537] VGAM1813 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1813 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1813 host target RNA into VGAM1813 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95538] VGAM1814 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1814 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1814 host target RNA into VGAM1814 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95539] VGAM1815 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1815 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1815 host target RNA into VGAM1815 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95540] It is appreciated that a function of VGR3128 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3128 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 1. Specific functions, and accordingly

utilities, of VGR3128 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3128 gene: VGAM1810 host target protein, VGAM1811 host target protein, VGAM1812 host target protein, VGAM1813 host target protein, VGAM1814 host target protein and VGAM1815 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1810, VGAM1811, VGAM1812, VGAM1813, VGAM1814 and VGAM1815.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3129(VGR3129) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95541] VGR3129 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3129 gene was

detected is described hereinabove with reference to Figs. 1-9.

[95542] VGR3129 gene encodes VGR3129 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95543] VGR3129 precursor RNA folds spatially, forming VGR3129 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3129 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3129 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95544] VGR3129 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1816 precursor RNA, VGAM1817 precursor RNA, VGAM1818 precursor RNA, VGAM1819 precursor RNA, VGAM1820 precursor RNA, VGAM1821 precursor RNA, VGAM1822 precursor RNA and VGAM1823 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95545] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1816 RNA, VGAM1817 RNA, VGAM1818 RNA, VGAM1819 RNA, VGAM1820 RNA, VGAM1821 RNA, VGAM1822 RNA and VGAM1823 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95546] VGAM1816 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1816 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1816 host target RNA into VGAM1816 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95547] VGAM1817 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1817 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1817 host target RNA into VGAM1817 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95548] VGAM1818 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1818 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1818 host target RNA into VGAM1818 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95549] VGAM1819 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1819 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1819 host target RNA into VGAM1819 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95550] VGAM1820 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1820 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1820 host target RNA into

VGAM1820 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95551] VGAM1821 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1821 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1821 host target RNA into VGAM1821 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95552] VGAM1822 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1822 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1822 host target RNA into VGAM1822 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95553] VGAM1823 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1823 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1823 host target RNA into VGAM1823 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95554] It is appreciated that a function of VGR3129 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3129 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3129 gene correlate with, and may be de-

duced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3129 gene: VGAM1816 host target protein, VGAM1817 host target protein, VGAM1818 host target protein, VGAM1819 host target protein, VGAM1820 host target protein, VGAM1821 host target protein, VGAM1822 host target protein and VGAM1823 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1816, VGAM1817, VGAM1818, VGAM1819, VGAM1820, VGAM1821, VGAM1822 and VGAM1823.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3130(VGR3130) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95555] VGR3130 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3130 gene was

detected is described hereinabove with reference to Figs. 1-9.

[95556] VGR3130 gene encodes VGR3130 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95557] VGR3130 precursor RNA folds spatially, forming VGR3130 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3130 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3130 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95558] VGR3130 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1824 precursor RNA, VGAM1825 precursor RNA and VGAM1826 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment,

corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95559] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1824 RNA, VGAM1825 RNA and VGAM1826 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95560] VGAM1824 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1824 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1824 host target RNA into VGAM1824 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95561] VGAM1825 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1825 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1825 host target RNA into VGAM1825 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95562] VGAM1826 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1826 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1826 host target RNA into VGAM1826 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95563] It is appreciated that a function of VGR3130 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3130 gene include diagnosis, prevention and treatment of viral infection by Cryphonectria Hypovirus. Specific functions, and accordingly utilities, of VGR3130 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3130 gene: VGAM1824 host target protein, VGAM1825 host target protein and VGAM1826 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1824, VGAM1825 and VGAM1826.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3131(VGR3131) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95564] VGR3131 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3131 gene was detected is described hereinabove with reference to Figs. 1-9.

[95565] VGR3131 gene encodes VGR3131 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95566] VGR3131 precursor RNA folds spatially, forming VGR3131 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3131 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3131 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95567] VGR3131 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1827 precursor RNA, VGAM1828 precursor RNA and VGAM1829 precursor RNA, herein

schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95568] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1827 RNA, VGAM1828 RNA and VGAM1829 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95569] VGAM1827 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1827 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1827 host target RNA into VGAM1827 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95570] VGAM1828 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1828 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1828 host target RNA into VGAM1828 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95571] VGAM1829 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1829 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1829 host target RNA into VGAM1829 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95572] It is appreciated that a function of VGR3131 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3131 gene include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGR3131 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3131 gene: VGAM1827 host target protein, VGAM1828 host target protein and VGAM1829 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1827, VGAM1828 and VGAM1829.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3132(VGR3132) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates ex-

pression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95573] VGR3132 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3132 gene was detected is described hereinabove with reference to Figs. 1-9.

[95574] VGR3132 gene encodes VGR3132 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95575] VGR3132 precursor RNA folds spatially, forming VGR3132 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3132 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3132 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95576] VGR3132 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1830 precursor RNA, VGAM1831 precursor RNA, VGAM1832 precursor RNA, VGAM1833 precursor RNA and VGAM1834 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95577] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1830 RNA, VGAM1831 RNA, VGAM1832 RNA, VGAM1833 RNA and VGAM1834 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95578] VGAM1830 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1830 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1830 host target RNA into VGAM1830 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95579] VGAM1831 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1831 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1831 host target RNA into VGAM1831 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95580] VGAM1832 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1832 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1832 host target RNA into VGAM1832 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95581] VGAM1833 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1833 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1833 host target RNA into VGAM1833 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95582] VGAM1834 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1834 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1834 host target RNA into VGAM1834 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95583] It is appreciated that a function of VGR3132 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3132 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3132 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3132 gene: VGAM1830 host target protein, VGAM1831 host target protein, VGAM1832 host target protein, VGAM1833 host target protein and VGAM1834 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with refer-

ence to VGAM1830, VGAM1831, VGAM1832, VGAM1833 and VGAM1834.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3133(VGR3133) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95584] VGR3133 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3133 gene was detected is described hereinabove with reference to Figs. 1-9.

[95585] VGR3133 gene encodes VGR3133 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95586] VGR3133 precursor RNA folds spatially, forming VGR3133 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3133 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3133 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95587] VGR3133 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1835 precursor RNA, VGAM1836 precursor RNA, VGAM1837 precursor RNA, VGAM1838 precursor RNA and VGAM1839 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95588] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1835 RNA, VGAM1836 RNA, VGAM1837 RNA, VGAM1838 RNA and VGAM1839 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95589] VGAM1835 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1835 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1835 host target RNA into VGAM1835 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95590] VGAM1836 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1836 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1836 host target RNA into VGAM1836 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95591] VGAM1837 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1837 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1837 host target RNA into VGAM1837 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95592] VGAM1838 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1838 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1838 host target RNA into VGAM1838 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95593] VGAM1839 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1839 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1839 host target RNA into VGAM1839 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95594] It is appreciated that a function of VGR3133 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3133 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR3133 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3133 gene: VGAM1835 host

target protein, VGAM1836 host target protein, VGAM1837 host target protein, VGAM1838 host target protein and VGAM1839 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1835, VGAM1836, VGAM1837, VGAM1838 and VGAM1839.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3134(VGR3134) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95595] VGR3134 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3134 gene was detected is described hereinabove with reference to Figs. 1-9.

[95596] VGR3134 gene encodes VGR3134 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95597] VGR3134 precursor RNA folds spatially, forming VGR3134 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3134 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3134 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95598] VGR3134 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1840 precursor RNA and VGAM1841 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95599] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1840 RNA and VGAM1841 RNA, herein schematically repre-

sented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95600] VGAM1840 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1840 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1840 host target RNA into VGAM1840 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95601] VGAM1841 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1841 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1841 host target RNA into

VGAM1841 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95602] It is appreciated that a function of VGR3134 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3134 gene include diagnosis, prevention and treatment of viral infection by Cowpea Mottle Virus. Specific functions, and accordingly utilities, of VGR3134 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3134 gene: VGAM1840 host target protein and VGAM1841 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1840 and VGAM1841.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3135(VGR3135) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expres-

sion of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95603] VGR3135 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3135 gene was detected is described hereinabove with reference to Figs. 1-9.

[95604] VGR3135 gene encodes VGR3135 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95605] VGR3135 precursor RNA folds spatially, forming VGR3135 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3135 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3135 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95606] VGR3135 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM1842 precursor RNA, VGAM1843 precursor RNA, VGAM1844 precursor RNA, VGAM1845 precursor RNA and VGAM1846 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95607] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1842 RNA, VGAM1843 RNA, VGAM1844 RNA, VGAM1845 RNA and VGAM1846 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95608] VGAM1842 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1842 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1842 host target RNA into VGAM1842 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95609] VGAM1843 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1843 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1843 host target RNA into VGAM1843 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95610] VGAM1844 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1844 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1844 host target RNA into VGAM1844 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95611] VGAM1845 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1845 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1845 host target RNA into VGAM1845 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95612] VGAM1846 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1846 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1846 host target RNA into VGAM1846 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95613] It is appreciated that a function of VGR3135 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3135 gene include diagnosis, prevention and treatment of viral infection by Chimpanzee Cytomegalovirus. Specific functions, and accordingly utilities, of VGR3135 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3135 gene: VGAM1842 host target protein, VGAM1843 host target protein, VGAM1844 host target protein, VGAM1845 host target protein and VGAM1846 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove

with reference to VGAM1842, VGAM1843, VGAM1844, VGAM1845 and VGAM1846.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3136(VGR3136) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95614] VGR3136 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3136 gene was detected is described hereinabove with reference to Figs. 1-9.

[95615] VGR3136 gene encodes VGR3136 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95616] VGR3136 precursor RNA folds spatially, forming VGR3136 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3136 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3136 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95617] VGR3136 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1847 precursor RNA, VGAM1848 precursor RNA, VGAM1849 precursor RNA, VGAM1850 precursor RNA, VGAM1851 precursor RNA, VGAM1852 precursor RNA and VGAM1853 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95618] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1847 RNA, VGAM1848 RNA, VGAM1849 RNA, VGAM1850 RNA, VGAM1851 RNA, VGAM1852 RNA and VGAM1853 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to

VGAM RNA of Fig. 1.

[95619] VGAM1847 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1847 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1847 host target RNA into VGAM1847 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95620] VGAM1848 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1848 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1848 host target RNA into VGAM1848 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95621] VGAM1849 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1849 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1849 host target RNA into VGAM1849 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95622] VGAM1850 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1850 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1850 host target RNA into

VGAM1850 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95623] VGAM1851 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1851 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1851 host target RNA into VGAM1851 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95624] VGAM1852 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1852 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1852 host target RNA into VGAM1852 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95625] VGAM1853 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1853 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1853 host target RNA into VGAM1853 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95626] It is appreciated that a function of VGR3136 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3136 gene include diagnosis, prevention and treatment of viral infection by Sonchus Yellow Net Virus. Specific functions, and accordingly utilities, of VGR3136 gene correlate with, and may

be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3136 gene: VGAM1847 host target protein, VGAM1848 host target protein, VGAM1849 host target protein, VGAM1850 host target protein, VGAM1851 host target protein, VGAM1852 host target protein and VGAM1853 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1847, VGAM1848, VGAM1849, VGAM1850, VGAM1851, VGAM1852 and VGAM1853.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3137(VGR3137) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95627] VGR3137 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3137 gene was

detected is described hereinabove with reference to Figs. 1-9.

[95628] VGR3137 gene encodes VGR3137 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95629] VGR3137 precursor RNA folds spatially, forming VGR3137 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3137 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3137 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95630] VGR3137 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1854 precursor RNA and VGAM1855 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95631] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1854 RNA and VGAM1855 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95632] VGAM1854 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1854 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1854 host target RNA into VGAM1854 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95633] VGAM1855 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1855 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1855 host target RNA into VGAM1855 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95634] It is appreciated that a function of VGR3137 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3137 gene include diagnosis, prevention and treatment of viral infection by Cowpea Chlorotic Mottle Virus. Specific functions, and accordingly utilities, of VGR3137 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3137 gene: VGAM1854 host target protein and VGAM1855 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1854 and VGAM1855.Fig. 9

further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3138(VGR3138) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95635] VGR3138 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3138 gene was detected is described hereinabove with reference to Figs. 1-9.

[95636] VGR3138 gene encodes VGR3138 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95637] VGR3138 precursor RNA folds spatially, forming VGR3138 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3138 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3138 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95638] VGR3138 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1856 precursor RNA, VGAM1857 precursor RNA, VGAM1858 precursor RNA, VGAM1859 precursor RNA, VGAM1860 precursor RNA and VGAM1861 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95639] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1856 RNA, VGAM1857 RNA, VGAM1858 RNA, VGAM1859 RNA, VGAM1860 RNA and VGAM1861 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95640] VGAM1856 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1856 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1856 host target RNA into VGAM1856 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95641] VGAM1857 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1857 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1857 host target RNA into VGAM1857 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95642] VGAM1858 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1858 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1858 host target RNA into VGAM1858 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95643] VGAM1859 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1859 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1859 host target RNA into VGAM1859 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95644] VGAM1860 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1860 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1860 host target RNA into VGAM1860 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95645] VGAM1861 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1861 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1861 host target RNA into VGAM1861 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95646] It is appreciated that a function of VGR3138 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3138 gene include diagnosis, prevention and treatment of viral infection by Rice Yellow Stunt Virus. Specific functions, and accordingly utilities, of VGR3138 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3138 gene: VGAM1856 host target protein, VGAM1857 host target protein, VGAM1858 host target protein, VGAM1859 host target protein, VGAM1860 host target protein and VGAM1861 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1856, VGAM1857, VGAM1858, VGAM1859, VGAM1860 and VGAM1861.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3139(VGR3139) viral

gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95647] VGR3139 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3139 gene was detected is described hereinabove with reference to Figs. 1-9.

[95648] VGR3139 gene encodes VGR3139 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95649] VGR3139 precursor RNA folds spatially, forming VGR3139 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3139 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3139 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[95650] VGR3139 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1863 precursor RNA, VGAM1864 precursor RNA, VGAM1865 precursor RNA, VGAM1866 precursor RNA, VGAM1867 precursor RNA and VGAM1868 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95651] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1863 RNA, VGAM1864 RNA, VGAM1865 RNA, VGAM1866 RNA, VGAM1867 RNA and VGAM1868 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95652] VGAM1863 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1863 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1863 host target RNA into VGAM1863 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95653] VGAM1864 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1864 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1864 host target RNA into VGAM1864 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95654] VGAM1865 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1865 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1865 host target RNA into VGAM1865 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95655] VGAM1866 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1866 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1866 host target RNA into VGAM1866 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95656] VGAM1867 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1867 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1867 host target RNA into VGAM1867 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95657] VGAM1868 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1868 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1868 host target RNA into VGAM1868 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95658] It is appreciated that a function of VGR3139 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3139 gene include diagnosis, prevention and treatment of viral infection by Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGR3139 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3139 gene: VGAM1863 host target protein, VGAM1864 host target protein, VGAM1865 host target protein, VGAM1866 host target protein, VGAM1867 host target protein and VGAM1868 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1863, VGAM1864, VGAM1865, VGAM1866, VGAM1867 and VGAM1868.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3140(VGR3140) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[95659] VGR3140 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3140 gene was detected is described hereinabove with reference to Figs. 1-9.

[95660] VGR3140 gene encodes VGR3140 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95661] VGR3140 precursor RNA folds spatially, forming VGR3140 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3140 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3140 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95662] VGR3140 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM

precursor RNAs, VGAM1870 precursor RNA, VGAM1871 precursor RNA, VGAM1872 precursor RNA, VGAM1873 precursor RNA, VGAM1874 precursor RNA, VGAM1875 precursor RNA, VGAM1876 precursor RNA and VGAM1877 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95663] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1870 RNA, VGAM1871 RNA, VGAM1872 RNA, VGAM1873 RNA, VGAM1874 RNA, VGAM1875 RNA, VGAM1876 RNA and VGAM1877 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95664] VGAM1870 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1870 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1870 host target RNA into VGAM1870 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95665] VGAM1871 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1871 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1871 host target RNA into VGAM1871 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95666] VGAM1872 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1872 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1872 host target RNA into VGAM1872 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95667] VGAM1873 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1873 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1873 host target RNA into VGAM1873 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95668] VGAM1874 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1874 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1874 host target RNA into VGAM1874 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95669] VGAM1875 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1875 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1875 host target RNA into VGAM1875 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95670] VGAM1876 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1876 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1876 host target RNA into VGAM1876 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95671] VGAM1877 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1877 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1877 host target RNA into VGAM1877 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95672] It is appreciated that a function of VGR3140 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3140 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR3140 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3140 gene: VGAM1870 host target protein, VGAM1871 host target protein, VGAM1872 host target protein, VGAM1873 host target protein, VGAM1874 host target protein, VGAM1875 host target protein, VGAM1876 host target protein and VGAM1877 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1870, VGAM1871, VGAM1872, VGAM1873, VGAM1874, VGAM1875, VGAM1876 and VGAM1877.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3141(VGR3141) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of

at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95673] VGR3141 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3141 gene was detected is described hereinabove with reference to Figs. 1-9.

[95674] VGR3141 gene encodes VGR3141 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95675] VGR3141 precursor RNA folds spatially, forming VGR3141 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3141 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3141 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95676] VGR3141 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM

precursor RNAs, VGAM1878 precursor RNA, VGAM1879 precursor RNA, VGAM1880 precursor RNA, VGAM1881 precursor RNA, VGAM1882 precursor RNA, VGAM1883 precursor RNA and VGAM1884 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95677] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1878 RNA, VGAM1879 RNA, VGAM1880 RNA, VGAM1881 RNA, VGAM1882 RNA, VGAM1883 RNA and VGAM1884 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95678] VGAM1878 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1878 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1878 host target RNA into VGAM1878 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95679] VGAM1879 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1879 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1879 host target RNA into VGAM1879 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95680] VGAM1880 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1880 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1880 host target RNA into VGAM1880 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95681] VGAM1881 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1881 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1881 host target RNA into VGAM1881 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95682] VGAM1882 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1882 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1882 host target RNA into VGAM1882 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95683] VGAM1883 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1883 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1883 host target RNA into VGAM1883 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95684] VGAM1884 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1884 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1884 host target RNA into VGAM1884 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95685] It is appreciated that a function of VGR3141 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3141 gene include diagnosis, prevention and treatment of viral infection by Bovine Respiratory Syncytial Virus. Specific functions, and accordingly utilities, of VGR3141 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3141 gene: VGAM1878 host target protein, VGAM1879 host target protein, VGAM1880 host target protein, VGAM1881 host target protein, VGAM1882 host target protein, VGAM1883 host target protein and VGAM1884 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1878, VGAM1879, VGAM1880, VGAM1881, VGAM1882, VGAM1883 and VGAM1884.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3142(VGR3142) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95686] VGR3142 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3142 gene was detected is described hereinabove with reference to Figs. 1-9.

[95687] VGR3142 gene encodes VGR3142 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95688] VGR3142 precursor RNA folds spatially, forming VGR3142 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3142 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3142 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95689] VGR3142 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1885 precursor RNA, VGAM1886 precursor RNA, VGAM1887 precursor RNA, VGAM1888 precursor RNA, VGAM1889 precursor RNA, VGAM1890 precursor RNA and VGAM1891 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95690] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1885

RNA, VGAM1886 RNA, VGAM1887 RNA, VGAM1888 RNA, VGAM1889 RNA, VGAM1890 RNA and VGAM1891 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95691] VGAM1885 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1885 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1885 host target RNA into VGAM1885 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95692] VGAM1886 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1886 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1886 host target RNA into VGAM1886 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95693] VGAM1887 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1887 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1887 host target RNA into VGAM1887 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95694] VGAM1888 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1888 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1888 host target RNA into VGAM1888 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95695] VGAM1889 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1889 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1889 host target RNA into VGAM1889 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95696] VGAM1890 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1890 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1890 host target RNA into VGAM1890 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95697] VGAM1891 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1891 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1891 host target RNA into VGAM1891 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95698] It is appreciated that a function of VGR3142 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3142 gene include diagnosis, prevention and treatment of viral infection by Newcastle Disease Virus. Specific functions, and accordingly utilities, of VGR3142 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3142 gene: VGAM1885 host target protein, VGAM1886 host target protein, VGAM1887 host target protein, VGAM1888 host target protein, VGAM1889 host target protein, VGAM1890 host target protein and VGAM1891 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1885, VGAM1886, VGAM1887, VGAM1888, VGAM1889, VGAM1890 and VGAM1891.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3143(VGR3143) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[95699] VGR3143 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3143 gene was detected is described hereinabove with reference to Figs. 1-9.

[95700] VGR3143 gene encodes VGR3143 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95701] VGR3143 precursor RNA folds spatially, forming VGR3143 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3143 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3143 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95702] VGR3143 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1892 precursor RNA and

VGAM1893 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95703] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1892 RNA and VGAM1893 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95704] VGAM1892 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1892 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1892 host target RNA into VGAM1892 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95705] VGAM1893 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1893 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1893 host target RNA into VGAM1893 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95706] It is appreciated that a function of VGR3143 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3143 gene include diagnosis, prevention and treatment of viral infection by Newcastle Disease Virus. Specific functions, and accordingly utilities, of VGR3143 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3143 gene: VGAM1892 host target protein and VGAM1893 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1892 and VGAM1893.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3144(VGR3144) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95707] VGR3144 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3144 gene was detected is described hereinabove with reference to Figs. 1-9.

[95708] VGR3144 gene encodes VGR3144 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95709] VGR3144 precursor RNA folds spatially, forming VGR3144 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3144 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3144 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95710] VGR3144 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1894 precursor RNA, VGAM1895 precursor RNA, VGAM1896 precursor RNA, VGAM1897 precursor RNA, VGAM1898 precursor RNA, VGAM1899 precursor RNA, VGAM1900 precursor RNA and VGAM1901 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95711] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1894 RNA, VGAM1895 RNA, VGAM1896 RNA, VGAM1897 RNA,

VGAM1898 RNA, VGAM1899 RNA, VGAM1900 RNA and VGAM1901 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95712] VGAM1894 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1894 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1894 host target RNA into VGAM1894 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95713] VGAM1895 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1895 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1895 host target RNA into VGAM1895 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95714] VGAM1896 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1896 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1896 host target RNA into VGAM1896 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95715] VGAM1897 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1897 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1897 host target RNA into VGAM1897 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95716] VGAM1898 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1898 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1898 host target RNA into VGAM1898 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95717] VGAM1899 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1899 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1899 host target RNA into VGAM1899 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95718] VGAM1900 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1900 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1900 host target RNA into VGAM1900 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95719] VGAM1901 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1901 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1901 host target RNA into VGAM1901 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95720] It is appreciated that a function of VGR3144 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3144 gene include diagnosis, prevention and treatment of viral infection by Respiratory Syncytial Virus. Specific functions, and accordingly utilities, of VGR3144 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3144 gene: VGAM1894 host target protein, VGAM1895 host target protein, VGAM1896 host target protein, VGAM1897 host target protein, VGAM1898 host target protein, VGAM1899 host target protein, VGAM1900 host target protein and VGAM1901 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1894, VGAM1895, VGAM1896, VGAM1897, VGAM1898, VGAM1899, VGAM1900 and VGAM1901.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3145(VGR3145) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95721] VGR3145 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3145 gene was detected is described hereinabove with reference to Figs. 1-9.

[95722] VGR3145 gene encodes VGR3145 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95723] VGR3145 precursor RNA folds spatially, forming VGR3145 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3145 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3145 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95724] VGR3145 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1902 precursor RNA, VGAM1903 precursor RNA and VGAM1904 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95725] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1902 RNA, VGAM1903 RNA and VGAM1904 RNA, herein schematically represented by VGAM1 RNA through VGAM3

RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95726] VGAM1902 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1902 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1902 host target RNA into VGAM1902 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95727] VGAM1903 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1903 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1903 host target RNA into

VGAM1903 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95728] VGAM1904 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1904 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1904 host target RNA into VGAM1904 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95729] It is appreciated that a function of VGR3145 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3145 gene include diagnosis, prevention and treatment of viral infection by Respiratory Syncytial Virus. Specific functions, and accordingly utilities, of VGR3145 gene correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3145 gene: VGAM1902 host target protein, VGAM1903 host target protein and VGAM1904 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1902, VGAM1903 and VGAM1904.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3146(VGR3146) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95730] VGR3146 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3146 gene was detected is described hereinabove with reference to Figs. 1-9.

[95731] VGR3146 gene encodes VGR3146 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[95732] VGR3146 precursor RNA folds spatially, forming VGR3146 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3146 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3146 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95733] VGR3146 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1905 precursor RNA and VGAM1906 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95734] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1905

RNA and VGAM1906 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95735] VGAM1905 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1905 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1905 host target RNA into VGAM1905 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95736] VGAM1906 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1906 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1906 host target RNA into VGAM1906 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95737] It is appreciated that a function of VGR3146 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3146 gene include diagnosis, prevention and treatment of viral infection by Sendai Virus. Specific functions, and accordingly utilities, of VGR3146 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3146 gene: VGAM1905 host target protein and VGAM1906 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1905 and VGAM1906.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3147(VGR3147) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like

genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95738] VGR3147 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3147 gene was detected is described hereinabove with reference to Figs. 1-9.

[95739] VGR3147 gene encodes VGR3147 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95740] VGR3147 precursor RNA folds spatially, forming VGR3147 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3147 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3147 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95741] VGR3147 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1907 precursor RNA, VGAM1908 precursor RNA, VGAM1909 precursor RNA, VGAM1910 precursor RNA, VGAM1911 precursor RNA, VGAM1912 precursor RNA and VGAM1913 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95742] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1907 RNA, VGAM1908 RNA, VGAM1909 RNA, VGAM1910 RNA, VGAM1911 RNA, VGAM1912 RNA and VGAM1913 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95743] VGAM1907 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1907 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1907 host target RNA into VGAM1907 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95744] VGAM1908 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1908 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1908 host target RNA into VGAM1908 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95745] VGAM1909 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1909 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1909 host target RNA into VGAM1909 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95746] VGAM1910 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1910 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1910 host target RNA into VGAM1910 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95747] VGAM1911 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1911 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1911 host target RNA into VGAM1911 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95748] VGAM1912 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1912 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1912 host target RNA into VGAM1912 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95749] VGAM1913 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1913 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1913 host target RNA into VGAM1913 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95750] It is appreciated that a function of VGR3147 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3147 gene include diagnosis, prevention and treatment of viral infection by Human Parainfluenza Virus 3. Specific functions, and accordingly utilities, of VGR3147 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3147 gene: VGAM1907 host target protein, VGAM1908 host target protein, VGAM1909 host target protein, VGAM1910 host target protein, VGAM1911 host target protein, VGAM1912 host

target protein and VGAM1913 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1907, VGAM1908, VGAM1909, VGAM1910, VGAM1911, VGAM1912 and VGAM1913.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3148(VGR3148) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95751] VGR3148 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3148 gene was detected is described hereinabove with reference to Figs. 1-9.

[95752] VGR3148 gene encodes VGR3148 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95753] VGR3148 precursor RNA folds spatially, forming VGR3148

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3148 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3148 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95754] VGR3148 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1914 precursor RNA and VGAM1915 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95755] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1914 RNA and VGAM1915 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of

which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95756] VGAM1914 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1914 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1914 host target RNA into VGAM1914 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95757] VGAM1915 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1915 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1915 host target RNA into VGAM1915 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95758] It is appreciated that a function of VGR3148 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3148 gene include diagnosis, prevention and treatment of viral infection by Human Parainfluenza Virus 3. Specific functions, and accordingly utilities, of VGR3148 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3148 gene: VGAM1914 host target protein and VGAM1915 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1914 and VGAM1915.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3149(VGR3149) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and

utility of which at least one host target gene is known in the art.

[95759] VGR3149 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3149 gene was detected is described hereinabove with reference to Figs. 1-9.

[95760] VGR3149 gene encodes VGR3149 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95761] VGR3149 precursor RNA folds spatially, forming VGR3149 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3149 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3149 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95762] VGR3149 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM

precursor RNAs, VGAM1916 precursor RNA, VGAM1917 precursor RNA and VGAM1918 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95763] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1916 RNA, VGAM1917 RNA and VGAM1918 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95764] VGAM1916 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1916 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1916 host target RNA into

VGAM1916 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95765] VGAM1917 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1917 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1917 host target RNA into VGAM1917 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95766] VGAM1918 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1918 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1918 host target RNA into VGAM1918 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95767] It is appreciated that a function of VGR3149 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3149 gene include diagnosis, prevention and treatment of viral infection by Human Parainfluenza Virus 1 Strain Washington/1964. Specific functions, and accordingly utilities, of VGR3149 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3149 gene: VGAM1916 host target protein, VGAM1917 host target protein and VGAM1918 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1916, VGAM1917 and VGAM1918.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record

3150(VGR3150) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95768] VGR3150 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3150 gene was detected is described hereinabove with reference to Figs. 1-9.

[95769] VGR3150 gene encodes VGR3150 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95770] VGR3150 precursor RNA folds spatially, forming VGR3150 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3150 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3150 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[95771] VGR3150 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1920 precursor RNA, VGAM1921 precursor RNA, VGAM1922 precursor RNA, VGAM1923 precursor RNA, VGAM1924 precursor RNA, VGAM1925 precursor RNA and VGAM1926 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95772] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1920 RNA, VGAM1921 RNA, VGAM1922 RNA, VGAM1923 RNA, VGAM1924 RNA, VGAM1925 RNA and VGAM1926 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95773] VGAM1920 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1920 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1920 host target RNA into VGAM1920 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95774] VGAM1921 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1921 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1921 host target RNA into VGAM1921 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95775] VGAM1922 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1922 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1922 host target RNA into VGAM1922 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95776] VGAM1923 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1923 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1923 host target RNA into VGAM1923 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95777] VGAM1924 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1924 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1924 host target RNA into VGAM1924 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95778] VGAM1925 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1925 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1925 host target RNA into VGAM1925 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95779] VGAM1926 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1926 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1926 host target RNA into VGAM1926 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95780] It is appreciated that a function of VGR3150 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3150 gene include diagnosis, prevention and treatment of viral infection by Canine Distemper Virus. Specific functions, and accordingly utilities, of VGR3150 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3150 gene: VGAM1920 host target protein, VGAM1921 host target protein, VGAM1922

host target protein, VGAM1923 host target protein, VGAM1924 host target protein, VGAM1925 host target protein and VGAM1926 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1920, VGAM1921, VGAM1922, VGAM1923, VGAM1924, VGAM1925 and VGAM1926.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3151(VGR3151) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95781] VGR3151 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3151 gene was detected is described hereinabove with reference to Figs. 1-9.

[95782] VGR3151 gene encodes VGR3151 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[95783] VGR3151 precursor RNA folds spatially, forming VGR3151 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3151 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3151 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95784] VGR3151 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1927 precursor RNA and VGAM1928 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95785] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1927

RNA and VGAM1928 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95786] VGAM1927 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1927 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1927 host target RNA into VGAM1927 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95787] VGAM1928 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1928 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1928 host target RNA into VGAM1928 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95788] It is appreciated that a function of VGR3151 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3151 gene include diagnosis, prevention and treatment of viral infection by Canine Distemper Virus. Specific functions, and accordingly utilities, of VGR3151 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3151 gene: VGAM1927 host target protein and VGAM1928 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1927 and VGAM1928.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3152(VGR3152) viral gene, which encodes an `operon-like` cluster of novel viral micro

RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95789] VGR3152 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3152 gene was detected is described hereinabove with reference to Figs. 1-9.

[95790] VGR3152 gene encodes VGR3152 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95791] VGR3152 precursor RNA folds spatially, forming VGR3152 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3152 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3152 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95792] VGR3152 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1930 precursor RNA, VGAM1931 precursor RNA, VGAM1932 precursor RNA, VGAM1933 precursor RNA, VGAM1934 precursor RNA, VGAM1935 precursor RNA and VGAM1936 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95793] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1930 RNA, VGAM1931 RNA, VGAM1932 RNA, VGAM1933 RNA, VGAM1934 RNA, VGAM1935 RNA and VGAM1936 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95794] VGAM1930 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1930 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1930 host target RNA into VGAM1930 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95795] VGAM1931 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1931 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1931 host target RNA into VGAM1931 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95796] VGAM1932 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1932 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1932 host target RNA into VGAM1932 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95797] VGAM1933 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1933 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1933 host target RNA into VGAM1933 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95798] VGAM1934 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1934 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1934 host target RNA into VGAM1934 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95799] VGAM1935 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1935 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1935 host target RNA into VGAM1935 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95800] VGAM1936 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1936 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1936 host target RNA into VGAM1936 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95801] It is appreciated that a function of VGR3152 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3152 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3152 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3152 gene: VGAM1930 host target protein, VGAM1931 host target protein, VGAM1932 host target protein, VGAM1933 host target protein,

VGAM1934 host target protein, VGAM1935 host target protein and VGAM1936 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1930, VGAM1931, VGAM1932, VGAM1933, VGAM1934, VGAM1935 and VGAM1936.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3153(VGR3153) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95802] VGR3153 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3153 gene was detected is described hereinabove with reference to Figs. 1-9.

[95803] VGR3153 gene encodes VGR3153 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95804] VGR3153 precursor RNA folds spatially, forming VGR3153 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3153 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3153 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95805] VGR3153 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1937 precursor RNA and VGAM1938 precursor RNA, herein schematically repre-

sented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95806] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1937 RNA and VGAM1938 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95807] VGAM1937 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1937 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1937 host target RNA into VGAM1937 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95808] VGAM1938 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1938 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1938 host target RNA into VGAM1938 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95809] It is appreciated that a function of VGR3153 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3153 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3153 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3153 gene: VGAM1937 host target protein and VGAM1938 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1937 and VGAM1938.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3154(VGR3154) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95810] VGR3154 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3154 gene was detected is described hereinabove with reference to Figs. 1-9.

[95811] VGR3154 gene encodes VGR3154 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95812] VGR3154 precursor RNA folds spatially, forming VGR3154 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3154 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3154 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95813] VGR3154 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1940 precursor RNA, VGAM1941 precursor RNA, VGAM1942 precursor RNA, VGAM1943 precursor RNA, VGAM1944 precursor RNA, VGAM1945 precursor RNA, VGAM1946 precursor RNA and VGAM1947 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95814] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1940 RNA, VGAM1941 RNA, VGAM1942 RNA, VGAM1943 RNA, VGAM1944 RNA, VGAM1945 RNA, VGAM1946 RNA and

VGAM1947 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95815] VGAM1940 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1940 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1940 host target RNA into VGAM1940 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95816] VGAM1941 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1941 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1941 host target RNA into VGAM1941 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95817] VGAM1942 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1942 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1942 host target RNA into VGAM1942 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95818] VGAM1943 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1943 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1943 host target RNA into VGAM1943 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95819] VGAM1944 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1944 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1944 host target RNA into VGAM1944 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95820] VGAM1945 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1945 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1945 host target RNA into VGAM1945 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95821] VGAM1946 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1946 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1946 host target RNA into VGAM1946 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95822] VGAM1947 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1947 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1947 host target RNA into VGAM1947 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95823] It is appreciated that a function of VGR3154 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3154 gene include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGR3154 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3154 gene: VGAM1940 host target protein, VGAM1941 host target protein, VGAM1942 host target protein, VGAM1943 host target protein, VGAM1944 host target protein, VGAM1945 host target protein, VGAM1946 host target protein and VGAM1947 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The

function of these host target genes is elaborated herein-above with reference to VGAM1940, VGAM1941, VGAM1942, VGAM1943, VGAM1944, VGAM1945, VGAM1946 and VGAM1947.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3155(VGR3155) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95824] VGR3155 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3155 gene was detected is described hereinabove with reference to Figs. 1-9.

[95825] VGR3155 gene encodes VGR3155 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95826] VGR3155 precursor RNA folds spatially, forming VGR3155 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3155 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3155 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95827] VGR3155 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1948 precursor RNA, VGAM1949 precursor RNA, VGAM1950 precursor RNA, VGAM1951 precursor RNA, VGAM1952 precursor RNA, VGAM1953 precursor RNA and VGAM1954 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95828] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1948 RNA, VGAM1949 RNA, VGAM1950 RNA, VGAM1951 RNA, VGAM1952 RNA, VGAM1953 RNA and VGAM1954 RNA,

herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95829] VGAM1948 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1948 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1948 host target RNA into VGAM1948 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95830] VGAM1949 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1949 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1949 host target RNA into VGAM1949 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95831] VGAM1950 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1950 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1950 host target RNA into VGAM1950 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95832] VGAM1951 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1951 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1951 host target RNA into VGAM1951 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95833] VGAM1952 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1952 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1952 host target RNA into VGAM1952 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95834] VGAM1953 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1953 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1953 host target RNA into VGAM1953 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95835] VGAM1954 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1954 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1954 host target RNA into VGAM1954 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95836] It is appreciated that a function of VGR3155 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3155 gene include diagnosis, prevention and treatment of viral infection by

Avian Paramyxovirus 6. Specific functions, and accordingly utilities, of VGR3155 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3155 gene: VGAM1948 host target protein, VGAM1949 host target protein, VGAM1950 host target protein, VGAM1951 host target protein, VGAM1952 host target protein, VGAM1953 host target protein and VGAM1954 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1948, VGAM1949, VGAM1950, VGAM1951, VGAM1952, VGAM1953 and VGAM1954.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3156(VGR3156) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95837] VGR3156 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3156 gene was detected is described hereinabove with reference to Figs. 1-9.

[95838] VGR3156 gene encodes VGR3156 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95839] VGR3156 precursor RNA folds spatially, forming VGR3156 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3156 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3156 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95840] VGR3156 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1955 precursor RNA, VGAM1956 precursor RNA, VGAM1957 precursor RNA, VGAM1958 precursor RNA, VGAM1959 precursor RNA and VGAM1960

precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95841] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1955 RNA, VGAM1956 RNA, VGAM1957 RNA, VGAM1958 RNA, VGAM1959 RNA and VGAM1960 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95842] VGAM1955 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1955 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1955 host target RNA into VGAM1955 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95843] VGAM1956 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1956 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1956 host target RNA into VGAM1956 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95844] VGAM1957 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1957 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1957 host target RNA into

VGAM1957 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95845] VGAM1958 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1958 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1958 host target RNA into VGAM1958 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95846] VGAM1959 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1959 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1959 host target RNA into VGAM1959 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95847] VGAM1960 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1960 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1960 host target RNA into VGAM1960 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95848] It is appreciated that a function of VGR3156 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3156 gene include diagnosis, prevention and treatment of viral infection by Macaca Mulatta Rhadinovirus. Specific functions, and accordingly utilities, of VGR3156 gene correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3156 gene: VGAM1955 host target protein, VGAM1956 host target protein, VGAM1957 host target protein, VGAM1958 host target protein, VGAM1959 host target protein and VGAM1960 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1955, VGAM1956, VGAM1957, VGAM1958, VGAM1959 and VGAM1960.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3157(VGR3157) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95849] VGR3157 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3157 gene was detected is described hereinabove with reference to Figs.

1-9.

[95850] VGR3157 gene encodes VGR3157 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95851] VGR3157 precursor RNA folds spatially, forming VGR3157 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3157 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3157 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95852] VGR3157 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM1961 precursor RNA, VGAM1962 precursor RNA and VGAM1963 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig.

1.

[95853] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1961 RNA, VGAM1962 RNA and VGAM1963 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95854] VGAM1961 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1961 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1961 host target RNA into VGAM1961 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95855] VGAM1962 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1962 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1962 host target RNA into VGAM1962 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95856] VGAM1963 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1963 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1963 host target RNA into VGAM1963 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95857] It is appreciated that a function of VGR3157 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3157 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3157 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3157 gene: VGAM1961 host target protein, VGAM1962 host target protein and VGAM1963 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1961, VGAM1962 and VGAM1963.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3158(VGR3158) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95858] VGR3158 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3158 gene was detected is described hereinabove with reference to Figs. 1-9.

[95859] VGR3158 gene encodes VGR3158 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95860] VGR3158 precursor RNA folds spatially, forming VGR3158 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3158 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3158 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95861] VGR3158 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1964 precursor RNA, VGAM1965 precursor RNA, VGAM1966 precursor RNA, VGAM1967 precursor RNA, VGAM1968 precursor RNA, VGAM1969

precursor RNA, VGAM1970 precursor RNA and VGAM1971 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95862] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1964 RNA, VGAM1965 RNA, VGAM1966 RNA, VGAM1967 RNA, VGAM1968 RNA, VGAM1969 RNA, VGAM1970 RNA and VGAM1971 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95863] VGAM1964 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1964 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1964 host target RNA into

VGAM1964 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95864] VGAM1965 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1965 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1965 host target RNA into VGAM1965 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95865] VGAM1966 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1966 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1966 host target RNA into VGAM1966 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95866] VGAM1967 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1967 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1967 host target RNA into VGAM1967 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95867] VGAM1968 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1968 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1968 host target RNA into VGAM1968 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95868] VGAM1969 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1969 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1969 host target RNA into VGAM1969 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95869] VGAM1970 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1970 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1970 host target RNA into VGAM1970 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95870] VGAM1971 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1971 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1971 host target RNA into VGAM1971 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95871] It is appreciated that a function of VGR3158 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3158 gene include diagnosis, prevention and treatment of viral infection by

Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR3158 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3158 gene: VGAM1964 host target protein, VGAM1965 host target protein, VGAM1966 host target protein, VGAM1967 host target protein, VGAM1968 host target protein, VGAM1969 host target protein, VGAM1970 host target protein and VGAM1971 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1964, VGAM1965, VGAM1966, VGAM1967, VGAM1968, VGAM1969, VGAM1970 and VGAM1971.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3159(VGR3159) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95872] VGR3159 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3159 gene was detected is described hereinabove with reference to Figs. 1-9.

[95873] VGR3159 gene encodes VGR3159 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95874] VGR3159 precursor RNA folds spatially, forming VGR3159 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3159 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3159 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95875] VGR3159 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1972 precursor RNA, VGAM1973 precursor RNA, VGAM1974 precursor RNA, VGAM1975 precursor RNA, VGAM1976 precursor RNA, VGAM1977

precursor RNA and VGAM1978 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95876] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1972 RNA, VGAM1973 RNA, VGAM1974 RNA, VGAM1975 RNA, VGAM1976 RNA, VGAM1977 RNA and VGAM1978 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95877] VGAM1972 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1972 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1972 host target RNA into

VGAM1972 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95878] VGAM1973 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1973 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1973 host target RNA into VGAM1973 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95879] VGAM1974 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1974 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1974 host target RNA into VGAM1974 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95880] VGAM1975 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1975 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1975 host target RNA into VGAM1975 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95881] VGAM1976 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1976 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1976 host target RNA into VGAM1976 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95882] VGAM1977 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1977 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1977 host target RNA into VGAM1977 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95883] VGAM1978 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1978 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1978 host target RNA into VGAM1978 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95884] It is appreciated that a function of VGR3159 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3159 gene include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3159 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3159 gene: VGAM1972 host target protein, VGAM1973 host target protein, VGAM1974 host target protein, VGAM1975 host target protein, VGAM1976 host target protein, VGAM1977 host target protein and VGAM1978 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove

with reference to VGAM1972, VGAM1973, VGAM1974, VGAM1975, VGAM1976, VGAM1977 and VGAM1978.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3160(VGR3160) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95885] VGR3160 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3160 gene was detected is described hereinabove with reference to Figs. 1-9.

[95886] VGR3160 gene encodes VGR3160 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95887] VGR3160 precursor RNA folds spatially, forming VGR3160 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3160 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3160 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95888] VGR3160 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1979 precursor RNA and VGAM1980 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95889] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1979 RNA and VGAM1980 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95890] VGAM1979 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM1979 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1979 host target RNA into VGAM1979 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95891] VGAM1980 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1980 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1980 host target RNA into VGAM1980 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95892] It is appreciated that a function of VGR3160 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3160 gene include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3160 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3160 gene: VGAM1979 host target protein and VGAM1980 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1979 and VGAM1980.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3161(VGR3161) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95893] VGR3161 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3161 gene was detected is described hereinabove with reference to Figs. 1-9.

[95894] VGR3161 gene encodes VGR3161 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95895] VGR3161 precursor RNA folds spatially, forming VGR3161 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3161 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3161 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95896] VGR3161 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM1981 precursor RNA, VGAM1982 precursor RNA, VGAM1983 precursor RNA, VGAM1984 precursor RNA, VGAM1985 precursor RNA, VGAM1986 precursor RNA and VGAM1987 precursor RNA, herein

schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95897] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1981 RNA, VGAM1982 RNA, VGAM1983 RNA, VGAM1984 RNA, VGAM1985 RNA, VGAM1986 RNA and VGAM1987 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95898] VGAM1981 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1981 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1981 host target RNA into VGAM1981 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95899] VGAM1982 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1982 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1982 host target RNA into VGAM1982 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95900] VGAM1983 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1983 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1983 host target RNA into

VGAM1983 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95901] VGAM1984 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1984 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1984 host target RNA into VGAM1984 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95902] VGAM1985 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1985 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM1985 host target RNA into VGAM1985 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95903] VGAM1986 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1986 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1986 host target RNA into VGAM1986 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95904] VGAM1987 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1987 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1987 host target RNA into VGAM1987 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95905] It is appreciated that a function of VGR3161 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3161 gene include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGR3161 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3161 gene: VGAM1981 host target protein, VGAM1982 host target protein, VGAM1983 host target protein, VGAM1984 host target protein, VGAM1985 host target protein, VGAM1986 host target protein and VGAM1987 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1981, VGAM1982, VGAM1983, VGAM1984,

VGAM1985, VGAM1986 and VGAM1987.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3162(VGR3162) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95906] VGR3162 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3162 gene was detected is described hereinabove with reference to Figs. 1-9.

[95907] VGR3162 gene encodes VGR3162 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95908] VGR3162 precursor RNA folds spatially, forming VGR3162 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3162 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3162 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95909] VGR3162 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM1988 precursor RNA and VGAM1989 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95910] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1988 RNA and VGAM1989 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95911] VGAM1988 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1988 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1988 host target RNA into VGAM1988 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95912] VGAM1989 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1989 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1989 host target RNA into VGAM1989 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95913] It is appreciated that a function of VGR3162 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3162 gene include

diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGR3162 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3162 gene: VGAM1988 host target protein and VGAM1989 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1988 and VGAM1989.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3163(VGR3163) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95914] VGR3163 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3163 gene was detected is described hereinabove with reference to Figs. 1-9.

[95915] VGR3163 gene encodes VGR3163 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95916] VGR3163 precursor RNA folds spatially, forming VGR3163 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3163 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3163 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95917] VGR3163 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM1990 precursor RNA, VGAM1991 precursor RNA, VGAM1992 precursor RNA, VGAM1993 precursor RNA, VGAM1994 precursor RNA, VGAM1995 precursor RNA, VGAM1996 precursor RNA and VGAM1997 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95918] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1990 RNA, VGAM1991 RNA, VGAM1992 RNA, VGAM1993 RNA, VGAM1994 RNA, VGAM1995 RNA, VGAM1996 RNA and VGAM1997 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95919] VGAM1990 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1990 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1990 host target RNA into VGAM1990 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95920] VGAM1991 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1991 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1991 host target RNA into VGAM1991 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95921] VGAM1992 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1992 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1992 host target RNA into VGAM1992 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95922] VGAM1993 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1993 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1993 host target RNA into VGAM1993 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95923] VGAM1994 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1994 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1994 host target RNA into VGAM1994 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95924] VGAM1995 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1995 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1995 host target RNA into VGAM1995 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95925] VGAM1996 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1996 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1996 host target RNA into VGAM1996 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95926] VGAM1997 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1997 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1997 host target RNA into VGAM1997 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95927] It is appreciated that a function of VGR3163 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3163 gene include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGR3163 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like`

cluster of VGR3163 gene: VGAM1990 host target protein, VGAM1991 host target protein, VGAM1992 host target protein, VGAM1993 host target protein, VGAM1994 host target protein, VGAM1995 host target protein, VGAM1996 host target protein and VGAM1997 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM1990, VGAM1991, VGAM1992, VGAM1993, VGAM1994, VGAM1995, VGAM1996 and VGAM1997.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3164(VGR3164) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95928] VGR3164 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3164 gene was detected is described hereinabove with reference to Figs. 1-9.

[95929] VGR3164 gene encodes VGR3164 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95930] VGR3164 precursor RNA folds spatially, forming VGR3164 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3164 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3164 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95931] VGR3164 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM1998 precursor RNA, VGAM1999 precursor RNA, VGAM2000 precursor RNA, VGAM2001 precursor RNA, VGAM2002 precursor RNA and VGAM2003 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM

FOLDED PRECURSOR RNA of Fig. 1.

[95932] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM1998 RNA, VGAM1999 RNA, VGAM2000 RNA, VGAM2001 RNA, VGAM2002 RNA and VGAM2003 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95933] VGAM1998 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM1998 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1998 host target RNA into VGAM1998 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95934] VGAM1999 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM1999 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM1999 host target RNA into VGAM1999 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95935] VGAM2000 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2000 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2000 host target RNA into VGAM2000 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95936] VGAM2001 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2001 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2001 host target RNA into VGAM2001 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95937] VGAM2002 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2002 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2002 host target RNA into VGAM2002 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95938] VGAM2003 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2003 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2003 host target RNA into VGAM2003 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95939] It is appreciated that a function of VGR3164 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3164 gene include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGR3164 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3164 gene: VGAM1998 host target protein, VGAM1999 host target protein, VGAM2000 host target

protein, VGAM2001 host target protein, VGAM2002 host target protein and VGAM2003 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM1998, VGAM1999, VGAM2000, VGAM2001, VGAM2002 and VGAM2003.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3165(VGR3165) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95940] VGR3165 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3165 gene was detected is described hereinabove with reference to Figs. 1-9.

[95941] VGR3165 gene encodes VGR3165 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95942] VGR3165 precursor RNA folds spatially, forming VGR3165

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3165 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3165 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95943] VGR3165 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2004 precursor RNA, VGAM2005 precursor RNA and VGAM2006 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95944] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2004 RNA, VGAM2005 RNA and VGAM2006 RNA, herein

schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95945] VGAM2004 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2004 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2004 host target RNA into VGAM2004 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95946] VGAM2005 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2005 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2005 host target RNA into VGAM2005 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95947] VGAM2006 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2006 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2006 host target RNA into VGAM2006 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95948] It is appreciated that a function of VGR3165 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3165 gene include diagnosis, prevention and treatment of viral infection by Chimpanzee Cytomegalovirus. Specific functions, and accordingly utilities, of VGR3165 gene correlate with, and

may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3165 gene: VGAM2004 host target protein, VGAM2005 host target protein and VGAM2006 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2004, VGAM2005 and VGAM2006.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3166(VGR3166) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95949] VGR3166 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3166 gene was detected is described hereinabove with reference to Figs. 1-9.

[95950] VGR3166 gene encodes VGR3166 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95951] VGR3166 precursor RNA folds spatially, forming VGR3166 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3166 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3166 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95952] VGR3166 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2007 precursor RNA, VGAM2008 precursor RNA, VGAM2009 precursor RNA, VGAM2010 precursor RNA, VGAM2011 precursor RNA, VGAM2012 precursor RNA, VGAM2013 precursor RNA and VGAM2014 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM

FOLDED PRECURSOR RNA of Fig. 1.

[95953] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2007 RNA, VGAM2008 RNA, VGAM2009 RNA, VGAM2010 RNA, VGAM2011 RNA, VGAM2012 RNA, VGAM2013 RNA and VGAM2014 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95954] VGAM2007 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2007 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2007 host target RNA into VGAM2007 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95955] VGAM2008 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2008 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2008 host target RNA into VGAM2008 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95956] VGAM2009 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2009 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2009 host target RNA into VGAM2009 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95957] VGAM2010 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2010 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2010 host target RNA into VGAM2010 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95958] VGAM2011 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2011 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2011 host target RNA into VGAM2011 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95959] VGAM2012 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2012 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2012 host target RNA into VGAM2012 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95960] VGAM2013 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2013 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2013 host target RNA into VGAM2013 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95961] VGAM2014 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2014 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2014 host target RNA into VGAM2014 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95962] It is appreciated that a function of VGR3166 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3166 gene include diagnosis, prevention and treatment of viral infection by Reston Ebola Virus (REBOV). Specific functions, and accordingly utilities, of VGR3166 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3166 gene: VGAM2007

host target protein, VGAM2008 host target protein, VGAM2009 host target protein, VGAM2010 host target protein, VGAM2011 host target protein, VGAM2012 host target protein, VGAM2013 host target protein and VGAM2014 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2007, VGAM2008, VGAM2009, VGAM2010, VGAM2011, VGAM2012, VGAM2013 and VGAM2014.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3167(VGR3167) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95963] VGR3167 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3167 gene was detected is described hereinabove with reference to Figs. 1-9.

[95964] VGR3167 gene encodes VGR3167 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95965] VGR3167 precursor RNA folds spatially, forming VGR3167 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3167 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3167 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95966] VGR3167 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2015 precursor RNA, VGAM2016 precursor RNA, VGAM2017 precursor RNA, VGAM2018 precursor RNA, VGAM2019 precursor RNA, VGAM2020 precursor RNA, VGAM2021 precursor RNA and VGAM2022 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95967] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2015 RNA, VGAM2016 RNA, VGAM2017 RNA, VGAM2018 RNA, VGAM2019 RNA, VGAM2020 RNA, VGAM2021 RNA and VGAM2022 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95968] VGAM2015 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2015 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2015 host target RNA into VGAM2015 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95969] VGAM2016 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2016 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2016 host target RNA into VGAM2016 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95970] VGAM2017 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2017 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2017 host target RNA into VGAM2017 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95971] VGAM2018 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2018 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2018 host target RNA into VGAM2018 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95972] VGAM2019 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2019 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2019 host target RNA into VGAM2019 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95973] VGAM2020 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2020 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2020 host target RNA into VGAM2020 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95974] VGAM2021 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2021 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2021 host target RNA into VGAM2021 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95975] VGAM2022 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2022 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2022 host target RNA into VGAM2022 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95976] It is appreciated that a function of VGR3167 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3167 gene include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGR3167 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR3167 gene: VGAM2015 host target protein, VGAM2016 host target protein, VGAM2017 host target protein, VGAM2018 host target protein, VGAM2019 host target protein, VGAM2020 host target protein, VGAM2021 host target protein and VGAM2022 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2015, VGAM2016, VGAM2017, VGAM2018, VGAM2019, VGAM2020, VGAM2021 and VGAM2022.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3168(VGR3168) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95977] VGR3168 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3168 gene was detected is described hereinabove with reference to Figs.

1-9.

[95978] VGR3168 gene encodes VGR3168 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95979] VGR3168 precursor RNA folds spatially, forming VGR3168 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3168 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3168 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95980] VGR3168 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2023 precursor RNA, VGAM2024 precursor RNA, VGAM2025 precursor RNA, VGAM2026 precursor RNA, VGAM2027 precursor RNA, VGAM2028 precursor RNA, VGAM2029 precursor RNA and VGAM2030 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95981] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2023 RNA, VGAM2024 RNA, VGAM2025 RNA, VGAM2026 RNA, VGAM2027 RNA, VGAM2028 RNA, VGAM2029 RNA and VGAM2030 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95982] VGAM2023 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2023 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2023 host target RNA into VGAM2023 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95983] VGAM2024 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2024 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2024 host target RNA into VGAM2024 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95984] VGAM2025 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2025 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2025 host target RNA into VGAM2025 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95985] VGAM2026 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2026 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2026 host target RNA into VGAM2026 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95986] VGAM2027 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2027 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2027 host target RNA into VGAM2027 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95987] VGAM2028 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2028 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2028 host target RNA into VGAM2028 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95988] VGAM2029 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2029 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2029 host target RNA into

VGAM2029 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95989] VGAM2030 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2030 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2030 host target RNA into VGAM2030 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95990] It is appreciated that a function of VGR3168 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3168 gene include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGR3168 gene correlate with, and may be deduced from, the identity of the host target genes,

which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3168 gene: VGAM2023 host target protein, VGAM2024 host target protein, VGAM2025 host target protein, VGAM2026 host target protein, VGAM2027 host target protein, VGAM2028 host target protein, VGAM2029 host target protein and VGAM2030 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2023, VGAM2024, VGAM2025, VGAM2026, VGAM2027, VGAM2028, VGAM2029 and VGAM2030.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3169(VGR3169) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[95991] VGR3169 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3169 gene was detected is described hereinabove with reference to Figs.

1-9.

[95992] VGR3169 gene encodes VGR3169 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[95993] VGR3169 precursor RNA folds spatially, forming VGR3169 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3169 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3169 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[95994] VGR3169 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2031 precursor RNA, VGAM2032 precursor RNA, VGAM2033 precursor RNA, VGAM2034 precursor RNA and VGAM2035 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment,

corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[95995] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2031 RNA, VGAM2032 RNA, VGAM2033 RNA, VGAM2034 RNA and VGAM2035 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[95996] VGAM2031 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2031 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2031 host target RNA into VGAM2031 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95997] VGAM2032 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2032 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2032 host target RNA into VGAM2032 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95998] VGAM2033 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2033 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2033 host target RNA into VGAM2033 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[95999] VGAM2034 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2034 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2034 host target RNA into VGAM2034 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96000] VGAM2035 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2035 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2035 host target RNA into VGAM2035 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96001] It is appreciated that a function of VGR3169 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3169 gene include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGR3169 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3169 gene: VGAM2031 host target protein, VGAM2032 host target protein, VGAM2033 host target protein, VGAM2034 host target protein and VGAM2035 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2031, VGAM2032, VGAM2033, VGAM2034 and VGAM2035.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3170(VGR3170) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one

host target gene, the function and utility of which at least one host target gene is known in the art.

[96002] VGR3170 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3170 gene was detected is described hereinabove with reference to Figs. 1-9.

[96003] VGR3170 gene encodes VGR3170 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96004] VGR3170 precursor RNA folds spatially, forming VGR3170 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3170 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3170 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96005] VGR3170 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM

precursor RNAs, VGAM2036 precursor RNA, VGAM2037 precursor RNA, VGAM2038 precursor RNA, VGAM2039 precursor RNA, VGAM2040 precursor RNA and VGAM2041 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96006] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2036 RNA, VGAM2037 RNA, VGAM2038 RNA, VGAM2039 RNA, VGAM2040 RNA and VGAM2041 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96007] VGAM2036 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2036 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2036 host target RNA into VGAM2036 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96008] VGAM2037 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2037 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2037 host target RNA into VGAM2037 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96009] VGAM2038 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2038 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2038 host target RNA into VGAM2038 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96010] VGAM2039 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2039 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2039 host target RNA into VGAM2039 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96011] VGAM2040 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2040 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2040 host target RNA into VGAM2040 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96012] VGAM2041 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2041 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2041 host target RNA into VGAM2041 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96013] It is appreciated that a function of VGR3170 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3170 gene include

diagnosis, prevention and treatment of viral infection by Marburg Virus. Specific functions, and accordingly utilities, of VGR3170 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3170 gene: VGAM2036 host target protein, VGAM2037 host target protein, VGAM2038 host target protein, VGAM2039 host target protein, VGAM2040 host target protein and VGAM2041 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2036, VGAM2037, VGAM2038, VGAM2039, VGAM2040 and VGAM2041.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3171(VGR3171) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96014] VGR3171 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3171 gene was detected is described hereinabove with reference to Figs. 1-9.

[96015] VGR3171 gene encodes VGR3171 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96016] VGR3171 precursor RNA folds spatially, forming VGR3171 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3171 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3171 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96017] VGR3171 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2042 precursor RNA, VGAM2043 precursor RNA, VGAM2044 precursor RNA, VGAM2045 precursor RNA, VGAM2046 precursor RNA, VGAM2047

precursor RNA, VGAM2048 precursor RNA and VGAM2049 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96018] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2042 RNA, VGAM2043 RNA, VGAM2044 RNA, VGAM2045 RNA, VGAM2046 RNA, VGAM2047 RNA, VGAM2048 RNA and VGAM2049 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96019] VGAM2042 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2042 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2042 host target RNA into

VGAM2042 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96020] VGAM2043 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2043 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2043 host target RNA into VGAM2043 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96021] VGAM2044 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2044 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2044 host target RNA into VGAM2044 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96022] VGAM2045 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2045 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2045 host target RNA into VGAM2045 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96023] VGAM2046 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2046 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2046 host target RNA into VGAM2046 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96024] VGAM2047 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2047 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2047 host target RNA into VGAM2047 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96025] VGAM2048 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2048 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2048 host target RNA into VGAM2048 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96026] VGAM2049 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2049 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2049 host target RNA into VGAM2049 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96027] It is appreciated that a function of VGR3171 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3171 gene include diagnosis, prevention and treatment of viral infection by

Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGR3171 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3171 gene: VGAM2042 host target protein, VGAM2043 host target protein, VGAM2044 host target protein, VGAM2045 host target protein, VGAM2046 host target protein, VGAM2047 host target protein, VGAM2048 host target protein and VGAM2049 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2042, VGAM2043, VGAM2044, VGAM2045, VGAM2046, VGAM2047, VGAM2048 and VGAM2049.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3172(VGR3172) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96028] VGR3172 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3172 gene was detected is described hereinabove with reference to Figs. 1-9.

[96029] VGR3172 gene encodes VGR3172 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96030] VGR3172 precursor RNA folds spatially, forming VGR3172 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3172 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3172 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96031] VGR3172 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2050 precursor RNA, VGAM2051 precursor RNA, VGAM2052 precursor RNA and VGAM2053 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96032] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2050 RNA, VGAM2051 RNA, VGAM2052 RNA and VGAM2053 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96033] VGAM2050 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2050 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2050 host target RNA into VGAM2050 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96034] VGAM2051 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2051 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2051 host target RNA into VGAM2051 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96035] VGAM2052 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2052 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2052 host target RNA into VGAM2052 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96036] VGAM2053 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2053 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2053 host target RNA into VGAM2053 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96037] It is appreciated that a function of VGR3172 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3172 gene include diagnosis, prevention and treatment of viral infection by Ovine Adenovirus A. Specific functions, and accordingly utilities, of VGR3172 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3172 gene: VGAM2050 host

target protein, VGAM2051 host target protein, VGAM2052 host target protein and VGAM2053 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM2050, VGAM2051, VGAM2052 and VGAM2053.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3173(VGR3173) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96038] VGR3173 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3173 gene was detected is described hereinabove with reference to Figs. 1-9.

[96039] VGR3173 gene encodes VGR3173 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[96040] VGR3173 precursor RNA folds spatially, forming VGR3173

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3173 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3173 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96041] VGR3173 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2054 precursor RNA, VGAM2055 precursor RNA, VGAM2056 precursor RNA, VGAM2057 precursor RNA, VGAM2058 precursor RNA, VGAM2059 precursor RNA, VGAM2060 precursor RNA and VGAM2061 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96042] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM2054 RNA, VGAM2055 RNA, VGAM2056 RNA, VGAM2057 RNA, VGAM2058 RNA, VGAM2059 RNA, VGAM2060 RNA and VGAM2061 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96043] VGAM2054 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2054 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2054 host target RNA into VGAM2054 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96044] VGAM2055 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2055 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2055 host target RNA into VGAM2055 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96045] VGAM2056 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2056 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2056 host target RNA into VGAM2056 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96046] VGAM2057 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2057 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2057 host target RNA into VGAM2057 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96047] VGAM2058 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2058 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2058 host target RNA into VGAM2058 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96048] VGAM2059 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2059 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2059 host target RNA into VGAM2059 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96049] VGAM2060 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2060 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2060 host target RNA into VGAM2060 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96050] VGAM2061 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2061 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2061 host target RNA into VGAM2061 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96051] It is appreciated that a function of VGR3173 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3173 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR3173 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3173 gene: VGAM2054 host target protein, VGAM2055 host target protein, VGAM2056 host target protein, VGAM2057 host target protein, VGAM2058 host target protein, VGAM2059 host target

protein, VGAM2060 host target protein and VGAM2061 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2054, VGAM2055, VGAM2056, VGAM2057, VGAM2058, VGAM2059, VGAM2060 and VGAM2061.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3174(VGR3174) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96052] VGR3174 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3174 gene was detected is described hereinabove with reference to Figs. 1-9.

[96053] VGR3174 gene encodes VGR3174 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96054] VGR3174 precursor RNA folds spatially, forming VGR3174

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3174 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3174 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96055] VGR3174 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2062 precursor RNA, VGAM2063 precursor RNA, VGAM2064 precursor RNA, VGAM2065 precursor RNA, VGAM2066 precursor RNA and VGAM2067 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96056] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2062

RNA, VGAM2063 RNA, VGAM2064 RNA, VGAM2065 RNA, VGAM2066 RNA and VGAM2067 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96057] VGAM2062 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2062 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2062 host target RNA into VGAM2062 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96058] VGAM2063 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2063 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2063 host target RNA into VGAM2063 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96059] VGAM2064 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2064 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2064 host target RNA into VGAM2064 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96060] VGAM2065 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2065 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2065 host target RNA into VGAM2065 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96061] VGAM2066 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2066 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2066 host target RNA into VGAM2066 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96062] VGAM2067 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2067 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2067 host target RNA into VGAM2067 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96063] It is appreciated that a function of VGR3174 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3174 gene include diagnosis, prevention and treatment of viral infection by Peanut Bud Necrosis Virus. Specific functions, and accordingly utilities, of VGR3174 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3174 gene: VGAM2062 host target protein, VGAM2063 host target protein, VGAM2064 host target protein, VGAM2065 host target protein, VGAM2066 host target protein and VGAM2067 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN.

The function of these host target genes is elaborated hereinabove with reference to VGAM2062, VGAM2063, VGAM2064, VGAM2065, VGAM2066 and VGAM2067.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3175(VGR3175) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96064] VGR3175 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3175 gene was detected is described hereinabove with reference to Figs. 1-9.

[96065] VGR3175 gene encodes VGR3175 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96066] VGR3175 precursor RNA folds spatially, forming VGR3175 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3175 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3175 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96067] VGR3175 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2068 precursor RNA, VGAM2069 precursor RNA, VGAM2070 precursor RNA, VGAM2071 precursor RNA, VGAM2072 precursor RNA, VGAM2073 precursor RNA and VGAM2074 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96068] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2068 RNA, VGAM2069 RNA, VGAM2070 RNA, VGAM2071 RNA, VGAM2072 RNA, VGAM2073 RNA and VGAM2074 RNA,

herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96069] VGAM2068 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2068 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2068 host target RNA into VGAM2068 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96070] VGAM2069 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2069 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2069 host target RNA into VGAM2069 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96071] VGAM2070 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2070 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2070 host target RNA into VGAM2070 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96072] VGAM2071 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2071 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2071 host target RNA into VGAM2071 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96073] VGAM2072 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2072 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2072 host target RNA into VGAM2072 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96074] VGAM2073 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2073 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2073 host target RNA into VGAM2073 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96075] VGAM2074 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2074 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2074 host target RNA into VGAM2074 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96076] It is appreciated that a function of VGR3175 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3175 gene include diagnosis, prevention and treatment of viral infection by

Monkeypox Virus. Specific functions, and accordingly utilities, of VGR3175 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3175 gene: VGAM2068 host target protein, VGAM2069 host target protein, VGAM2070 host target protein, VGAM2071 host target protein, VGAM2072 host target protein, VGAM2073 host target protein and VGAM2074 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2068, VGAM2069, VGAM2070, VGAM2071, VGAM2072, VGAM2073 and VGAM2074.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3176(VGR3176) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96077] VGR3176 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3176 gene was detected is described hereinabove with reference to Figs. 1-9.

[96078] VGR3176 gene encodes VGR3176 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96079] VGR3176 precursor RNA folds spatially, forming VGR3176 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3176 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3176 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96080] VGR3176 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2075 precursor RNA, VGAM2076 precursor RNA, VGAM2077 precursor RNA, VGAM2078 precursor RNA, VGAM2079 precursor RNA, VGAM2080

precursor RNA, VGAM2081 precursor RNA and VGAM2082 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96081] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2075 RNA, VGAM2076 RNA, VGAM2077 RNA, VGAM2078 RNA, VGAM2079 RNA, VGAM2080 RNA, VGAM2081 RNA and VGAM2082 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96082] VGAM2075 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2075 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2075 host target RNA into

VGAM2075 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96083] VGAM2076 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2076 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2076 host target RNA into VGAM2076 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96084] VGAM2077 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2077 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2077 host target RNA into VGAM2077 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96085] VGAM2078 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2078 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2078 host target RNA into VGAM2078 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96086] VGAM2079 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2079 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2079 host target RNA into VGAM2079 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96087] VGAM2080 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2080 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2080 host target RNA into VGAM2080 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96088] VGAM2081 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2081 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2081 host target RNA into VGAM2081 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96089] VGAM2082 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2082 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2082 host target RNA into VGAM2082 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96090] It is appreciated that a function of VGR3176 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3176 gene include diagnosis, prevention and treatment of viral infection by

Variola Virus. Specific functions, and accordingly utilities, of VGR3176 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3176 gene: VGAM2075 host target protein, VGAM2076 host target protein, VGAM2077 host target protein, VGAM2078 host target protein, VGAM2079 host target protein, VGAM2080 host target protein, VGAM2081 host target protein and VGAM2082 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2075, VGAM2076, VGAM2077, VGAM2078, VGAM2079, VGAM2080, VGAM2081 and VGAM2082.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3177(VGR3177) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96091] VGR3177 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3177 gene was detected is described hereinabove with reference to Figs. 1-9.

[96092] VGR3177 gene encodes VGR3177 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96093] VGR3177 precursor RNA folds spatially, forming VGR3177 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3177 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3177 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96094] VGR3177 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2083 precursor RNA and VGAM2084 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3

FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96095] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2083 RNA and VGAM2084 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96096] VGAM2083 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2083 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2083 host target RNA into VGAM2083 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96097] VGAM2084 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2084 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2084 host target RNA into VGAM2084 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96098] It is appreciated that a function of VGR3177 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3177 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3177 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3177 gene: VGAM2083 host target protein and VGAM2084 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The func-

tion of these host target genes is elaborated hereinabove with reference to VGAM2083 and VGAM2084.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3178(VGR3178) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96099] VGR3178 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3178 gene was detected is described hereinabove with reference to Figs. 1-9.

[96100] VGR3178 gene encodes VGR3178 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96101] VGR3178 precursor RNA folds spatially, forming VGR3178 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3178 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3178 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96102] VGR3178 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2085 precursor RNA, VGAM2086 precursor RNA, VGAM2087 precursor RNA, VGAM2088 precursor RNA, VGAM2089 precursor RNA, VGAM2090 precursor RNA, VGAM2091 precursor RNA and VGAM2092 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96103] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2085 RNA, VGAM2086 RNA, VGAM2087 RNA, VGAM2088 RNA, VGAM2089 RNA, VGAM2090 RNA, VGAM2091 RNA and VGAM2092 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96104] VGAM2085 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2085 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2085 host target RNA into VGAM2085 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96105] VGAM2086 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2086 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2086 host target RNA into

VGAM2086 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96106] VGAM2087 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2087 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2087 host target RNA into VGAM2087 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96107] VGAM2088 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2088 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2088 host target RNA into VGAM2088 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96108] VGAM2089 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2089 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2089 host target RNA into VGAM2089 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96109] VGAM2090 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2090 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2090 host target RNA into VGAM2090 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96110] VGAM2091 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2091 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2091 host target RNA into VGAM2091 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96111] VGAM2092 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2092 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2092 host target RNA into VGAM2092 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96112] It is appreciated that a function of VGR3178 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3178 gene include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGR3178 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3178 gene: VGAM2085 host target protein, VGAM2086 host target protein, VGAM2087 host target protein, VGAM2088 host target protein, VGAM2089 host target protein, VGAM2090 host target protein, VGAM2091 host target protein and VGAM2092 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes

is elaborated hereinabove with reference to VGAM2085, VGAM2086, VGAM2087, VGAM2088, VGAM2089, VGAM2090, VGAM2091 and VGAM2092.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3179(VGR3179) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96113] VGR3179 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3179 gene was detected is described hereinabove with reference to Figs. 1-9.

[96114] VGR3179 gene encodes VGR3179 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96115] VGR3179 precursor RNA folds spatially, forming VGR3179 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3179 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3179 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96116] VGR3179 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2093 precursor RNA, VGAM2094 precursor RNA, VGAM2095 precursor RNA, VGAM2096 precursor RNA, VGAM2097 precursor RNA, VGAM2098 precursor RNA, VGAM2099 precursor RNA and VGAM2100 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96117] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2093 RNA, VGAM2094 RNA, VGAM2095 RNA, VGAM2096 RNA, VGAM2097 RNA, VGAM2098 RNA, VGAM2099 RNA and VGAM2100 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96118] VGAM2093 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2093 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2093 host target RNA into VGAM2093 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96119] VGAM2094 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2094 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2094 host target RNA into

VGAM2094 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96120] VGAM2095 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2095 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2095 host target RNA into VGAM2095 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96121] VGAM2096 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2096 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2096 host target RNA into VGAM2096 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96122] VGAM2097 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2097 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2097 host target RNA into VGAM2097 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96123] VGAM2098 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2098 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2098 host target RNA into VGAM2098 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96124] VGAM2099 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2099 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2099 host target RNA into VGAM2099 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96125] VGAM2100 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2100 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2100 host target RNA into VGAM2100 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96126] It is appreciated that a function of VGR3179 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3179 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3179 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3179 gene: VGAM2093 host target protein, VGAM2094 host target protein, VGAM2095 host target protein, VGAM2096 host target protein, VGAM2097 host target protein, VGAM2098 host target protein, VGAM2099 host target protein and VGAM2100 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes

is elaborated hereinabove with reference to VGAM2093, VGAM2094, VGAM2095, VGAM2096, VGAM2097, VGAM2098, VGAM2099 and VGAM2100.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3180(VGR3180) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96127] VGR3180 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3180 gene was detected is described hereinabove with reference to Figs. 1-9.

[96128] VGR3180 gene encodes VGR3180 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96129] VGR3180 precursor RNA folds spatially, forming VGR3180 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3180 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3180 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96130] VGR3180 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2101 precursor RNA, VGAM2102 precursor RNA, VGAM2103 precursor RNA and VGAM2104 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96131] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2101 RNA, VGAM2102 RNA, VGAM2103 RNA and VGAM2104 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96132] VGAM2101 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2101 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2101 host target RNA into VGAM2101 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96133] VGAM2102 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2102 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2102 host target RNA into VGAM2102 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96134] VGAM2103 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2103 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2103 host target RNA into VGAM2103 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96135] VGAM2104 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2104 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2104 host target RNA into VGAM2104 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96136] It is appreciated that a function of VGR3180 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3180 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3180 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3180 gene: VGAM2101 host target protein, VGAM2102 host target protein, VGAM2103 host target protein and VGAM2104 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2101, VGAM2102, VGAM2103 and VGAM2104.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3181(VGR3181) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one

host target gene, the function and utility of which at least one host target gene is known in the art.

[96137] VGR3181 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3181 gene was detected is described hereinabove with reference to Figs. 1-9.

[96138] VGR3181 gene encodes VGR3181 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96139] VGR3181 precursor RNA folds spatially, forming VGR3181 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3181 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3181 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96140] VGR3181 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM

precursor RNAs, VGAM2105 precursor RNA, VGAM2106 precursor RNA, VGAM2107 precursor RNA, VGAM2108 precursor RNA, VGAM2109 precursor RNA, VGAM2110 precursor RNA and VGAM2111 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96141] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2105 RNA, VGAM2106 RNA, VGAM2107 RNA, VGAM2108 RNA, VGAM2109 RNA, VGAM2110 RNA and VGAM2111 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96142] VGAM2105 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2105 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2105 host target RNA into VGAM2105 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96143] VGAM2106 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2106 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2106 host target RNA into VGAM2106 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96144] VGAM2107 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2107 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2107 host target RNA into VGAM2107 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96145] VGAM2108 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2108 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2108 host target RNA into VGAM2108 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96146] VGAM2109 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2109 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2109 host target RNA into VGAM2109 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96147] VGAM2110 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2110 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2110 host target RNA into VGAM2110 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96148] VGAM2111 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2111 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2111 host target RNA into VGAM2111 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96149] It is appreciated that a function of VGR3181 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3181 gene include diagnosis, prevention and treatment of viral infection by Grapevine Chrome Mosaic Virus. Specific functions, and accordingly utilities, of VGR3181 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3181 gene: VGAM2105 host target protein, VGAM2106 host target protein, VGAM2107 host target protein, VGAM2108 host target protein, VGAM2109 host target protein, VGAM2110 host target protein and VGAM2111 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2105, VGAM2106, VGAM2107, VGAM2108, VGAM2109, VGAM2110 and VGAM2111.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3182(VGR3182) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96150] VGR3182 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3182 gene was detected is described hereinabove with reference to Figs. 1-9.

[96151] VGR3182 gene encodes VGR3182 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96152] VGR3182 precursor RNA folds spatially, forming VGR3182 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3182 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3182 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96153] VGR3182 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2112 precursor RNA and VGAM2113 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96154] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2112 RNA and VGAM2113 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96155] VGAM2112 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2112 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2112 host target RNA into VGAM2112 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96156] VGAM2113 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2113 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2113 host target RNA into VGAM2113 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96157] It is appreciated that a function of VGR3182 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3182 gene include diagnosis, prevention and treatment of viral infection by Grapevine Chrome Mosaic Virus. Specific functions, and accordingly utilities, of VGR3182 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3182 gene: VGAM2112 host target protein and VGAM2113 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2112 and VGAM2113.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3183(VGR3183) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[96158] VGR3183 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3183 gene was detected is described hereinabove with reference to Figs. 1-9.

[96159] VGR3183 gene encodes VGR3183 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96160] VGR3183 precursor RNA folds spatially, forming VGR3183 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3183 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3183 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96161] VGR3183 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2114 precursor RNA, VGAM2115

precursor RNA, VGAM2116 precursor RNA, VGAM2117 precursor RNA, VGAM2118 precursor RNA, VGAM2119 precursor RNA, VGAM2120 precursor RNA and VGAM2121 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96162] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2114 RNA, VGAM2115 RNA, VGAM2116 RNA, VGAM2117 RNA, VGAM2118 RNA, VGAM2119 RNA, VGAM2120 RNA and VGAM2121 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96163] VGAM2114 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2114 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2114 host target RNA into VGAM2114 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96164] VGAM2115 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2115 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2115 host target RNA into VGAM2115 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96165] VGAM2116 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2116 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2116 host target RNA into VGAM2116 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96166] VGAM2117 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2117 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2117 host target RNA into VGAM2117 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96167] VGAM2118 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2118 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2118 host target RNA into VGAM2118 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96168] VGAM2119 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2119 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2119 host target RNA into VGAM2119 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96169] VGAM2120 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2120 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2120 host target RNA into VGAM2120 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96170] VGAM2121 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2121 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2121 host target RNA into VGAM2121 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96171] It is appreciated that a function of VGR3183 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3183 gene include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGR3183 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3183 gene: VGAM2114 host target protein, VGAM2115 host target protein, VGAM2116 host target protein, VGAM2117 host target protein, VGAM2118 host target protein, VGAM2119 host target protein, VGAM2120 host target protein and VGAM2121 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2114, VGAM2115, VGAM2116, VGAM2117, VGAM2118, VGAM2119, VGAM2120 and VGAM2121.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3184(VGR3184) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[96172] VGR3184 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3184 gene was detected is described hereinabove with reference to Figs. 1-9.

[96173] VGR3184 gene encodes VGR3184 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96174] VGR3184 precursor RNA folds spatially, forming VGR3184 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3184 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3184 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96175] VGR3184 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2122 precursor RNA, VGAM2123

precursor RNA and VGAM2124 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96176] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2122 RNA, VGAM2123 RNA and VGAM2124 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96177] VGAM2122 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2122 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2122 host target RNA into VGAM2122 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96178] VGAM2123 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2123 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2123 host target RNA into VGAM2123 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96179] VGAM2124 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2124 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2124 host target RNA into

VGAM2124 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96180] It is appreciated that a function of VGR3184 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3184 gene include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGR3184 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3184 gene: VGAM2122 host target protein, VGAM2123 host target protein and VGAM2124 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2122, VGAM2123 and VGAM2124.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3185(VGR3185) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes,

each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96181] VGR3185 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3185 gene was detected is described hereinabove with reference to Figs. 1-9.

[96182] VGR3185 gene encodes VGR3185 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96183] VGR3185 precursor RNA folds spatially, forming VGR3185 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3185 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3185 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96184] VGR3185 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2125 precursor RNA, VGAM2126 precursor RNA, VGAM2127 precursor RNA, VGAM2128 precursor RNA, VGAM2129 precursor RNA, VGAM2130 precursor RNA, VGAM2131 precursor RNA and VGAM2132 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96185] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2125 RNA, VGAM2126 RNA, VGAM2127 RNA, VGAM2128 RNA, VGAM2129 RNA, VGAM2130 RNA, VGAM2131 RNA and VGAM2132 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96186] VGAM2125 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2125 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2125 host target RNA into VGAM2125 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96187] VGAM2126 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2126 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2126 host target RNA into VGAM2126 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96188] VGAM2127 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2127 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2127 host target RNA into VGAM2127 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96189] VGAM2128 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2128 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2128 host target RNA into VGAM2128 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96190] VGAM2129 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2129 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2129 host target RNA into VGAM2129 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96191] VGAM2130 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2130 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2130 host target RNA into VGAM2130 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96192] VGAM2131 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2131 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2131 host target RNA into VGAM2131 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96193] VGAM2132 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2132 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2132 host target RNA into VGAM2132 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96194] It is appreciated that a function of VGR3185 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3185 gene include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGR3185 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3185 gene: VGAM2125 host target protein, VGAM2126 host target protein, VGAM2127 host target protein, VGAM2128 host target protein, VGAM2129 host target protein, VGAM2130 host target protein, VGAM2131 host target protein and VGAM2132 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2125, VGAM2126, VGAM2127, VGAM2128, VGAM2129, VGAM2130, VGAM2131 and VGAM2132.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3186(VGR3186) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-

like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96195] VGR3186 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3186 gene was detected is described hereinabove with reference to Figs. 1-9.

[96196] VGR3186 gene encodes VGR3186 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96197] VGR3186 precursor RNA folds spatially, forming VGR3186 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3186 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3186 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96198] VGR3186 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2133 precursor RNA, VGAM2134 precursor RNA and VGAM2135 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96199] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2133 RNA, VGAM2134 RNA and VGAM2135 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96200] VGAM2133 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2133 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2133 host target RNA into VGAM2133 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96201] VGAM2134 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2134 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2134 host target RNA into VGAM2134 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96202] VGAM2135 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2135 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2135 host target RNA into VGAM2135 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96203] It is appreciated that a function of VGR3186 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3186 gene include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGR3186 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3186 gene: VGAM2133 host target protein, VGAM2134 host target protein and VGAM2135 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2133, VGAM2134 and VGAM2135.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to

here as Viral Genomic Record 3187(VGR3187) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96204] VGR3187 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3187 gene was detected is described hereinabove with reference to Figs. 1-9.

[96205] VGR3187 gene encodes VGR3187 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96206] VGR3187 precursor RNA folds spatially, forming VGR3187 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3187 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3187 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[96207] VGR3187 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2136 precursor RNA, VGAM2137 precursor RNA, VGAM2138 precursor RNA, VGAM2139 precursor RNA, VGAM2140 precursor RNA, VGAM2141 precursor RNA, VGAM2142 precursor RNA and VGAM2143 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96208] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2136 RNA, VGAM2137 RNA, VGAM2138 RNA, VGAM2139 RNA, VGAM2140 RNA, VGAM2141 RNA, VGAM2142 RNA and VGAM2143 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96209] VGAM2136 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2136 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2136 host target RNA into VGAM2136 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96210] VGAM2137 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2137 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2137 host target RNA into VGAM2137 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96211] VGAM2138 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2138 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2138 host target RNA into VGAM2138 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96212] VGAM2139 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2139 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2139 host target RNA into VGAM2139 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96213] VGAM2140 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2140 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2140 host target RNA into VGAM2140 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96214] VGAM2141 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2141 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2141 host target RNA into VGAM2141 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96215] VGAM2142 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2142 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2142 host target RNA into VGAM2142 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96216] VGAM2143 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2143 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2143 host target RNA into VGAM2143 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96217] It is appreciated that a function of VGR3187 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3187 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR3187 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3187 gene: VGAM2136 host target protein, VGAM2137 host target protein, VGAM2138 host target protein, VGAM2139 host target protein, VGAM2140 host target protein, VGAM2141 host target protein, VGAM2142 host target protein and VGAM2143 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2136, VGAM2137, VGAM2138, VGAM2139, VGAM2140, VGAM2141, VGAM2142 and VGAM2143.Fig. 9 further provides a conceptual description of novel bioinformati-

cally detected regulatory viral gene, referred to here as Viral Genomic Record 3188(VGR3188) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96218] VGR3188 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3188 gene was detected is described hereinabove with reference to Figs. 1-9.

[96219] VGR3188 gene encodes VGR3188 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96220] VGR3188 precursor RNA folds spatially, forming VGR3188 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3188 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3188 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-re-

versed sequence of the second half thereof, as is well known in the art.

[96221] VGR3188 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2144 precursor RNA and VGAM2145 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96222] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2144 RNA and VGAM2145 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96223] VGAM2144 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2144 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2144 host target RNA into VGAM2144 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96224] VGAM2145 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2145 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2145 host target RNA into VGAM2145 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96225] It is appreciated that a function of VGR3188 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3188 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utili-

ties, of VGR3188 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3188 gene: VGAM2144 host target protein and VGAM2145 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2144 and VGAM2145.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3189(VGR3189) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96226] VGR3189 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3189 gene was detected is described hereinabove with reference to Figs. 1-9.

[96227] VGR3189 gene encodes VGR3189 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96228] VGR3189 precursor RNA folds spatially, forming VGR3189 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3189 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3189 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96229] VGR3189 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2146 precursor RNA, VGAM2147 precursor RNA, VGAM2148 precursor RNA, VGAM2149 precursor RNA, VGAM2150 precursor RNA, VGAM2151 precursor RNA and VGAM2152 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig.

1.

[96230] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2146 RNA, VGAM2147 RNA, VGAM2148 RNA, VGAM2149 RNA, VGAM2150 RNA, VGAM2151 RNA and VGAM2152 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96231] VGAM2146 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2146 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2146 host target RNA into VGAM2146 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96232] VGAM2147 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2147 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2147 host target RNA into VGAM2147 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96233] VGAM2148 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2148 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2148 host target RNA into VGAM2148 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96234] VGAM2149 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2149 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2149 host target RNA into VGAM2149 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96235] VGAM2150 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2150 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2150 host target RNA into VGAM2150 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96236] VGAM2151 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2151 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2151 host target RNA into VGAM2151 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96237] VGAM2152 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2152 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2152 host target RNA into VGAM2152 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96238] It is appreciated that a function of VGR3189 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3189 gene include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR3189 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3189 gene: VGAM2146 host target protein, VGAM2147 host target protein, VGAM2148 host target protein, VGAM2149 host target protein, VGAM2150 host target protein, VGAM2151 host target protein and VGAM2152 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2146, VGAM2147, VGAM2148, VGAM2149, VGAM2150, VGAM2151 and VGAM2152.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3190(VGR3190) viral

gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96239] VGR3190 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3190 gene was detected is described hereinabove with reference to Figs. 1-9.

[96240] VGR3190 gene encodes VGR3190 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96241] VGR3190 precursor RNA folds spatially, forming VGR3190 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3190 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3190 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[96242] VGR3190 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2153 precursor RNA and VGAM2154 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96243] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2153 RNA and VGAM2154 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96244] VGAM2153 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2153 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2153 host target RNA into VGAM2153 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96245] VGAM2154 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2154 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2154 host target RNA into VGAM2154 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96246] It is appreciated that a function of VGR3190 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3190 gene include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR3190 gene correlate with, and may

be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3190 gene: VGAM2153 host target protein and VGAM2154 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2153 and VGAM2154.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3191(VGR3191) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96247] VGR3191 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3191 gene was detected is described hereinabove with reference to Figs. 1-9.

[96248] VGR3191 gene encodes VGR3191 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[96249] VGR3191 precursor RNA folds spatially, forming VGR3191 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3191 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3191 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96250] VGR3191 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2155 precursor RNA, VGAM2156 precursor RNA, VGAM2157 precursor RNA, VGAM2158 precursor RNA, VGAM2159 precursor RNA and VGAM2160 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96251] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2155 RNA, VGAM2156 RNA, VGAM2157 RNA, VGAM2158 RNA, VGAM2159 RNA and VGAM2160 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96252] VGAM2155 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2155 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2155 host target RNA into VGAM2155 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96253] VGAM2156 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2156 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2156 host target RNA into VGAM2156 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96254] VGAM2157 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2157 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2157 host target RNA into VGAM2157 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96255] VGAM2158 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2158 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2158 host target RNA into VGAM2158 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96256] VGAM2159 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2159 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2159 host target RNA into VGAM2159 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96257] VGAM2160 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2160 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2160 host target RNA into VGAM2160 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96258] It is appreciated that a function of VGR3191 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3191 gene include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGR3191 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3191 gene: VGAM2155 host target protein, VGAM2156 host target protein, VGAM2157 host target protein, VGAM2158 host target protein, VGAM2159 host target protein and VGAM2160 host target

protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2155, VGAM2156, VGAM2157, VGAM2158, VGAM2159 and VGAM2160.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3192(VGR3192) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96259] VGR3192 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3192 gene was detected is described hereinabove with reference to Figs. 1-9.

[96260] VGR3192 gene encodes VGR3192 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96261] VGR3192 precursor RNA folds spatially, forming VGR3192 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3192 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3192 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96262] VGR3192 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2161 precursor RNA, VGAM2162 precursor RNA, VGAM2163 precursor RNA, VGAM2164 precursor RNA, VGAM2165 precursor RNA, VGAM2166 precursor RNA, VGAM2167 precursor RNA and VGAM2168 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96263] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2161

RNA, VGAM2162 RNA, VGAM2163 RNA, VGAM2164 RNA, VGAM2165 RNA, VGAM2166 RNA, VGAM2167 RNA and VGAM2168 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96264] VGAM2161 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2161 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2161 host target RNA into VGAM2161 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96265] VGAM2162 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2162 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2162 host target RNA into VGAM2162 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96266] VGAM2163 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2163 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2163 host target RNA into VGAM2163 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96267] VGAM2164 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2164 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2164 host target RNA into VGAM2164 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96268] VGAM2165 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2165 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2165 host target RNA into VGAM2165 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96269] VGAM2166 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2166 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2166 host target RNA into VGAM2166 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96270] VGAM2167 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2167 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2167 host target RNA into VGAM2167 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96271] VGAM2168 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2168 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2168 host target RNA into VGAM2168 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96272] It is appreciated that a function of VGR3192 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3192 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGR3192 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3192 gene: VGAM2161 host target protein, VGAM2162 host target protein, VGAM2163 host target protein, VGAM2164 host target protein, VGAM2165 host target protein, VGAM2166 host target protein, VGAM2167 host target protein and VGAM2168

host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2161, VGAM2162, VGAM2163, VGAM2164, VGAM2165, VGAM2166, VGAM2167 and VGAM2168.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3193(VGR3193) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96273] VGR3193 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3193 gene was detected is described hereinabove with reference to Figs. 1-9.

[96274] VGR3193 gene encodes VGR3193 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96275] VGR3193 precursor RNA folds spatially, forming VGR3193 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3193 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3193 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96276] VGR3193 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2169 precursor RNA, VGAM2170 precursor RNA, VGAM2171 precursor RNA, VGAM2172 precursor RNA and VGAM2173 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96277] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2169 RNA, VGAM2170 RNA, VGAM2171 RNA, VGAM2172 RNA

and VGAM2173 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96278] VGAM2169 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2169 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2169 host target RNA into VGAM2169 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96279] VGAM2170 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2170 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2170 host target RNA into VGAM2170 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96280] VGAM2171 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2171 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2171 host target RNA into VGAM2171 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96281] VGAM2172 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2172 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2172 host target RNA into VGAM2172 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96282] VGAM2173 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2173 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2173 host target RNA into VGAM2173 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96283] It is appreciated that a function of VGR3193 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3193 gene include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utili-

ties, of VGR3193 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3193 gene: VGAM2169 host target protein, VGAM2170 host target protein, VGAM2171 host target protein, VGAM2172 host target protein and VGAM2173 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2169, VGAM2170, VGAM2171, VGAM2172 and VGAM2173.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3194(VGR3194) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96284] VGR3194 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3194 gene was detected is described hereinabove with reference to Figs.

1-9.

[96285] VGR3194 gene encodes VGR3194 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96286] VGR3194 precursor RNA folds spatially, forming VGR3194 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3194 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3194 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96287] VGR3194 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2174 precursor RNA, VGAM2175 precursor RNA, VGAM2176 precursor RNA, VGAM2177 precursor RNA, VGAM2178 precursor RNA and VGAM2179 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96288] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2174 RNA, VGAM2175 RNA, VGAM2176 RNA, VGAM2177 RNA, VGAM2178 RNA and VGAM2179 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96289] VGAM2174 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2174 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2174 host target RNA into VGAM2174 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96290] VGAM2175 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2175 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2175 host target RNA into VGAM2175 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96291] VGAM2176 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2176 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2176 host target RNA into VGAM2176 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96292] VGAM2177 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2177 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2177 host target RNA into VGAM2177 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96293] VGAM2178 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2178 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2178 host target RNA into VGAM2178 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96294] VGAM2179 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2179 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2179 host target RNA into VGAM2179 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96295] It is appreciated that a function of VGR3194 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3194 gene include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGR3194 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3194 gene: VGAM2174 host

target protein, VGAM2175 host target protein, VGAM2176 host target protein, VGAM2177 host target protein, VGAM2178 host target protein and VGAM2179 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2174, VGAM2175, VGAM2176, VGAM2177, VGAM2178 and VGAM2179.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3195(VGR3195) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96296] VGR3195 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3195 gene was detected is described hereinabove with reference to Figs. 1-9.

[96297] VGR3195 gene encodes VGR3195 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[96298] VGR3195 precursor RNA folds spatially, forming VGR3195 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3195 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3195 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96299] VGR3195 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2180 precursor RNA, VGAM2181 precursor RNA, VGAM2182 precursor RNA and VGAM2183 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96300] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM2180 RNA, VGAM2181 RNA, VGAM2182 RNA and VGAM2183 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96301] VGAM2180 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2180 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2180 host target RNA into VGAM2180 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96302] VGAM2181 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2181 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2181 host target RNA into VGAM2181 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96303] VGAM2182 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2182 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2182 host target RNA into VGAM2182 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96304] VGAM2183 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2183 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2183 host target RNA into VGAM2183 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96305] It is appreciated that a function of VGR3195 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3195 gene include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGR3195 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3195 gene: VGAM2180 host target protein, VGAM2181 host target protein, VGAM2182 host target protein and VGAM2183 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2180, VGAM2181,

VGAM2182 and VGAM2183.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3196(VGR3196) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96306] VGR3196 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3196 gene was detected is described hereinabove with reference to Figs. 1-9.

[96307] VGR3196 gene encodes VGR3196 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96308] VGR3196 precursor RNA folds spatially, forming VGR3196 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3196 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3196 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96309] VGR3196 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2184 precursor RNA, VGAM2185 precursor RNA, VGAM2186 precursor RNA, VGAM2187 precursor RNA, VGAM2188 precursor RNA, VGAM2189 precursor RNA, VGAM2190 precursor RNA and VGAM2191 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96310] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2184 RNA, VGAM2185 RNA, VGAM2186 RNA, VGAM2187 RNA, VGAM2188 RNA, VGAM2189 RNA, VGAM2190 RNA and VGAM2191 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96311] VGAM2184 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2184 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2184 host target RNA into VGAM2184 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96312] VGAM2185 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2185 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2185 host target RNA into VGAM2185 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96313] VGAM2186 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2186 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2186 host target RNA into VGAM2186 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96314] VGAM2187 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2187 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2187 host target RNA into VGAM2187 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96315] VGAM2188 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2188 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2188 host target RNA into VGAM2188 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96316] VGAM2189 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2189 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2189 host target RNA into

VGAM2189 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96317] VGAM2190 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2190 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2190 host target RNA into VGAM2190 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96318] VGAM2191 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2191 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2191 host target RNA into VGAM2191 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96319] It is appreciated that a function of VGR3196 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3196 gene include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGR3196 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3196 gene: VGAM2184 host target protein, VGAM2185 host target protein, VGAM2186 host target protein, VGAM2187 host target protein, VGAM2188 host target protein, VGAM2189 host target protein, VGAM2190 host target protein and VGAM2191 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2184, VGAM2185, VGAM2186, VGAM2187, VGAM2188,

VGAM2189, VGAM2190 and VGAM2191.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3197(VGR3197) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96320] VGR3197 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3197 gene was detected is described hereinabove with reference to Figs. 1-9.

[96321] VGR3197 gene encodes VGR3197 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96322] VGR3197 precursor RNA folds spatially, forming VGR3197 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3197 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3197 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96323] VGR3197 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2192 precursor RNA, VGAM2193 precursor RNA and VGAM2194 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96324] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2192 RNA, VGAM2193 RNA and VGAM2194 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96325] VGAM2192 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2192 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2192 host target RNA into VGAM2192 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96326] VGAM2193 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2193 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2193 host target RNA into VGAM2193 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96327] VGAM2194 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2194 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2194 host target RNA into VGAM2194 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96328] It is appreciated that a function of VGR3197 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3197 gene include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGR3197 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3197 gene: VGAM2192 host target protein, VGAM2193 host target protein and VGAM2194 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2192, VGAM2193 and VGAM2194.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3198(VGR3198) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96329] VGR3198 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3198 gene was detected is described hereinabove with reference to Figs. 1-9.

[96330] VGR3198 gene encodes VGR3198 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96331] VGR3198 precursor RNA folds spatially, forming VGR3198 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3198 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3198 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96332] VGR3198 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2195 precursor RNA, VGAM2196 precursor RNA, VGAM2197 precursor RNA, VGAM2198 precursor RNA and VGAM2199 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96333] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2195 RNA, VGAM2196 RNA, VGAM2197 RNA, VGAM2198 RNA and VGAM2199 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[96334] VGAM2195 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2195 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2195 host target RNA into VGAM2195 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96335] VGAM2196 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2196 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2196 host target RNA into VGAM2196 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96336] VGAM2197 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2197 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2197 host target RNA into VGAM2197 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96337] VGAM2198 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2198 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2198 host target RNA into

VGAM2198 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96338] VGAM2199 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2199 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2199 host target RNA into VGAM2199 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96339] It is appreciated that a function of VGR3198 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3198 gene include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGR3198 gene correlate with, and may be deduced from, the identity of the host target genes,

which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3198 gene: VGAM2195 host target protein, VGAM2196 host target protein, VGAM2197 host target protein, VGAM2198 host target protein and VGAM2199 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2195, VGAM2196, VGAM2197, VGAM2198 and VGAM2199.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3199(VGR3199) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96340] VGR3199 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3199 gene was detected is described hereinabove with reference to Figs. 1-9.

[96341] VGR3199 gene encodes VGR3199 precursor RNA, herein

designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96342] VGR3199 precursor RNA folds spatially, forming VGR3199 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3199 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3199 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96343] VGR3199 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2200 precursor RNA, VGAM2201 precursor RNA, VGAM2202 precursor RNA, VGAM2203 precursor RNA, VGAM2204 precursor RNA, VGAM2205 precursor RNA and VGAM2206 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig.

1.

[96344] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2200 RNA, VGAM2201 RNA, VGAM2202 RNA, VGAM2203 RNA, VGAM2204 RNA, VGAM2205 RNA and VGAM2206 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96345] VGAM2200 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2200 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2200 host target RNA into VGAM2200 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96346] VGAM2201 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2201 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2201 host target RNA into VGAM2201 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96347] VGAM2202 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2202 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2202 host target RNA into VGAM2202 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96348] VGAM2203 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2203 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2203 host target RNA into VGAM2203 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96349] VGAM2204 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2204 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2204 host target RNA into VGAM2204 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96350] VGAM2205 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2205 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2205 host target RNA into VGAM2205 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96351] VGAM2206 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2206 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2206 host target RNA into VGAM2206 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96352] It is appreciated that a function of VGR3199 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3199 gene include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGR3199 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3199 gene: VGAM2200 host target protein, VGAM2201 host target protein, VGAM2202 host target protein, VGAM2203 host target protein, VGAM2204 host target protein, VGAM2205 host target protein and VGAM2206 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2200, VGAM2201, VGAM2202, VGAM2203, VGAM2204, VGAM2205 and VGAM2206.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3200(VGR3200) viral gene, which en-

codes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96353] VGR3200 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3200 gene was detected is described hereinabove with reference to Figs. 1-9.

[96354] VGR3200 gene encodes VGR3200 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96355] VGR3200 precursor RNA folds spatially, forming VGR3200 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3200 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3200 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96356] VGR3200 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2207 precursor RNA, VGAM2208 precursor RNA, VGAM2209 precursor RNA, VGAM2210 precursor RNA, VGAM2211 precursor RNA, VGAM2212 precursor RNA, VGAM2213 precursor RNA and VGAM2214 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96357] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2207 RNA, VGAM2208 RNA, VGAM2209 RNA, VGAM2210 RNA, VGAM2211 RNA, VGAM2212 RNA, VGAM2213 RNA and VGAM2214 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96358] VGAM2207 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2207 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2207 host target RNA into VGAM2207 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96359] VGAM2208 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2208 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2208 host target RNA into VGAM2208 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96360] VGAM2209 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2209 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2209 host target RNA into VGAM2209 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96361] VGAM2210 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2210 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2210 host target RNA into VGAM2210 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96362] VGAM2211 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2211 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2211 host target RNA into VGAM2211 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96363] VGAM2212 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2212 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2212 host target RNA into VGAM2212 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96364] VGAM2213 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2213 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2213 host target RNA into VGAM2213 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96365] VGAM2214 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2214 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2214 host target RNA into VGAM2214 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96366] It is appreciated that a function of VGR3200 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3200 gene include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGR3200 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3200 gene: VGAM2207 host target protein, VGAM2208 host target protein, VGAM2209 host target protein, VGAM2210 host target protein, VGAM2211 host target protein, VGAM2212 host target protein, VGAM2213 host target protein and VGAM2214 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2207, VGAM2208, VGAM2209, VGAM2210, VGAM2211, VGAM2212, VGAM2213 and VGAM2214.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3201(VGR3201) viral gene, which en-

codes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96367] VGR3201 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3201 gene was detected is described hereinabove with reference to Figs. 1-9.

[96368] VGR3201 gene encodes VGR3201 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96369] VGR3201 precursor RNA folds spatially, forming VGR3201 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3201 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3201 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96370] VGR3201 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2215 precursor RNA, VGAM2216 precursor RNA, VGAM2217 precursor RNA, VGAM2218 precursor RNA, VGAM2219 precursor RNA and VGAM2220 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96371] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2215 RNA, VGAM2216 RNA, VGAM2217 RNA, VGAM2218 RNA, VGAM2219 RNA and VGAM2220 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96372] VGAM2215 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2215 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2215 host target RNA into VGAM2215 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96373] VGAM2216 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2216 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2216 host target RNA into VGAM2216 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96374] VGAM2217 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2217 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2217 host target RNA into VGAM2217 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96375] VGAM2218 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2218 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2218 host target RNA into VGAM2218 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96376] VGAM2219 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2219 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2219 host target RNA into VGAM2219 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96377] VGAM2220 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2220 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2220 host target RNA into VGAM2220 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96378] It is appreciated that a function of VGR3201 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3201 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR3201 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3201 gene: VGAM2215 host target protein, VGAM2216 host target protein, VGAM2217 host target protein, VGAM2218 host target protein, VGAM2219 host target protein and VGAM2220 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2215, VGAM2216, VGAM2217, VGAM2218, VGAM2219 and VGAM2220.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3202(VGR3202) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known

in the art.

[96379] VGR3202 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3202 gene was detected is described hereinabove with reference to Figs. 1-9.

[96380] VGR3202 gene encodes VGR3202 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96381] VGR3202 precursor RNA folds spatially, forming VGR3202 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3202 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3202 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96382] VGR3202 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2221 precursor RNA, VGAM2222

precursor RNA, VGAM2223 precursor RNA, VGAM2224 precursor RNA, VGAM2225 precursor RNA, VGAM2226 precursor RNA, VGAM2227 precursor RNA and VGAM2228 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96383] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2221 RNA, VGAM2222 RNA, VGAM2223 RNA, VGAM2224 RNA, VGAM2225 RNA, VGAM2226 RNA, VGAM2227 RNA and VGAM2228 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96384] VGAM2221 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2221 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2221 host target RNA into VGAM2221 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96385] VGAM2222 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2222 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2222 host target RNA into VGAM2222 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96386] VGAM2223 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2223 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2223 host target RNA into VGAM2223 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96387] VGAM2224 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2224 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2224 host target RNA into VGAM2224 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96388] VGAM2225 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2225 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2225 host target RNA into VGAM2225 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96389] VGAM2226 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2226 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2226 host target RNA into VGAM2226 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96390] VGAM2227 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2227 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2227 host target RNA into VGAM2227 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96391] VGAM2228 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2228 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2228 host target RNA into VGAM2228 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96392] It is appreciated that a function of VGR3202 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3202 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3202 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3202 gene: VGAM2221 host target protein, VGAM2222 host target protein, VGAM2223 host target protein, VGAM2224 host target protein, VGAM2225 host target protein, VGAM2226 host target protein, VGAM2227 host target protein and VGAM2228 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2221, VGAM2222, VGAM2223, VGAM2224, VGAM2225, VGAM2226, VGAM2227 and VGAM2228.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3203(VGR3203) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of

which at least one host target gene is known in the art.

[96393] VGR3203 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3203 gene was detected is described hereinabove with reference to Figs. 1-9.

[96394] VGR3203 gene encodes VGR3203 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96395] VGR3203 precursor RNA folds spatially, forming VGR3203 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3203 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3203 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96396] VGR3203 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2229 precursor RNA, VGAM2230

precursor RNA and VGAM2231 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96397] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2229 RNA, VGAM2230 RNA and VGAM2231 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96398] VGAM2229 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2229 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2229 host target RNA into VGAM2229 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96399] VGAM2230 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2230 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2230 host target RNA into VGAM2230 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96400] VGAM2231 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2231 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2231 host target RNA into

VGAM2231 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96401] It is appreciated that a function of VGR3203 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3203 gene include diagnosis, prevention and treatment of viral infection by Potato Aucuba Mosaic Virus. Specific functions, and accordingly utilities, of VGR3203 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3203 gene: VGAM2229 host target protein, VGAM2230 host target protein and VGAM2231 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2229, VGAM2230 and VGAM2231.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3204(VGR3204) viral gene, which encodes an `operon-like` cluster of novel viral mi-

cro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96402] VGR3204 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3204 gene was detected is described hereinabove with reference to Figs. 1-9.

[96403] VGR3204 gene encodes VGR3204 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96404] VGR3204 precursor RNA folds spatially, forming VGR3204 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3204 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3204 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96405] VGR3204 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2232 precursor RNA, VGAM2233 precursor RNA, VGAM2234 precursor RNA, VGAM2235 precursor RNA, VGAM2236 precursor RNA, VGAM2237 precursor RNA, VGAM2238 precursor RNA and VGAM2239 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96406] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2232 RNA, VGAM2233 RNA, VGAM2234 RNA, VGAM2235 RNA, VGAM2236 RNA, VGAM2237 RNA, VGAM2238 RNA and VGAM2239 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96407] VGAM2232 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2232 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2232 host target RNA into VGAM2232 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96408] VGAM2233 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2233 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2233 host target RNA into VGAM2233 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96409] VGAM2234 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2234 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2234 host target RNA into VGAM2234 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96410] VGAM2235 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2235 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2235 host target RNA into VGAM2235 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96411] VGAM2236 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2236 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2236 host target RNA into VGAM2236 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96412] VGAM2237 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2237 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2237 host target RNA into VGAM2237 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96413] VGAM2238 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2238 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2238 host target RNA into VGAM2238 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96414] VGAM2239 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2239 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2239 host target RNA into VGAM2239 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96415] It is appreciated that a function of VGR3204 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3204 gene include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGR3204 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3204 gene: VGAM2232 host target protein, VGAM2233 host target protein, VGAM2234 host target protein, VGAM2235 host target protein, VGAM2236 host target protein, VGAM2237 host target protein, VGAM2238 host target protein and VGAM2239 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2232, VGAM2233, VGAM2234, VGAM2235, VGAM2236, VGAM2237, VGAM2238 and VGAM2239.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3205(VGR3205) viral

gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96416] VGR3205 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3205 gene was detected is described hereinabove with reference to Figs. 1-9.

[96417] VGR3205 gene encodes VGR3205 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96418] VGR3205 precursor RNA folds spatially, forming VGR3205 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3205 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3205 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[96419] VGR3205 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2240 precursor RNA, VGAM2241 precursor RNA, VGAM2242 precursor RNA, VGAM2243 precursor RNA, VGAM2244 precursor RNA, VGAM2245 precursor RNA and VGAM2246 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96420] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2240 RNA, VGAM2241 RNA, VGAM2242 RNA, VGAM2243 RNA, VGAM2244 RNA, VGAM2245 RNA and VGAM2246 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96421] VGAM2240 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2240 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2240 host target RNA into VGAM2240 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96422] VGAM2241 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2241 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2241 host target RNA into VGAM2241 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96423] VGAM2242 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2242 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2242 host target RNA into VGAM2242 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96424] VGAM2243 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2243 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2243 host target RNA into VGAM2243 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96425] VGAM2244 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2244 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2244 host target RNA into VGAM2244 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96426] VGAM2245 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2245 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2245 host target RNA into VGAM2245 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96427] VGAM2246 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2246 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2246 host target RNA into VGAM2246 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96428] It is appreciated that a function of VGR3205 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3205 gene include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGR3205 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3205 gene: VGAM2240 host target protein, VGAM2241 host target protein,

VGAM2242 host target protein, VGAM2243 host target protein, VGAM2244 host target protein, VGAM2245 host target protein and VGAM2246 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2240, VGAM2241, VGAM2242, VGAM2243, VGAM2244, VGAM2245 and VGAM2246.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3206(VGR3206) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96429] VGR3206 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3206 gene was detected is described hereinabove with reference to Figs. 1-9.

[96430] VGR3206 gene encodes VGR3206 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[96431] VGR3206 precursor RNA folds spatially, forming VGR3206 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3206 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3206 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96432] VGR3206 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2247 precursor RNA, VGAM2248 precursor RNA, VGAM2249 precursor RNA, VGAM2250 precursor RNA, VGAM2251 precursor RNA, VGAM2252 precursor RNA and VGAM2253 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96433] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2247 RNA, VGAM2248 RNA, VGAM2249 RNA, VGAM2250 RNA, VGAM2251 RNA, VGAM2252 RNA and VGAM2253 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96434] VGAM2247 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2247 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2247 host target RNA into VGAM2247 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96435] VGAM2248 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2248 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2248 host target RNA into VGAM2248 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96436] VGAM2249 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2249 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2249 host target RNA into VGAM2249 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96437] VGAM2250 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2250 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2250 host target RNA into VGAM2250 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96438] VGAM2251 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2251 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2251 host target RNA into VGAM2251 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96439] VGAM2252 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2252 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2252 host target RNA into VGAM2252 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96440] VGAM2253 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2253 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2253 host target RNA into VGAM2253 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96441] It is appreciated that a function of VGR3206 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3206 gene include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGR3206 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3206 gene: VGAM2247 host target protein, VGAM2248 host target protein, VGAM2249 host target protein, VGAM2250 host target protein, VGAM2251 host target protein, VGAM2252 host target protein and VGAM2253 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2247, VGAM2248, VGAM2249, VGAM2250, VGAM2251, VGAM2252 and VGAM2253.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3207(VGR3207) viral gene, which encodes an `operon-like` cluster of novel vi-

ral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96442] VGR3207 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3207 gene was detected is described hereinabove with reference to Figs. 1-9.

[96443] VGR3207 gene encodes VGR3207 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96444] VGR3207 precursor RNA folds spatially, forming VGR3207 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3207 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3207 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96445] VGR3207 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2254 precursor RNA and VGAM2255 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96446] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2254 RNA and VGAM2255 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96447] VGAM2254 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2254 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2254 host target RNA into

VGAM2254 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96448] VGAM2255 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2255 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2255 host target RNA into VGAM2255 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96449] It is appreciated that a function of VGR3207 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3207 gene include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGR3207 gene correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3207 gene: VGAM2254 host target protein and VGAM2255 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM2254 and VGAM2255.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3208(VGR3208) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96450] VGR3208 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3208 gene was detected is described hereinabove with reference to Figs. 1-9.

[96451] VGR3208 gene encodes VGR3208 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96452] VGR3208 precursor RNA folds spatially, forming VGR3208 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3208 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3208 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96453] VGR3208 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2256 precursor RNA, VGAM2257 precursor RNA and VGAM2258 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96454] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2256

RNA, VGAM2257 RNA and VGAM2258 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96455] VGAM2256 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2256 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2256 host target RNA into VGAM2256 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96456] VGAM2257 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2257 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2257 host target RNA into VGAM2257 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96457] VGAM2258 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2258 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2258 host target RNA into VGAM2258 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96458] It is appreciated that a function of VGR3208 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3208 gene include diagnosis, prevention and treatment of viral infection by Oat Chlorotic Stunt Virus. Specific functions, and accord-

ingly utilities, of VGR3208 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3208 gene: VGAM2256 host target protein, VGAM2257 host target protein and VGAM2258 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2256, VGAM2257 and VGAM2258.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3209(VGR3209) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96459] VGR3209 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3209 gene was detected is described hereinabove with reference to Figs. 1-9.

[96460] VGR3209 gene encodes VGR3209 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96461] VGR3209 precursor RNA folds spatially, forming VGR3209 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3209 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3209 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96462] VGR3209 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2259 precursor RNA, VGAM2260 precursor RNA, VGAM2261 precursor RNA, VGAM2262 precursor RNA, VGAM2263 precursor RNA, VGAM2264 precursor RNA, VGAM2265 precursor RNA and VGAM2266 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96463] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2259 RNA, VGAM2260 RNA, VGAM2261 RNA, VGAM2262 RNA, VGAM2263 RNA, VGAM2264 RNA, VGAM2265 RNA and VGAM2266 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96464] VGAM2259 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2259 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2259 host target RNA into VGAM2259 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96465] VGAM2260 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2260 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2260 host target RNA into VGAM2260 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96466] VGAM2261 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2261 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2261 host target RNA into VGAM2261 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96467] VGAM2262 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2262 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2262 host target RNA into VGAM2262 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96468] VGAM2263 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2263 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2263 host target RNA into VGAM2263 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96469] VGAM2264 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2264 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2264 host target RNA into VGAM2264 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96470] VGAM2265 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2265 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2265 host target RNA into VGAM2265 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96471] VGAM2266 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2266 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2266 host target RNA into VGAM2266 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96472] It is appreciated that a function of VGR3209 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3209 gene include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR3209 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR3209 gene: VGAM2259 host target protein, VGAM2260 host target protein, VGAM2261 host target protein, VGAM2262 host target protein, VGAM2263 host target protein, VGAM2264 host target protein, VGAM2265 host target protein and VGAM2266 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2259, VGAM2260, VGAM2261, VGAM2262, VGAM2263, VGAM2264, VGAM2265 and VGAM2266.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3210(VGR3210) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96473] VGR3210 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3210 gene was detected is described hereinabove with reference to Figs. 1-9.

[96474] VGR3210 gene encodes VGR3210 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96475] VGR3210 precursor RNA folds spatially, forming VGR3210 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3210 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3210 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96476] VGR3210 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2267 precursor RNA, VGAM2268 precursor RNA, VGAM2269 precursor RNA, VGAM2270 precursor RNA, VGAM2271 precursor RNA, VGAM2272 precursor RNA, VGAM2273 precursor RNA and VGAM2274 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96477] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2267 RNA, VGAM2268 RNA, VGAM2269 RNA, VGAM2270 RNA, VGAM2271 RNA, VGAM2272 RNA, VGAM2273 RNA and VGAM2274 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96478] VGAM2267 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2267 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2267 host target RNA into VGAM2267 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96479] VGAM2268 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2268 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2268 host target RNA into VGAM2268 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96480] VGAM2269 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2269 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2269 host target RNA into VGAM2269 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96481] VGAM2270 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2270 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2270 host target RNA into VGAM2270 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96482] VGAM2271 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2271 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2271 host target RNA into VGAM2271 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96483] VGAM2272 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2272 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2272 host target RNA into VGAM2272 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96484] VGAM2273 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2273 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2273 host target RNA into VGAM2273 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96485] VGAM2274 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2274 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2274 host target RNA into VGAM2274 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96486] It is appreciated that a function of VGR3210 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3210 gene include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR3210 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR3210 gene: VGAM2267 host target protein, VGAM2268 host target protein, VGAM2269 host target protein, VGAM2270 host target protein, VGAM2271 host target protein, VGAM2272 host target protein, VGAM2273 host target protein and VGAM2274 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2267, VGAM2268, VGAM2269, VGAM2270, VGAM2271, VGAM2272, VGAM2273 and VGAM2274.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3211(VGR3211) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96487] VGR3211 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3211 gene was detected is described hereinabove with reference to Figs. 1-9.

[96488] VGR3211 gene encodes VGR3211 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96489] VGR3211 precursor RNA folds spatially, forming VGR3211 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3211 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3211 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96490] VGR3211 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2275 precursor RNA, VGAM2276 precursor RNA, VGAM2277 precursor RNA, VGAM2278 precursor RNA, VGAM2279 precursor RNA and VGAM2280 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM

FOLDED PRECURSOR RNA of Fig. 1.

[96491] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2275 RNA, VGAM2276 RNA, VGAM2277 RNA, VGAM2278 RNA, VGAM2279 RNA and VGAM2280 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96492] VGAM2275 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2275 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2275 host target RNA into VGAM2275 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96493] VGAM2276 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2276 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2276 host target RNA into VGAM2276 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96494] VGAM2277 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2277 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2277 host target RNA into VGAM2277 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96495] VGAM2278 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2278 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2278 host target RNA into VGAM2278 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96496] VGAM2279 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2279 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2279 host target RNA into VGAM2279 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96497] VGAM2280 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2280 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2280 host target RNA into VGAM2280 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96498] It is appreciated that a function of VGR3211 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3211 gene include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGR3211 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3211 gene: VGAM2275 host target protein, VGAM2276 host target protein, VGAM2277

host target protein, VGAM2278 host target protein, VGAM2279 host target protein and VGAM2280 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2275, VGAM2276, VGAM2277, VGAM2278, VGAM2279 and VGAM2280.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3212(VGR3212) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96499] VGR3212 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3212 gene was detected is described hereinabove with reference to Figs. 1-9.

[96500] VGR3212 gene encodes VGR3212 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96501] VGR3212 precursor RNA folds spatially, forming VGR3212 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3212 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3212 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96502] VGR3212 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2281 precursor RNA, VGAM2282 precursor RNA, VGAM2283 precursor RNA, VGAM2284 precursor RNA, VGAM2285 precursor RNA, VGAM2286 precursor RNA, VGAM2287 precursor RNA and VGAM2288 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96503] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2281 RNA, VGAM2282 RNA, VGAM2283 RNA, VGAM2284 RNA, VGAM2285 RNA, VGAM2286 RNA, VGAM2287 RNA and VGAM2288 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96504] VGAM2281 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2281 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2281 host target RNA into VGAM2281 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96505] VGAM2282 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2282 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2282 host target RNA into VGAM2282 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96506] VGAM2283 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2283 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2283 host target RNA into VGAM2283 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96507] VGAM2284 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2284 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2284 host target RNA into VGAM2284 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96508] VGAM2285 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2285 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2285 host target RNA into VGAM2285 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96509] VGAM2286 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2286 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2286 host target RNA into VGAM2286 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96510] VGAM2287 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2287 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2287 host target RNA into VGAM2287 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96511] VGAM2288 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2288 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2288 host target RNA into VGAM2288 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96512] It is appreciated that a function of VGR3212 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3212 gene include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGR3212 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3212 gene: VGAM2281 host target protein, VGAM2282 host target protein, VGAM2283 host target protein, VGAM2284 host target protein,

VGAM2285 host target protein, VGAM2286 host target protein, VGAM2287 host target protein and VGAM2288 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2281, VGAM2282, VGAM2283, VGAM2284, VGAM2285, VGAM2286, VGAM2287 and VGAM2288.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3213(VGR3213) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96513] VGR3213 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3213 gene was detected is described hereinabove with reference to Figs. 1-9.

[96514] VGR3213 gene encodes VGR3213 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96515] VGR3213 precursor RNA folds spatially, forming VGR3213 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3213 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3213 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96516] VGR3213 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2289 precursor RNA, VGAM2290 precursor RNA, VGAM2291 precursor RNA, VGAM2292 precursor RNA, VGAM2293 precursor RNA and VGAM2294 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96517] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM2289 RNA, VGAM2290 RNA, VGAM2291 RNA, VGAM2292 RNA, VGAM2293 RNA and VGAM2294 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96518] VGAM2289 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2289 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2289 host target RNA into VGAM2289 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96519] VGAM2290 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2290 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2290 host target RNA into VGAM2290 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96520] VGAM2291 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2291 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2291 host target RNA into VGAM2291 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96521] VGAM2292 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2292 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2292 host target RNA into VGAM2292 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96522] VGAM2293 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2293 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2293 host target RNA into VGAM2293 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96523] VGAM2294 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2294 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2294 host target RNA into VGAM2294 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96524] It is appreciated that a function of VGR3213 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3213 gene include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGR3213 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3213 gene: VGAM2289 host target protein, VGAM2290 host target protein, VGAM2291 host target protein, VGAM2292 host target protein, VGAM2293 host target protein and VGAM2294 host target protein, herein schematically represented by VGAM1 HOST

TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2289, VGAM2290, VGAM2291, VGAM2292, VGAM2293 and VGAM2294.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3214(VGR3214) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96525] VGR3214 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3214 gene was detected is described hereinabove with reference to Figs. 1-9.

[96526] VGR3214 gene encodes VGR3214 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96527] VGR3214 precursor RNA folds spatially, forming VGR3214 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3214 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3214 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96528] VGR3214 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2295 precursor RNA, VGAM2296 precursor RNA, VGAM2297 precursor RNA, VGAM2298 precursor RNA, VGAM2299 precursor RNA, VGAM2300 precursor RNA, VGAM2301 precursor RNA and VGAM2302 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96529] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2295 RNA, VGAM2296 RNA, VGAM2297 RNA, VGAM2298 RNA,

VGAM2299 RNA, VGAM2300 RNA, VGAM2301 RNA and VGAM2302 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96530] VGAM2295 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2295 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2295 host target RNA into VGAM2295 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96531] VGAM2296 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2296 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2296 host target RNA into VGAM2296 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96532] VGAM2297 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2297 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2297 host target RNA into VGAM2297 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96533] VGAM2298 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2298 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2298 host target RNA into VGAM2298 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96534] VGAM2299 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2299 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2299 host target RNA into VGAM2299 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96535] VGAM2300 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2300 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2300 host target RNA into VGAM2300 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96536] VGAM2301 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2301 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2301 host target RNA into VGAM2301 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96537] VGAM2302 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2302 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2302 host target RNA into VGAM2302 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96538] It is appreciated that a function of VGR3214 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3214 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR3214 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3214 gene: VGAM2295 host target protein, VGAM2296 host target protein, VGAM2297 host target protein, VGAM2298 host target protein, VGAM2299 host target protein, VGAM2300 host target protein, VGAM2301 host target protein and VGAM2302 host target protein, herein schematically represented by

VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2295, VGAM2296, VGAM2297, VGAM2298, VGAM2299, VGAM2300, VGAM2301 and VGAM2302.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3215(VGR3215) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96539] VGR3215 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3215 gene was detected is described hereinabove with reference to Figs. 1-9.

[96540] VGR3215 gene encodes VGR3215 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96541] VGR3215 precursor RNA folds spatially, forming VGR3215 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3215 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3215 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96542] VGR3215 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2303 precursor RNA, VGAM2304 precursor RNA, VGAM2305 precursor RNA and VGAM2306 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96543] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2303 RNA, VGAM2304 RNA, VGAM2305 RNA and VGAM2306 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corre-

sponding to VGAM RNA of Fig. 1.

[96544] VGAM2303 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2303 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2303 host target RNA into VGAM2303 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96545] VGAM2304 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2304 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2304 host target RNA into VGAM2304 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96546] VGAM2305 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2305 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2305 host target RNA into VGAM2305 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96547] VGAM2306 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2306 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2306 host target RNA into

VGAM2306 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96548] It is appreciated that a function of VGR3215 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3215 gene include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGR3215 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3215 gene: VGAM2303 host target protein, VGAM2304 host target protein, VGAM2305 host target protein and VGAM2306 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2303, VGAM2304, VGAM2305 and VGAM2306.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3216(VGR3216) viral gene, which encodes an

`operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96549] VGR3216 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3216 gene was detected is described hereinabove with reference to Figs. 1-9.

[96550] VGR3216 gene encodes VGR3216 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96551] VGR3216 precursor RNA folds spatially, forming VGR3216 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3216 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3216 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96552] VGR3216 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2307 precursor RNA, VGAM2308 precursor RNA, VGAM2309 precursor RNA, VGAM2310 precursor RNA, VGAM2311 precursor RNA, VGAM2312 precursor RNA and VGAM2313 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96553] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2307 RNA, VGAM2308 RNA, VGAM2309 RNA, VGAM2310 RNA, VGAM2311 RNA, VGAM2312 RNA and VGAM2313 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96554] VGAM2307 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2307 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2307 host target RNA into VGAM2307 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96555] VGAM2308 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2308 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2308 host target RNA into VGAM2308 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96556] VGAM2309 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2309 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2309 host target RNA into VGAM2309 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96557] VGAM2310 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2310 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2310 host target RNA into VGAM2310 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96558] VGAM2311 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2311 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2311 host target RNA into VGAM2311 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96559] VGAM2312 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2312 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2312 host target RNA into VGAM2312 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96560] VGAM2313 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2313 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2313 host target RNA into VGAM2313 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96561] It is appreciated that a function of VGR3216 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3216 gene include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGR3216 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3216 gene: VGAM2307 host target protein, VGAM2308 host target protein, VGAM2309 host target protein, VGAM2310 host target protein,

VGAM2311 host target protein, VGAM2312 host target protein and VGAM2313 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2307, VGAM2308, VGAM2309, VGAM2310, VGAM2311, VGAM2312 and VGAM2313.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3217(VGR3217) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96562] VGR3217 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3217 gene was detected is described hereinabove with reference to Figs. 1-9.

[96563] VGR3217 gene encodes VGR3217 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96564] VGR3217 precursor RNA folds spatially, forming VGR3217 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3217 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3217 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96565] VGR3217 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2314 precursor RNA and VGAM2315 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96566] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2314 RNA and VGAM2315 RNA, herein schematically repre-

sented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96567] VGAM2314 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2314 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2314 host target RNA into VGAM2314 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96568] VGAM2315 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2315 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2315 host target RNA into

VGAM2315 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96569] It is appreciated that a function of VGR3217 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3217 gene include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGR3217 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3217 gene: VGAM2314 host target protein and VGAM2315 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2314 and VGAM2315.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3218(VGR3218) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expres-

sion of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96570] VGR3218 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3218 gene was detected is described hereinabove with reference to Figs. 1-9.

[96571] VGR3218 gene encodes VGR3218 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96572] VGR3218 precursor RNA folds spatially, forming VGR3218 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3218 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3218 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96573] VGR3218 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2316 precursor RNA, VGAM2317 precursor RNA, VGAM2318 precursor RNA, VGAM2319 precursor RNA, VGAM2320 precursor RNA, VGAM2321 precursor RNA, VGAM2322 precursor RNA and VGAM2323 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96574] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2316 RNA, VGAM2317 RNA, VGAM2318 RNA, VGAM2319 RNA, VGAM2320 RNA, VGAM2321 RNA, VGAM2322 RNA and VGAM2323 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96575] VGAM2316 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2316 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2316 host target RNA into VGAM2316 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96576] VGAM2317 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2317 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2317 host target RNA into VGAM2317 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96577] VGAM2318 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2318 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2318 host target RNA into VGAM2318 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96578] VGAM2319 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2319 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2319 host target RNA into VGAM2319 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96579] VGAM2320 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2320 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2320 host target RNA into VGAM2320 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96580] VGAM2321 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2321 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2321 host target RNA into VGAM2321 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96581] VGAM2322 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2322 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2322 host target RNA into VGAM2322 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96582] VGAM2323 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2323 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2323 host target RNA into VGAM2323 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96583] It is appreciated that a function of VGR3218 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3218 gene include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR3218 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3218 gene: VGAM2316 host target protein, VGAM2317 host target protein, VGAM2318 host target protein, VGAM2319 host target protein, VGAM2320 host target protein, VGAM2321 host target protein, VGAM2322 host target protein and VGAM2323 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2316, VGAM2317, VGAM2318, VGAM2319, VGAM2320, VGAM2321, VGAM2322 and VGAM2323.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3219(VGR3219) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-

like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96584] VGR3219 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3219 gene was detected is described hereinabove with reference to Figs. 1-9.

[96585] VGR3219 gene encodes VGR3219 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96586] VGR3219 precursor RNA folds spatially, forming VGR3219 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3219 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3219 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96587] VGR3219 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2324 precursor RNA, VGAM2325 precursor RNA, VGAM2326 precursor RNA, VGAM2327 precursor RNA and VGAM2328 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96588] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2324 RNA, VGAM2325 RNA, VGAM2326 RNA, VGAM2327 RNA and VGAM2328 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96589] VGAM2324 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2324 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2324 host target RNA into VGAM2324 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96590] VGAM2325 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2325 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2325 host target RNA into VGAM2325 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96591] VGAM2326 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2326 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2326 host target RNA into VGAM2326 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96592] VGAM2327 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2327 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2327 host target RNA into VGAM2327 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96593] VGAM2328 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2328 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2328 host target RNA into VGAM2328 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96594] It is appreciated that a function of VGR3219 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3219 gene include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGR3219 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3219 gene: VGAM2324 host target protein, VGAM2325 host target protein, VGAM2326 host target protein, VGAM2327 host target protein and VGAM2328 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with refer-

ence to VGAM2324, VGAM2325, VGAM2326, VGAM2327 and VGAM2328.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3220(VGR3220) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96595] VGR3220 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3220 gene was detected is described hereinabove with reference to Figs. 1-9.

[96596] VGR3220 gene encodes VGR3220 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96597] VGR3220 precursor RNA folds spatially, forming VGR3220 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3220 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3220 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96598] VGR3220 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2329 precursor RNA, VGAM2330 precursor RNA, VGAM2331 precursor RNA, VGAM2332 precursor RNA, VGAM2333 precursor RNA, VGAM2334 precursor RNA, VGAM2335 precursor RNA and VGAM2336 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96599] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2329 RNA, VGAM2330 RNA, VGAM2331 RNA, VGAM2332 RNA, VGAM2333 RNA, VGAM2334 RNA, VGAM2335 RNA and VGAM2336 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[96600] VGAM2329 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2329 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2329 host target RNA into VGAM2329 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96601] VGAM2330 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2330 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2330 host target RNA into VGAM2330 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96602] VGAM2331 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2331 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2331 host target RNA into VGAM2331 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96603] VGAM2332 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2332 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2332 host target RNA into

VGAM2332 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96604] VGAM2333 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2333 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2333 host target RNA into VGAM2333 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96605] VGAM2334 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2334 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2334 host target RNA into VGAM2334 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96606] VGAM2335 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2335 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2335 host target RNA into VGAM2335 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96607] VGAM2336 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2336 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2336 host target RNA into VGAM2336 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96608] It is appreciated that a function of VGR3220 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3220 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3220 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3220 gene: VGAM2329 host target protein, VGAM2330 host target protein, VGAM2331 host target protein, VGAM2332 host target protein, VGAM2333 host target protein, VGAM2334 host target protein, VGAM2335 host target protein and VGAM2336 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2329,

VGAM2330, VGAM2331, VGAM2332, VGAM2333, VGAM2334, VGAM2335 and VGAM2336.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3221(VGR3221) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96609] VGR3221 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3221 gene was detected is described hereinabove with reference to Figs. 1-9.

[96610] VGR3221 gene encodes VGR3221 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96611] VGR3221 precursor RNA folds spatially, forming VGR3221 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3221 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3221 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96612] VGR3221 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2337 precursor RNA, VGAM2338 precursor RNA, VGAM2339 precursor RNA, VGAM2340 precursor RNA, VGAM2341 precursor RNA, VGAM2342 precursor RNA, VGAM2343 precursor RNA and VGAM2344 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96613] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2337 RNA, VGAM2338 RNA, VGAM2339 RNA, VGAM2340 RNA, VGAM2341 RNA, VGAM2342 RNA, VGAM2343 RNA and VGAM2344 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[96614] VGAM2337 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2337 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2337 host target RNA into VGAM2337 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96615] VGAM2338 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2338 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2338 host target RNA into VGAM2338 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96616] VGAM2339 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2339 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2339 host target RNA into VGAM2339 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96617] VGAM2340 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2340 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2340 host target RNA into

VGAM2340 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96618] VGAM2341 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2341 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2341 host target RNA into VGAM2341 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96619] VGAM2342 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2342 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2342 host target RNA into VGAM2342 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96620] VGAM2343 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2343 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2343 host target RNA into VGAM2343 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96621] VGAM2344 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2344 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2344 host target RNA into VGAM2344 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96622] It is appreciated that a function of VGR3221 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3221 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3221 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3221 gene: VGAM2337 host target protein, VGAM2338 host target protein, VGAM2339 host target protein, VGAM2340 host target protein, VGAM2341 host target protein, VGAM2342 host target protein, VGAM2343 host target protein and VGAM2344 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2337,

VGAM2338, VGAM2339, VGAM2340, VGAM2341, VGAM2342, VGAM2343 and VGAM2344.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3222(VGR3222) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96623] VGR3222 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3222 gene was detected is described hereinabove with reference to Figs. 1-9.

[96624] VGR3222 gene encodes VGR3222 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96625] VGR3222 precursor RNA folds spatially, forming VGR3222 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3222 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3222 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96626] VGR3222 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2345 precursor RNA, VGAM2346 precursor RNA, VGAM2347 precursor RNA, VGAM2348 precursor RNA, VGAM2349 precursor RNA, VGAM2350 precursor RNA, VGAM2351 precursor RNA and VGAM2352 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96627] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2345 RNA, VGAM2346 RNA, VGAM2347 RNA, VGAM2348 RNA, VGAM2349 RNA, VGAM2350 RNA, VGAM2351 RNA and VGAM2352 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[96628] VGAM2345 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2345 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2345 host target RNA into VGAM2345 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96629] VGAM2346 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2346 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2346 host target RNA into VGAM2346 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96630] VGAM2347 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2347 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2347 host target RNA into VGAM2347 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96631] VGAM2348 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2348 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2348 host target RNA into

VGAM2348 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96632] VGAM2349 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2349 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2349 host target RNA into VGAM2349 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96633] VGAM2350 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2350 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2350 host target RNA into VGAM2350 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96634] VGAM2351 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2351 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2351 host target RNA into VGAM2351 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96635] VGAM2352 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2352 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2352 host target RNA into VGAM2352 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96636] It is appreciated that a function of VGR3222 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3222 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3222 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3222 gene: VGAM2345 host target protein, VGAM2346 host target protein, VGAM2347 host target protein, VGAM2348 host target protein, VGAM2349 host target protein, VGAM2350 host target protein, VGAM2351 host target protein and VGAM2352 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2345,

VGAM2346, VGAM2347, VGAM2348, VGAM2349, VGAM2350, VGAM2351 and VGAM2352.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3223(VGR3223) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96637] VGR3223 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3223 gene was detected is described hereinabove with reference to Figs. 1-9.

[96638] VGR3223 gene encodes VGR3223 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96639] VGR3223 precursor RNA folds spatially, forming VGR3223 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3223 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3223 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96640] VGR3223 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2353 precursor RNA, VGAM2354 precursor RNA, VGAM2355 precursor RNA, VGAM2356 precursor RNA, VGAM2357 precursor RNA, VGAM2358 precursor RNA, VGAM2359 precursor RNA and VGAM2360 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96641] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2353 RNA, VGAM2354 RNA, VGAM2355 RNA, VGAM2356 RNA, VGAM2357 RNA, VGAM2358 RNA, VGAM2359 RNA and VGAM2360 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM

RNAs corresponding to VGAM RNA of Fig. 1.

[96642] VGAM2353 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2353 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2353 host target RNA into VGAM2353 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96643] VGAM2354 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2354 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2354 host target RNA into VGAM2354 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96644] VGAM2355 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2355 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2355 host target RNA into VGAM2355 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96645] VGAM2356 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2356 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2356 host target RNA into

VGAM2356 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96646] VGAM2357 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2357 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2357 host target RNA into VGAM2357 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96647] VGAM2358 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2358 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2358 host target RNA into VGAM2358 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96648] VGAM2359 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2359 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2359 host target RNA into VGAM2359 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96649] VGAM2360 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2360 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2360 host target RNA into VGAM2360 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96650] It is appreciated that a function of VGR3223 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3223 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3223 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3223 gene: VGAM2353 host target protein, VGAM2354 host target protein, VGAM2355 host target protein, VGAM2356 host target protein, VGAM2357 host target protein, VGAM2358 host target protein, VGAM2359 host target protein and VGAM2360 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2353,

VGAM2354, VGAM2355, VGAM2356, VGAM2357, VGAM2358, VGAM2359 and VGAM2360.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3224(VGR3224) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96651] VGR3224 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3224 gene was detected is described hereinabove with reference to Figs. 1-9.

[96652] VGR3224 gene encodes VGR3224 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96653] VGR3224 precursor RNA folds spatially, forming VGR3224 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3224 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3224 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96654] VGR3224 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2361 precursor RNA, VGAM2362 precursor RNA, VGAM2363 precursor RNA and VGAM2364 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96655] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2361 RNA, VGAM2362 RNA, VGAM2363 RNA and VGAM2364 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96656] VGAM2361 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2361 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2361 host target RNA into VGAM2361 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96657] VGAM2362 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2362 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2362 host target RNA into VGAM2362 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96658] VGAM2363 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2363 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2363 host target RNA into VGAM2363 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96659] VGAM2364 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2364 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2364 host target RNA into VGAM2364 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96660] It is appreciated that a function of VGR3224 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3224 gene include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGR3224 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3224 gene: VGAM2361 host target protein, VGAM2362 host target protein, VGAM2363 host target protein and VGAM2364 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2361, VGAM2362, VGAM2363 and VGAM2364.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3225(VGR3225) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[96661] VGR3225 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3225 gene was detected is described hereinabove with reference to Figs. 1-9.

[96662] VGR3225 gene encodes VGR3225 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96663] VGR3225 precursor RNA folds spatially, forming VGR3225 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3225 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3225 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96664] VGR3225 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2365 precursor RNA, VGAM2366

precursor RNA, VGAM2367 precursor RNA, VGAM2368 precursor RNA, VGAM2369 precursor RNA, VGAM2370 precursor RNA, VGAM2371 precursor RNA and VGAM2372 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96665] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2365 RNA, VGAM2366 RNA, VGAM2367 RNA, VGAM2368 RNA, VGAM2369 RNA, VGAM2370 RNA, VGAM2371 RNA and VGAM2372 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96666] VGAM2365 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2365 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2365 host target RNA into VGAM2365 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96667] VGAM2366 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2366 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2366 host target RNA into VGAM2366 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96668] VGAM2367 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2367 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2367 host target RNA into VGAM2367 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96669] VGAM2368 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2368 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2368 host target RNA into VGAM2368 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96670] VGAM2369 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2369 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2369 host target RNA into VGAM2369 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96671] VGAM2370 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2370 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2370 host target RNA into VGAM2370 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96672] VGAM2371 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2371 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2371 host target RNA into VGAM2371 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96673] VGAM2372 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2372 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2372 host target RNA into VGAM2372 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96674] It is appreciated that a function of VGR3225 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3225 gene include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGR3225 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3225 gene: VGAM2365 host target protein, VGAM2366 host target protein, VGAM2367 host target protein, VGAM2368 host target protein, VGAM2369 host target protein, VGAM2370 host target protein, VGAM2371 host target protein and VGAM2372 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2365, VGAM2366, VGAM2367, VGAM2368, VGAM2369, VGAM2370, VGAM2371 and VGAM2372.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3226(VGR3226) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of

which at least one host target gene is known in the art.

[96675] VGR3226 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3226 gene was detected is described hereinabove with reference to Figs. 1-9.

[96676] VGR3226 gene encodes VGR3226 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96677] VGR3226 precursor RNA folds spatially, forming VGR3226 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3226 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3226 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96678] VGR3226 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2373 precursor RNA, VGAM2374

precursor RNA, VGAM2375 precursor RNA, VGAM2376 precursor RNA, VGAM2377 precursor RNA, VGAM2378 precursor RNA and VGAM2379 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96679] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2373 RNA, VGAM2374 RNA, VGAM2375 RNA, VGAM2376 RNA, VGAM2377 RNA, VGAM2378 RNA and VGAM2379 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96680] VGAM2373 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2373 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2373 host target RNA into VGAM2373 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96681] VGAM2374 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2374 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2374 host target RNA into VGAM2374 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96682] VGAM2375 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2375 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2375 host target RNA into VGAM2375 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96683] VGAM2376 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2376 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2376 host target RNA into VGAM2376 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96684] VGAM2377 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2377 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2377 host target RNA into VGAM2377 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96685] VGAM2378 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2378 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2378 host target RNA into VGAM2378 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96686] VGAM2379 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2379 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2379 host target RNA into VGAM2379 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96687] It is appreciated that a function of VGR3226 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3226 gene include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGR3226 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3226 gene: VGAM2373 host target protein, VGAM2374 host target protein, VGAM2375 host target protein, VGAM2376 host target protein, VGAM2377 host target protein, VGAM2378 host target protein and VGAM2379 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2373, VGAM2374, VGAM2375, VGAM2376, VGAM2377, VGAM2378 and VGAM2379.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3227(VGR3227) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96688] VGR3227 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3227 gene was detected is described hereinabove with reference to Figs. 1-9.

[96689] VGR3227 gene encodes VGR3227 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96690] VGR3227 precursor RNA folds spatially, forming VGR3227 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3227 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3227 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96691] VGR3227 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2380 precursor RNA, VGAM2381 precursor RNA, VGAM2382 precursor RNA, VGAM2383 precursor RNA, VGAM2384 precursor RNA, VGAM2385 precursor RNA and VGAM2386 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96692] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2380 RNA, VGAM2381 RNA, VGAM2382 RNA, VGAM2383 RNA,

VGAM2384 RNA, VGAM2385 RNA and VGAM2386 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96693] VGAM2380 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2380 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2380 host target RNA into VGAM2380 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96694] VGAM2381 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2381 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2381 host target RNA into VGAM2381 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96695] VGAM2382 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2382 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2382 host target RNA into VGAM2382 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96696] VGAM2383 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2383 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2383 host target RNA into VGAM2383 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96697] VGAM2384 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2384 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2384 host target RNA into VGAM2384 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96698] VGAM2385 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2385 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2385 host target RNA into VGAM2385 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96699] VGAM2386 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2386 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2386 host target RNA into VGAM2386 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96700] It is appreciated that a function of VGR3227 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3227 gene include

diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3227 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3227 gene: VGAM2380 host target protein, VGAM2381 host target protein, VGAM2382 host target protein, VGAM2383 host target protein, VGAM2384 host target protein, VGAM2385 host target protein and VGAM2386 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2380, VGAM2381, VGAM2382, VGAM2383, VGAM2384, VGAM2385 and VGAM2386.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3228(VGR3228) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96701] VGR3228 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3228 gene was detected is described hereinabove with reference to Figs. 1-9.

[96702] VGR3228 gene encodes VGR3228 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96703] VGR3228 precursor RNA folds spatially, forming VGR3228 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3228 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3228 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96704] VGR3228 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2387 precursor RNA and VGAM2388 precursor RNA, herein schematically repre-

sented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96705] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2387 RNA and VGAM2388 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96706] VGAM2387 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2387 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2387 host target RNA into VGAM2387 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96707] VGAM2388 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2388 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2388 host target RNA into VGAM2388 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96708] It is appreciated that a function of VGR3228 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3228 gene include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGR3228 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3228 gene: VGAM2387 host target protein and VGAM2388 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2387 and VGAM2388.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3229(VGR3229) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96709] VGR3229 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3229 gene was detected is described hereinabove with reference to Figs. 1-9.

[96710] VGR3229 gene encodes VGR3229 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96711] VGR3229 precursor RNA folds spatially, forming VGR3229 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3229 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3229 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96712] VGR3229 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2389 precursor RNA, VGAM2390 precursor RNA, VGAM2391 precursor RNA, VGAM2392 precursor RNA, VGAM2393 precursor RNA, VGAM2394 precursor RNA, VGAM2395 precursor RNA and VGAM2396 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96713] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2389 RNA, VGAM2390 RNA, VGAM2391 RNA, VGAM2392 RNA, VGAM2393 RNA, VGAM2394 RNA, VGAM2395 RNA and

VGAM2396 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96714] VGAM2389 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2389 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2389 host target RNA into VGAM2389 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96715] VGAM2390 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2390 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2390 host target RNA into VGAM2390 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96716] VGAM2391 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2391 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2391 host target RNA into VGAM2391 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96717] VGAM2392 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2392 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2392 host target RNA into VGAM2392 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96718] VGAM2393 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2393 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2393 host target RNA into VGAM2393 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96719] VGAM2394 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2394 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2394 host target RNA into VGAM2394 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96720] VGAM2395 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2395 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2395 host target RNA into VGAM2395 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96721] VGAM2396 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2396 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2396 host target RNA into VGAM2396 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96722] It is appreciated that a function of VGR3229 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3229 gene include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGR3229 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3229 gene: VGAM2389 host target protein, VGAM2390 host target protein, VGAM2391 host target protein, VGAM2392 host target protein, VGAM2393 host target protein, VGAM2394 host target protein, VGAM2395 host target protein and VGAM2396 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2389, VGAM2390, VGAM2391, VGAM2392, VGAM2393, VGAM2394, VGAM2395 and VGAM2396.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3230(VGR3230) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96723] VGR3230 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3230 gene was detected is described hereinabove with reference to Figs. 1-9.

[96724] VGR3230 gene encodes VGR3230 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96725] VGR3230 precursor RNA folds spatially, forming VGR3230 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3230 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3230 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96726] VGR3230 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2397 precursor RNA, VGAM2398 precursor RNA, VGAM2399 precursor RNA, VGAM2400 precursor RNA, VGAM2401 precursor RNA, VGAM2402 precursor RNA, VGAM2403 precursor RNA and VGAM2404 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96727] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2397 RNA, VGAM2398 RNA, VGAM2399 RNA, VGAM2400 RNA, VGAM2401 RNA, VGAM2402 RNA, VGAM2403 RNA and

VGAM2404 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96728] VGAM2397 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2397 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2397 host target RNA into VGAM2397 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96729] VGAM2398 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2398 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2398 host target RNA into VGAM2398 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96730] VGAM2399 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2399 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2399 host target RNA into VGAM2399 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96731] VGAM2400 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2400 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2400 host target RNA into VGAM2400 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96732] VGAM2401 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2401 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2401 host target RNA into VGAM2401 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96733] VGAM2402 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2402 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2402 host target RNA into VGAM2402 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96734] VGAM2403 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2403 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2403 host target RNA into VGAM2403 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96735] VGAM2404 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2404 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2404 host target RNA into VGAM2404 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96736] It is appreciated that a function of VGR3230 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3230 gene include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGR3230 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3230 gene: VGAM2397 host target protein, VGAM2398 host target protein, VGAM2399 host target protein, VGAM2400 host target protein, VGAM2401 host target protein, VGAM2402 host target protein, VGAM2403 host target protein and VGAM2404 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2397, VGAM2398, VGAM2399, VGAM2400, VGAM2401, VGAM2402, VGAM2403 and VGAM2404.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3231(VGR3231) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96737] VGR3231 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3231 gene was detected is described hereinabove with reference to Figs. 1-9.

[96738] VGR3231 gene encodes VGR3231 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96739] VGR3231 precursor RNA folds spatially, forming VGR3231 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3231 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3231 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96740] VGR3231 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2405 precursor RNA, VGAM2406 precursor RNA, VGAM2407 precursor RNA, VGAM2408 precursor RNA, VGAM2409 precursor RNA, VGAM2410 precursor RNA, VGAM2411 precursor RNA and VGAM2412 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96741] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2405 RNA, VGAM2406 RNA, VGAM2407 RNA, VGAM2408 RNA, VGAM2409 RNA, VGAM2410 RNA, VGAM2411 RNA and

VGAM2412 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96742] VGAM2405 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2405 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2405 host target RNA into VGAM2405 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96743] VGAM2406 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2406 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2406 host target RNA into VGAM2406 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96744] VGAM2407 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2407 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2407 host target RNA into VGAM2407 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96745] VGAM2408 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2408 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2408 host target RNA into VGAM2408 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96746] VGAM2409 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2409 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2409 host target RNA into VGAM2409 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96747] VGAM2410 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2410 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2410 host target RNA into VGAM2410 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96748] VGAM2411 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2411 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2411 host target RNA into VGAM2411 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96749] VGAM2412 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2412 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2412 host target RNA into VGAM2412 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96750] It is appreciated that a function of VGR3231 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3231 gene include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGR3231 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3231 gene: VGAM2405 host target protein, VGAM2406 host target protein, VGAM2407 host target protein, VGAM2408 host target protein, VGAM2409 host target protein, VGAM2410 host target protein, VGAM2411 host target protein and VGAM2412 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2405, VGAM2406, VGAM2407, VGAM2408, VGAM2409, VGAM2410, VGAM2411 and VGAM2412.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3232(VGR3232) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96751] VGR3232 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3232 gene was detected is described hereinabove with reference to Figs. 1-9.

[96752] VGR3232 gene encodes VGR3232 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96753] VGR3232 precursor RNA folds spatially, forming VGR3232 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3232 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3232 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96754] VGR3232 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2413 precursor RNA, VGAM2414 precursor RNA, VGAM2415 precursor RNA, VGAM2416 precursor RNA, VGAM2417 precursor RNA, VGAM2418 precursor RNA, VGAM2419 precursor RNA and VGAM2420 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96755] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2413 RNA, VGAM2414 RNA, VGAM2415 RNA, VGAM2416 RNA, VGAM2417 RNA, VGAM2418 RNA, VGAM2419 RNA and

VGAM2420 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96756] VGAM2413 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2413 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2413 host target RNA into VGAM2413 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96757] VGAM2414 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2414 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2414 host target RNA into VGAM2414 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96758] VGAM2415 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2415 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2415 host target RNA into VGAM2415 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96759] VGAM2416 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2416 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2416 host target RNA into VGAM2416 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96760] VGAM2417 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2417 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2417 host target RNA into VGAM2417 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96761] VGAM2418 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2418 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2418 host target RNA into VGAM2418 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96762] VGAM2419 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2419 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2419 host target RNA into VGAM2419 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96763] VGAM2420 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2420 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2420 host target RNA into VGAM2420 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96764] It is appreciated that a function of VGR3232 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3232 gene include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGR3232 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3232 gene: VGAM2413 host target protein, VGAM2414 host target protein, VGAM2415 host target protein, VGAM2416 host target protein, VGAM2417 host target protein, VGAM2418 host target protein, VGAM2419 host target protein and VGAM2420 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2413, VGAM2414, VGAM2415, VGAM2416, VGAM2417, VGAM2418, VGAM2419 and VGAM2420.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3233(VGR3233) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96765] VGR3233 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3233 gene was detected is described hereinabove with reference to Figs. 1-9.

[96766] VGR3233 gene encodes VGR3233 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96767] VGR3233 precursor RNA folds spatially, forming VGR3233 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3233 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3233 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96768] VGR3233 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2421 precursor RNA, VGAM2422 precursor RNA, VGAM2423 precursor RNA, VGAM2424 precursor RNA, VGAM2425 precursor RNA, VGAM2426 precursor RNA, VGAM2427 precursor RNA and VGAM2428 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96769] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2421 RNA, VGAM2422 RNA, VGAM2423 RNA, VGAM2424 RNA, VGAM2425 RNA, VGAM2426 RNA, VGAM2427 RNA and

VGAM2428 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96770] VGAM2421 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2421 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2421 host target RNA into VGAM2421 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96771] VGAM2422 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2422 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2422 host target RNA into VGAM2422 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96772] VGAM2423 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2423 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2423 host target RNA into VGAM2423 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96773] VGAM2424 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2424 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2424 host target RNA into VGAM2424 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96774] VGAM2425 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2425 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2425 host target RNA into VGAM2425 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96775] VGAM2426 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2426 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2426 host target RNA into VGAM2426 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96776] VGAM2427 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2427 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2427 host target RNA into VGAM2427 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96777] VGAM2428 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2428 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2428 host target RNA into VGAM2428 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96778] It is appreciated that a function of VGR3233 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3233 gene include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGR3233 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3233 gene: VGAM2421 host target protein, VGAM2422 host target protein, VGAM2423 host target protein, VGAM2424 host target protein, VGAM2425 host target protein, VGAM2426 host target protein, VGAM2427 host target protein and VGAM2428 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2421, VGAM2422, VGAM2423, VGAM2424, VGAM2425, VGAM2426, VGAM2427 and VGAM2428.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3234(VGR3234) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96779] VGR3234 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3234 gene was detected is described hereinabove with reference to Figs. 1-9.

[96780] VGR3234 gene encodes VGR3234 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96781] VGR3234 precursor RNA folds spatially, forming VGR3234 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3234 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3234 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96782] VGR3234 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2429 precursor RNA, VGAM2430 precursor RNA, VGAM2431 precursor RNA, VGAM2432 precursor RNA, VGAM2433 precursor RNA, VGAM2434 precursor RNA, VGAM2435 precursor RNA and VGAM2436 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96783] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2429 RNA, VGAM2430 RNA, VGAM2431 RNA, VGAM2432 RNA, VGAM2433 RNA, VGAM2434 RNA, VGAM2435 RNA and

VGAM2436 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96784] VGAM2429 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2429 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2429 host target RNA into VGAM2429 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96785] VGAM2430 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2430 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2430 host target RNA into VGAM2430 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96786] VGAM2431 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2431 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2431 host target RNA into VGAM2431 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96787] VGAM2432 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2432 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2432 host target RNA into VGAM2432 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96788] VGAM2433 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2433 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2433 host target RNA into VGAM2433 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96789] VGAM2434 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2434 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2434 host target RNA into VGAM2434 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96790] VGAM2435 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2435 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2435 host target RNA into VGAM2435 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96791] VGAM2436 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2436 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2436 host target RNA into VGAM2436 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96792] It is appreciated that a function of VGR3234 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3234 gene include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGR3234 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3234 gene: VGAM2429 host target protein, VGAM2430 host target protein, VGAM2431 host target protein, VGAM2432 host target protein, VGAM2433 host target protein, VGAM2434 host target protein, VGAM2435 host target protein and VGAM2436 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST

TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2429, VGAM2430, VGAM2431, VGAM2432, VGAM2433, VGAM2434, VGAM2435 and VGAM2436.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3235(VGR3235) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96793] VGR3235 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3235 gene was detected is described hereinabove with reference to Figs. 1-9.

[96794] VGR3235 gene encodes VGR3235 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96795] VGR3235 precursor RNA folds spatially, forming VGR3235 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3235 folded precursor RNA comprises a plurality of what is known in

the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3235 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96796] VGR3235 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2437 precursor RNA, VGAM2438 precursor RNA, VGAM2439 precursor RNA, VGAM2440 precursor RNA, VGAM2441 precursor RNA and VGAM2442 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96797] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2437 RNA, VGAM2438 RNA, VGAM2439 RNA, VGAM2440 RNA, VGAM2441 RNA and VGAM2442 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA,

each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96798] VGAM2437 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2437 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2437 host target RNA into VGAM2437 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96799] VGAM2438 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2438 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2438 host target RNA into

VGAM2438 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96800] VGAM2439 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2439 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2439 host target RNA into VGAM2439 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96801] VGAM2440 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2440 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2440 host target RNA into VGAM2440 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96802] VGAM2441 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2441 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2441 host target RNA into VGAM2441 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96803] VGAM2442 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2442 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2442 host target RNA into VGAM2442 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96804] It is appreciated that a function of VGR3235 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3235 gene include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGR3235 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3235 gene: VGAM2437 host target protein, VGAM2438 host target protein, VGAM2439 host target protein, VGAM2440 host target protein, VGAM2441 host target protein and VGAM2442 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2437, VGAM2438, VGAM2439, VGAM2440, VGAM2441 and VGAM2442.Fig.

9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3236(VGR3236) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96805] VGR3236 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3236 gene was detected is described hereinabove with reference to Figs. 1-9.

[96806] VGR3236 gene encodes VGR3236 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96807] VGR3236 precursor RNA folds spatially, forming VGR3236 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3236 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3236 precursor RNA comprises a plurality of seg-

ments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96808] VGR3236 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2443 precursor RNA, VGAM2444 precursor RNA, VGAM2445 precursor RNA, VGAM2446 precursor RNA, VGAM2447 precursor RNA, VGAM2448 precursor RNA, VGAM2449 precursor RNA and VGAM2450 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96809] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2443 RNA, VGAM2444 RNA, VGAM2445 RNA, VGAM2446 RNA, VGAM2447 RNA, VGAM2448 RNA, VGAM2449 RNA and VGAM2450 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96810] VGAM2443 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2443 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2443 host target RNA into VGAM2443 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96811] VGAM2444 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2444 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2444 host target RNA into VGAM2444 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96812] VGAM2445 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2445 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2445 host target RNA into VGAM2445 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96813] VGAM2446 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2446 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2446 host target RNA into VGAM2446 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96814] VGAM2447 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2447 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2447 host target RNA into VGAM2447 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96815] VGAM2448 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2448 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2448 host target RNA into

VGAM2448 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96816] VGAM2449 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2449 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2449 host target RNA into VGAM2449 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96817] VGAM2450 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2450 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2450 host target RNA into VGAM2450 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96818] It is appreciated that a function of VGR3236 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3236 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3236 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3236 gene: VGAM2443 host target protein, VGAM2444 host target protein, VGAM2445 host target protein, VGAM2446 host target protein, VGAM2447 host target protein, VGAM2448 host target protein, VGAM2449 host target protein and VGAM2450 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2443, VGAM2444, VGAM2445, VGAM2446, VGAM2447,

VGAM2448, VGAM2449 and VGAM2450.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3237(VGR3237) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96819] VGR3237 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3237 gene was detected is described hereinabove with reference to Figs. 1-9.

[96820] VGR3237 gene encodes VGR3237 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96821] VGR3237 precursor RNA folds spatially, forming VGR3237 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3237 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3237 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96822] VGR3237 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2451 precursor RNA, VGAM2452 precursor RNA, VGAM2453 precursor RNA, VGAM2454 precursor RNA, VGAM2455 precursor RNA, VGAM2456 precursor RNA, VGAM2457 precursor RNA and VGAM2458 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96823] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2451 RNA, VGAM2452 RNA, VGAM2453 RNA, VGAM2454 RNA, VGAM2455 RNA, VGAM2456 RNA, VGAM2457 RNA and VGAM2458 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96824] VGAM2451 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2451 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2451 host target RNA into VGAM2451 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96825] VGAM2452 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2452 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2452 host target RNA into VGAM2452 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96826] VGAM2453 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2453 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2453 host target RNA into VGAM2453 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96827] VGAM2454 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2454 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2454 host target RNA into VGAM2454 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96828] VGAM2455 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2455 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2455 host target RNA into VGAM2455 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96829] VGAM2456 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2456 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2456 host target RNA into VGAM2456 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96830] VGAM2457 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2457 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2457 host target RNA into VGAM2457 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96831] VGAM2458 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2458 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2458 host target RNA into VGAM2458 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96832] It is appreciated that a function of VGR3237 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3237 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3237 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3237 gene: VGAM2451 host target protein, VGAM2452 host target protein, VGAM2453 host target protein, VGAM2454 host target protein,

VGAM2455 host target protein, VGAM2456 host target protein, VGAM2457 host target protein and VGAM2458 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2451, VGAM2452, VGAM2453, VGAM2454, VGAM2455, VGAM2456, VGAM2457 and VGAM2458.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3238(VGR3238) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96833] VGR3238 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3238 gene was detected is described hereinabove with reference to Figs. 1-9.

[96834] VGR3238 gene encodes VGR3238 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96835] VGR3238 precursor RNA folds spatially, forming VGR3238 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3238 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3238 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96836] VGR3238 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2459 precursor RNA, VGAM2460 precursor RNA, VGAM2461 precursor RNA, VGAM2462 precursor RNA, VGAM2463 precursor RNA, VGAM2464 precursor RNA, VGAM2465 precursor RNA and VGAM2466 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96837] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2459 RNA, VGAM2460 RNA, VGAM2461 RNA, VGAM2462 RNA, VGAM2463 RNA, VGAM2464 RNA, VGAM2465 RNA and VGAM2466 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96838] VGAM2459 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2459 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2459 host target RNA into VGAM2459 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96839] VGAM2460 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2460 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2460 host target RNA into VGAM2460 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96840] VGAM2461 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2461 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2461 host target RNA into VGAM2461 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96841] VGAM2462 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2462 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2462 host target RNA into VGAM2462 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96842] VGAM2463 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2463 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2463 host target RNA into VGAM2463 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96843] VGAM2464 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2464 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2464 host target RNA into VGAM2464 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96844] VGAM2465 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2465 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2465 host target RNA into VGAM2465 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96845] VGAM2466 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2466 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2466 host target RNA into VGAM2466 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96846] It is appreciated that a function of VGR3238 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3238 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3238 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3238 gene: VGAM2459 host target protein, VGAM2460 host target protein, VGAM2461 host target protein, VGAM2462 host target protein,

VGAM2463 host target protein, VGAM2464 host target protein, VGAM2465 host target protein and VGAM2466 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2459, VGAM2460, VGAM2461, VGAM2462, VGAM2463, VGAM2464, VGAM2465 and VGAM2466.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3239(VGR3239) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96847] VGR3239 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3239 gene was detected is described hereinabove with reference to Figs. 1-9.

[96848] VGR3239 gene encodes VGR3239 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96849] VGR3239 precursor RNA folds spatially, forming VGR3239 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3239 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3239 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96850] VGR3239 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2467 precursor RNA, VGAM2468 precursor RNA, VGAM2469 precursor RNA, VGAM2470 precursor RNA, VGAM2471 precursor RNA, VGAM2472 precursor RNA, VGAM2473 precursor RNA and VGAM2474 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96851] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2467 RNA, VGAM2468 RNA, VGAM2469 RNA, VGAM2470 RNA, VGAM2471 RNA, VGAM2472 RNA, VGAM2473 RNA and VGAM2474 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96852] VGAM2467 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2467 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2467 host target RNA into VGAM2467 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96853] VGAM2468 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2468 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2468 host target RNA into VGAM2468 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96854] VGAM2469 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2469 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2469 host target RNA into VGAM2469 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96855] VGAM2470 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2470 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2470 host target RNA into VGAM2470 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96856] VGAM2471 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2471 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2471 host target RNA into VGAM2471 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96857] VGAM2472 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2472 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2472 host target RNA into VGAM2472 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96858] VGAM2473 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2473 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2473 host target RNA into VGAM2473 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96859] VGAM2474 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2474 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2474 host target RNA into VGAM2474 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96860] It is appreciated that a function of VGR3239 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3239 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3239 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3239 gene: VGAM2467 host target protein, VGAM2468 host target protein, VGAM2469 host target protein, VGAM2470 host target protein,

VGAM2471 host target protein, VGAM2472 host target protein, VGAM2473 host target protein and VGAM2474 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2467, VGAM2468, VGAM2469, VGAM2470, VGAM2471, VGAM2472, VGAM2473 and VGAM2474.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3240(VGR3240) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96861] VGR3240 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3240 gene was detected is described hereinabove with reference to Figs. 1-9.

[96862] VGR3240 gene encodes VGR3240 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96863] VGR3240 precursor RNA folds spatially, forming VGR3240 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3240 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3240 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96864] VGR3240 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2475 precursor RNA, VGAM2476 precursor RNA, VGAM2477 precursor RNA, VGAM2478 precursor RNA, VGAM2479 precursor RNA, VGAM2480 precursor RNA, VGAM2481 precursor RNA and VGAM2482 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96865] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2475 RNA, VGAM2476 RNA, VGAM2477 RNA, VGAM2478 RNA, VGAM2479 RNA, VGAM2480 RNA, VGAM2481 RNA and VGAM2482 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96866] VGAM2475 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2475 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2475 host target RNA into VGAM2475 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96867] VGAM2476 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2476 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2476 host target RNA into VGAM2476 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96868] VGAM2477 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2477 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2477 host target RNA into VGAM2477 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96869] VGAM2478 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2478 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2478 host target RNA into VGAM2478 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96870] VGAM2479 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2479 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2479 host target RNA into VGAM2479 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96871] VGAM2480 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2480 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2480 host target RNA into VGAM2480 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96872] VGAM2481 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2481 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2481 host target RNA into VGAM2481 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96873] VGAM2482 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2482 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2482 host target RNA into VGAM2482 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96874] It is appreciated that a function of VGR3240 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3240 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3240 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3240 gene: VGAM2475 host target protein, VGAM2476 host target protein, VGAM2477 host target protein, VGAM2478 host target protein,

VGAM2479 host target protein, VGAM2480 host target protein, VGAM2481 host target protein and VGAM2482 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2475, VGAM2476, VGAM2477, VGAM2478, VGAM2479, VGAM2480, VGAM2481 and VGAM2482.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3241(VGR3241) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96875] VGR3241 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3241 gene was detected is described hereinabove with reference to Figs. 1-9.

[96876] VGR3241 gene encodes VGR3241 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96877] VGR3241 precursor RNA folds spatially, forming VGR3241 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3241 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3241 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96878] VGR3241 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2483 precursor RNA, VGAM2484 precursor RNA, VGAM2485 precursor RNA, VGAM2486 precursor RNA, VGAM2487 precursor RNA, VGAM2488 precursor RNA, VGAM2489 precursor RNA and VGAM2490 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96879] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2483 RNA, VGAM2484 RNA, VGAM2485 RNA, VGAM2486 RNA, VGAM2487 RNA, VGAM2488 RNA, VGAM2489 RNA and VGAM2490 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96880] VGAM2483 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2483 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2483 host target RNA into VGAM2483 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96881] VGAM2484 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2484 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2484 host target RNA into VGAM2484 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96882] VGAM2485 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2485 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2485 host target RNA into VGAM2485 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96883] VGAM2486 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2486 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2486 host target RNA into VGAM2486 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96884] VGAM2487 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2487 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2487 host target RNA into VGAM2487 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96885] VGAM2488 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2488 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2488 host target RNA into VGAM2488 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96886] VGAM2489 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2489 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2489 host target RNA into VGAM2489 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96887] VGAM2490 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2490 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2490 host target RNA into VGAM2490 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96888] It is appreciated that a function of VGR3241 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3241 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3241 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3241 gene: VGAM2483 host target protein, VGAM2484 host target protein, VGAM2485 host target protein, VGAM2486 host target protein,

VGAM2487 host target protein, VGAM2488 host target protein, VGAM2489 host target protein and VGAM2490 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2483, VGAM2484, VGAM2485, VGAM2486, VGAM2487, VGAM2488, VGAM2489 and VGAM2490.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3242(VGR3242) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96889] VGR3242 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3242 gene was detected is described hereinabove with reference to Figs. 1-9.

[96890] VGR3242 gene encodes VGR3242 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96891] VGR3242 precursor RNA folds spatially, forming VGR3242 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3242 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3242 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96892] VGR3242 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2491 precursor RNA, VGAM2492 precursor RNA, VGAM2493 precursor RNA, VGAM2494 precursor RNA, VGAM2495 precursor RNA, VGAM2496 precursor RNA, VGAM2497 precursor RNA and VGAM2498 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96893] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2491 RNA, VGAM2492 RNA, VGAM2493 RNA, VGAM2494 RNA, VGAM2495 RNA, VGAM2496 RNA, VGAM2497 RNA and VGAM2498 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96894] VGAM2491 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2491 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2491 host target RNA into VGAM2491 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96895] VGAM2492 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2492 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2492 host target RNA into VGAM2492 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96896] VGAM2493 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2493 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2493 host target RNA into VGAM2493 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96897] VGAM2494 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2494 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2494 host target RNA into VGAM2494 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96898] VGAM2495 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2495 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2495 host target RNA into VGAM2495 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96899] VGAM2496 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2496 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2496 host target RNA into VGAM2496 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96900] VGAM2497 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2497 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2497 host target RNA into VGAM2497 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96901] VGAM2498 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2498 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2498 host target RNA into VGAM2498 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96902] It is appreciated that a function of VGR3242 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3242 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3242 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3242 gene: VGAM2491 host target protein, VGAM2492 host target protein, VGAM2493 host target protein, VGAM2494 host target protein,

VGAM2495 host target protein, VGAM2496 host target protein, VGAM2497 host target protein and VGAM2498 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2491, VGAM2492, VGAM2493, VGAM2494, VGAM2495, VGAM2496, VGAM2497 and VGAM2498.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3243(VGR3243) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96903] VGR3243 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3243 gene was detected is described hereinabove with reference to Figs. 1-9.

[96904] VGR3243 gene encodes VGR3243 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96905] VGR3243 precursor RNA folds spatially, forming VGR3243 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3243 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3243 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96906] VGR3243 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2499 precursor RNA, VGAM2500 precursor RNA, VGAM2501 precursor RNA, VGAM2502 precursor RNA, VGAM2503 precursor RNA, VGAM2504 precursor RNA, VGAM2505 precursor RNA and VGAM2506 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96907] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2499 RNA, VGAM2500 RNA, VGAM2501 RNA, VGAM2502 RNA, VGAM2503 RNA, VGAM2504 RNA, VGAM2505 RNA and VGAM2506 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96908] VGAM2499 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2499 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2499 host target RNA into VGAM2499 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96909] VGAM2500 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2500 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2500 host target RNA into VGAM2500 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96910] VGAM2501 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2501 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2501 host target RNA into VGAM2501 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96911] VGAM2502 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2502 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2502 host target RNA into VGAM2502 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96912] VGAM2503 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2503 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2503 host target RNA into VGAM2503 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96913] VGAM2504 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2504 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2504 host target RNA into VGAM2504 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96914] VGAM2505 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2505 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2505 host target RNA into VGAM2505 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96915] VGAM2506 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2506 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2506 host target RNA into VGAM2506 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96916] It is appreciated that a function of VGR3243 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3243 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3243 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3243 gene: VGAM2499 host target protein, VGAM2500 host target protein, VGAM2501 host target protein, VGAM2502 host target protein,

VGAM2503 host target protein, VGAM2504 host target protein, VGAM2505 host target protein and VGAM2506 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2499, VGAM2500, VGAM2501, VGAM2502, VGAM2503, VGAM2504, VGAM2505 and VGAM2506.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3244(VGR3244) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96917] VGR3244 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3244 gene was detected is described hereinabove with reference to Figs. 1-9.

[96918] VGR3244 gene encodes VGR3244 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96919] VGR3244 precursor RNA folds spatially, forming VGR3244 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3244 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3244 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96920] VGR3244 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2507 precursor RNA, VGAM2508 precursor RNA, VGAM2509 precursor RNA, VGAM2510 precursor RNA, VGAM2511 precursor RNA, VGAM2512 precursor RNA, VGAM2513 precursor RNA and VGAM2514 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96921] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2507 RNA, VGAM2508 RNA, VGAM2509 RNA, VGAM2510 RNA, VGAM2511 RNA, VGAM2512 RNA, VGAM2513 RNA and VGAM2514 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96922] VGAM2507 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2507 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2507 host target RNA into VGAM2507 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96923] VGAM2508 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2508 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2508 host target RNA into VGAM2508 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96924] VGAM2509 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2509 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2509 host target RNA into VGAM2509 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96925] VGAM2510 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2510 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2510 host target RNA into VGAM2510 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96926] VGAM2511 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2511 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2511 host target RNA into VGAM2511 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96927] VGAM2512 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2512 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2512 host target RNA into VGAM2512 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96928] VGAM2513 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2513 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2513 host target RNA into VGAM2513 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96929] VGAM2514 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2514 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2514 host target RNA into VGAM2514 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96930] It is appreciated that a function of VGR3244 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3244 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3244 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3244 gene: VGAM2507 host target protein, VGAM2508 host target protein, VGAM2509 host target protein, VGAM2510 host target protein,

VGAM2511 host target protein, VGAM2512 host target protein, VGAM2513 host target protein and VGAM2514 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2507, VGAM2508, VGAM2509, VGAM2510, VGAM2511, VGAM2512, VGAM2513 and VGAM2514.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3245(VGR3245) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96931] VGR3245 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3245 gene was detected is described hereinabove with reference to Figs. 1-9.

[96932] VGR3245 gene encodes VGR3245 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96933] VGR3245 precursor RNA folds spatially, forming VGR3245 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3245 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3245 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96934] VGR3245 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2515 precursor RNA, VGAM2516 precursor RNA, VGAM2517 precursor RNA, VGAM2518 precursor RNA, VGAM2519 precursor RNA, VGAM2520 precursor RNA, VGAM2521 precursor RNA and VGAM2522 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96935] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2515 RNA, VGAM2516 RNA, VGAM2517 RNA, VGAM2518 RNA, VGAM2519 RNA, VGAM2520 RNA, VGAM2521 RNA and VGAM2522 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96936] VGAM2515 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2515 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2515 host target RNA into VGAM2515 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96937] VGAM2516 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2516 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2516 host target RNA into VGAM2516 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96938] VGAM2517 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2517 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2517 host target RNA into VGAM2517 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96939] VGAM2518 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2518 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2518 host target RNA into VGAM2518 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96940] VGAM2519 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2519 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2519 host target RNA into VGAM2519 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96941] VGAM2520 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2520 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2520 host target RNA into VGAM2520 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96942] VGAM2521 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2521 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2521 host target RNA into VGAM2521 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96943] VGAM2522 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2522 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2522 host target RNA into VGAM2522 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96944] It is appreciated that a function of VGR3245 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3245 gene include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3245 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3245 gene: VGAM2515 host target protein, VGAM2516 host target protein, VGAM2517 host target protein, VGAM2518 host target protein,

VGAM2519 host target protein, VGAM2520 host target protein, VGAM2521 host target protein and VGAM2522 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2515, VGAM2516, VGAM2517, VGAM2518, VGAM2519, VGAM2520, VGAM2521 and VGAM2522.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3246(VGR3246) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96945] VGR3246 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3246 gene was detected is described hereinabove with reference to Figs. 1-9.

[96946] VGR3246 gene encodes VGR3246 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96947] VGR3246 precursor RNA folds spatially, forming VGR3246 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3246 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3246 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96948] VGR3246 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2523 precursor RNA, VGAM2524 precursor RNA, VGAM2525 precursor RNA, VGAM2526 precursor RNA and VGAM2527 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96949] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM2523 RNA, VGAM2524 RNA, VGAM2525 RNA, VGAM2526 RNA and VGAM2527 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96950] VGAM2523 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2523 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2523 host target RNA into VGAM2523 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96951] VGAM2524 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2524 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2524 host target RNA into VGAM2524 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96952] VGAM2525 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2525 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2525 host target RNA into VGAM2525 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96953] VGAM2526 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2526 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2526 host target RNA into VGAM2526 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96954] VGAM2527 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2527 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2527 host target RNA into VGAM2527 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96955] It is appreciated that a function of VGR3246 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3246 gene include

diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGR3246 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3246 gene: VGAM2523 host target protein, VGAM2524 host target protein, VGAM2525 host target protein, VGAM2526 host target protein and VGAM2527 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2523, VGAM2524, VGAM2525, VGAM2526 and VGAM2527.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3247(VGR3247) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96956] VGR3247 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3247 gene was detected is described hereinabove with reference to Figs. 1-9.

[96957] VGR3247 gene encodes VGR3247 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96958] VGR3247 precursor RNA folds spatially, forming VGR3247 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3247 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3247 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96959] VGR3247 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2530 precursor RNA and VGAM2531 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs

being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96960] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2530 RNA and VGAM2531 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96961] VGAM2530 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2530 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2530 host target RNA into VGAM2530 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96962] VGAM2531 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2531 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2531 host target RNA into VGAM2531 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96963] It is appreciated that a function of VGR3247 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3247 gene include diagnosis, prevention and treatment of viral infection by Pepper Ringspot Virus. Specific functions, and accordingly utilities, of VGR3247 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3247 gene: VGAM2530 host target protein and VGAM2531 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove

with reference to VGAM2530 and VGAM2531.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3248(VGR3248) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96964] VGR3248 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3248 gene was detected is described hereinabove with reference to Figs. 1-9.

[96965] VGR3248 gene encodes VGR3248 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96966] VGR3248 precursor RNA folds spatially, forming VGR3248 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3248 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of

VGR3248 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96967] VGR3248 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2532 precursor RNA, VGAM2533 precursor RNA, VGAM2534 precursor RNA and VGAM2535 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96968] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2532 RNA, VGAM2533 RNA, VGAM2534 RNA and VGAM2535 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96969] VGAM2532 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2532 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2532 host target RNA into VGAM2532 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96970] VGAM2533 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2533 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2533 host target RNA into VGAM2533 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96971] VGAM2534 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2534 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2534 host target RNA into VGAM2534 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96972] VGAM2535 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2535 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2535 host target RNA into VGAM2535 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96973] It is appreciated that a function of VGR3248 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3248 gene include diagnosis, prevention and treatment of viral infection by Rio Bravo Virus. Specific functions, and accordingly utilities, of VGR3248 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3248 gene: VGAM2532 host target protein, VGAM2533 host target protein, VGAM2534 host target protein and VGAM2535 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2532, VGAM2533, VGAM2534 and VGAM2535.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3249(VGR3249) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[96974] VGR3249 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3249 gene was detected is described hereinabove with reference to Figs. 1-9.

[96975] VGR3249 gene encodes VGR3249 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96976] VGR3249 precursor RNA folds spatially, forming VGR3249 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3249 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3249 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96977] VGR3249 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2536 precursor RNA, VGAM2537

precursor RNA and VGAM2538 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96978] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2536 RNA, VGAM2537 RNA and VGAM2538 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96979] VGAM2536 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2536 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2536 host target RNA into VGAM2536 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96980] VGAM2537 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2537 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2537 host target RNA into VGAM2537 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96981] VGAM2538 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2538 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2538 host target RNA into

VGAM2538 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96982] It is appreciated that a function of VGR3249 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3249 gene include diagnosis, prevention and treatment of viral infection by Pestivirus Reindeer-1. Specific functions, and accordingly utilities, of VGR3249 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3249 gene: VGAM2536 host target protein, VGAM2537 host target protein and VGAM2538 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2536, VGAM2537 and VGAM2538.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3250(VGR3250) viral gene, which encodes an `operon-like` cluster of novel viral mi-

cro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96983] VGR3250 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3250 gene was detected is described hereinabove with reference to Figs. 1-9.

[96984] VGR3250 gene encodes VGR3250 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96985] VGR3250 precursor RNA folds spatially, forming VGR3250 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3250 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3250 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96986] VGR3250 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2539 precursor RNA and VGAM2540 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96987] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2539 RNA and VGAM2540 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96988] VGAM2539 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2539 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2539 host target RNA into

VGAM2539 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96989] VGAM2540 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2540 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2540 host target RNA into VGAM2540 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96990] It is appreciated that a function of VGR3250 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3250 gene include diagnosis, prevention and treatment of viral infection by Pestivirus Giraffe-1. Specific functions, and accordingly utilities, of VGR3250 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3250 gene: VGAM2539 host target protein and VGAM2540 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2539 and VGAM2540.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3251(VGR3251) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[96991] VGR3251 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3251 gene was detected is described hereinabove with reference to Figs. 1-9.

[96992] VGR3251 gene encodes VGR3251 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[96993] VGR3251 precursor RNA folds spatially, forming VGR3251 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3251 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3251 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[96994] VGR3251 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2541 precursor RNA, VGAM2542 precursor RNA, VGAM2543 precursor RNA, VGAM2544 precursor RNA, VGAM2545 precursor RNA, VGAM2546 precursor RNA and VGAM2547 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[96995] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2541 RNA, VGAM2542 RNA, VGAM2543 RNA, VGAM2544 RNA, VGAM2545 RNA, VGAM2546 RNA and VGAM2547 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[96996] VGAM2541 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2541 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2541 host target RNA into VGAM2541 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96997] VGAM2542 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2542 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2542 host target RNA into VGAM2542 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96998] VGAM2543 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2543 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2543 host target RNA into VGAM2543 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[96999] VGAM2544 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2544 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2544 host target RNA into VGAM2544 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97000] VGAM2545 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2545 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2545 host target RNA into VGAM2545 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97001] VGAM2546 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2546 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2546 host target RNA into VGAM2546 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97002] VGAM2547 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2547 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2547 host target RNA into VGAM2547 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97003] It is appreciated that a function of VGR3251 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3251 gene include diagnosis, prevention and treatment of viral infection by Langat Virus. Specific functions, and accordingly utilities, of VGR3251 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3251 gene: VGAM2541 host target protein, VGAM2542 host target protein, VGAM2543 host target protein, VGAM2544 host target protein, VGAM2545 host target protein, VGAM2546 host target protein and VGAM2547 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2541, VGAM2542, VGAM2543, VGAM2544, VGAM2545, VGAM2546 and VGAM2547.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3252(VGR3252) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of

at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97004] VGR3252 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3252 gene was detected is described hereinabove with reference to Figs. 1-9.

[97005] VGR3252 gene encodes VGR3252 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97006] VGR3252 precursor RNA folds spatially, forming VGR3252 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3252 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3252 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97007] VGR3252 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM

precursor RNAs, VGAM2548 precursor RNA, VGAM2549 precursor RNA and VGAM2550 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97008] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2548 RNA, VGAM2549 RNA and VGAM2550 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97009] VGAM2548 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2548 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2548 host target RNA into

VGAM2548 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97010] VGAM2549 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2549 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2549 host target RNA into VGAM2549 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97011] VGAM2550 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2550 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2550 host target RNA into VGAM2550 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97012] It is appreciated that a function of VGR3252 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3252 gene include diagnosis, prevention and treatment of viral infection by Saccharomyces Cerevisiae Virus L-A. Specific functions, and accordingly utilities, of VGR3252 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3252 gene: VGAM2548 host target protein, VGAM2549 host target protein and VGAM2550 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2548, VGAM2549 and VGAM2550.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3253(VGR3253) viral gene,

which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97013] VGR3253 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3253 gene was detected is described hereinabove with reference to Figs. 1-9.

[97014] VGR3253 gene encodes VGR3253 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97015] VGR3253 precursor RNA folds spatially, forming VGR3253 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3253 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3253 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well

known in the art.

[97016] VGR3253 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2552 precursor RNA and VGAM2553 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97017] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2552 RNA and VGAM2553 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97018] VGAM2552 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2552 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2552 host target RNA into VGAM2552 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97019] VGAM2553 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2553 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2553 host target RNA into VGAM2553 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97020] It is appreciated that a function of VGR3253 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3253 gene include diagnosis, prevention and treatment of viral infection by Rice Ragged Stunt Virus. Specific functions, and accordingly utilities, of VGR3253 gene correlate with, and may

be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3253 gene: VGAM2552 host target protein and VGAM2553 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2552 and VGAM2553.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3254(VGR3254) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97021] VGR3254 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3254 gene was detected is described hereinabove with reference to Figs. 1-9.

[97022] VGR3254 gene encodes VGR3254 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-

cally several hundred nucleotides long.

[97023] VGR3254 precursor RNA folds spatially, forming VGR3254 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3254 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3254 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97024] VGR3254 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2554 precursor RNA, VGAM2555 precursor RNA and VGAM2556 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97025] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM2554 RNA, VGAM2555 RNA and VGAM2556 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97026] VGAM2554 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2554 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2554 host target RNA into VGAM2554 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97027] VGAM2555 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2555 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2555 host target RNA into VGAM2555 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97028] VGAM2556 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2556 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2556 host target RNA into VGAM2556 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97029] It is appreciated that a function of VGR3254 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3254 gene include diagnosis, prevention and treatment of viral infection by

Plautia Stali Intestine Virus. Specific functions, and accordingly utilities, of VGR3254 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3254 gene: VGAM2554 host target protein, VGAM2555 host target protein and VGAM2556 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2554, VGAM2555 and VGAM2556.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3255(VGR3255) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97030] VGR3255 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3255 gene was detected is described hereinabove with reference to Figs.

1-9.

[97031] VGR3255 gene encodes VGR3255 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97032] VGR3255 precursor RNA folds spatially, forming VGR3255 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3255 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3255 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97033] VGR3255 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2557 precursor RNA, VGAM2558 precursor RNA, VGAM2559 precursor RNA, VGAM2560 precursor RNA, VGAM2561 precursor RNA, VGAM2562 precursor RNA and VGAM2563 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97034] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2557 RNA, VGAM2558 RNA, VGAM2559 RNA, VGAM2560 RNA, VGAM2561 RNA, VGAM2562 RNA and VGAM2563 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97035] VGAM2557 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2557 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2557 host target RNA into VGAM2557 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97036] VGAM2558 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2558 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2558 host target RNA into VGAM2558 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97037] VGAM2559 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2559 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2559 host target RNA into VGAM2559 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97038] VGAM2560 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2560 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2560 host target RNA into VGAM2560 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97039] VGAM2561 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2561 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2561 host target RNA into VGAM2561 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97040] VGAM2562 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2562 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2562 host target RNA into VGAM2562 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97041] VGAM2563 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2563 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2563 host target RNA into

VGAM2563 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97042] It is appreciated that a function of VGR3255 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3255 gene include diagnosis, prevention and treatment of viral infection by Himetobi P Virus. Specific functions, and accordingly utilities, of VGR3255 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3255 gene: VGAM2557 host target protein, VGAM2558 host target protein, VGAM2559 host target protein, VGAM2560 host target protein, VGAM2561 host target protein, VGAM2562 host target protein and VGAM2563 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2557, VGAM2558, VGAM2559, VGAM2560, VGAM2561, VGAM2562 and VGAM2563.Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3256(VGR3256) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97043] VGR3256 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3256 gene was detected is described hereinabove with reference to Figs. 1-9.

[97044] VGR3256 gene encodes VGR3256 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97045] VGR3256 precursor RNA folds spatially, forming VGR3256 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3256 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3256 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97046] VGR3256 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2564 precursor RNA, VGAM2565 precursor RNA, VGAM2566 precursor RNA, VGAM2567 precursor RNA, VGAM2568 precursor RNA, VGAM2569 precursor RNA, VGAM2570 precursor RNA and VGAM2571 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97047] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2564 RNA, VGAM2565 RNA, VGAM2566 RNA, VGAM2567 RNA, VGAM2568 RNA, VGAM2569 RNA, VGAM2570 RNA and VGAM2571 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97048] VGAM2564 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2564 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2564 host target RNA into VGAM2564 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97049] VGAM2565 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2565 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2565 host target RNA into VGAM2565 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97050] VGAM2566 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2566 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2566 host target RNA into VGAM2566 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97051] VGAM2567 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2567 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2567 host target RNA into VGAM2567 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97052] VGAM2568 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2568 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2568 host target RNA into VGAM2568 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97053] VGAM2569 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2569 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2569 host target RNA into VGAM2569 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97054] VGAM2570 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2570 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2570 host target RNA into VGAM2570 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97055] VGAM2571 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2571 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2571 host target RNA into

VGAM2571 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97056] It is appreciated that a function of VGR3256 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3256 gene include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGR3256 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3256 gene: VGAM2564 host target protein, VGAM2565 host target protein, VGAM2566 host target protein, VGAM2567 host target protein, VGAM2568 host target protein, VGAM2569 host target protein, VGAM2570 host target protein and VGAM2571 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2564, VGAM2565, VGAM2566, VGAM2567, VGAM2568, VGAM2569, VGAM2570 and VGAM2571.Fig. 9 further

provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3257(VGR3257) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97057] VGR3257 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3257 gene was detected is described hereinabove with reference to Figs. 1-9.

[97058] VGR3257 gene encodes VGR3257 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97059] VGR3257 precursor RNA folds spatially, forming VGR3257 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3257 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3257 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97060] VGR3257 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2572 precursor RNA, VGAM2573 precursor RNA, VGAM2574 precursor RNA, VGAM2575 precursor RNA, VGAM2576 precursor RNA, VGAM2577 precursor RNA and VGAM2578 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97061] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2572 RNA, VGAM2573 RNA, VGAM2574 RNA, VGAM2575 RNA, VGAM2576 RNA, VGAM2577 RNA and VGAM2578 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97062] VGAM2572 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2572 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2572 host target RNA into VGAM2572 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97063] VGAM2573 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2573 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2573 host target RNA into VGAM2573 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97064] VGAM2574 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2574 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2574 host target RNA into VGAM2574 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97065] VGAM2575 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2575 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2575 host target RNA into VGAM2575 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97066] VGAM2576 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2576 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2576 host target RNA into VGAM2576 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97067] VGAM2577 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2577 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2577 host target RNA into VGAM2577 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97068] VGAM2578 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2578 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2578 host target RNA into VGAM2578 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97069] It is appreciated that a function of VGR3257 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3257 gene include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGR3257 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR3257 gene: VGAM2572 host target protein, VGAM2573 host target protein, VGAM2574 host target protein, VGAM2575 host target protein, VGAM2576 host target protein, VGAM2577 host target protein and VGAM2578 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2572, VGAM2573, VGAM2574, VGAM2575, VGAM2576, VGAM2577 and VGAM2578.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3258(VGR3258) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97070] VGR3258 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3258 gene was detected is described hereinabove with reference to Figs. 1-9.

[97071] VGR3258 gene encodes VGR3258 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97072] VGR3258 precursor RNA folds spatially, forming VGR3258 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3258 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3258 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97073] VGR3258 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2579 precursor RNA, VGAM2580 precursor RNA, VGAM2581 precursor RNA, VGAM2582 precursor RNA and VGAM2583 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig.

1.

[97074] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2579 RNA, VGAM2580 RNA, VGAM2581 RNA, VGAM2582 RNA and VGAM2583 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97075] VGAM2579 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2579 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2579 host target RNA into VGAM2579 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97076] VGAM2580 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2580 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2580 host target RNA into VGAM2580 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97077] VGAM2581 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2581 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2581 host target RNA into VGAM2581 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97078] VGAM2582 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2582 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2582 host target RNA into VGAM2582 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97079] VGAM2583 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2583 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2583 host target RNA into VGAM2583 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97080] It is appreciated that a function of VGR3258 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3258 gene include diagnosis, prevention and treatment of viral infection by Triatoma Virus. Specific functions, and accordingly utilities, of VGR3258 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3258 gene: VGAM2579 host target protein, VGAM2580 host target protein, VGAM2581 host target protein, VGAM2582 host target protein and VGAM2583 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2579, VGAM2580, VGAM2581, VGAM2582 and VGAM2583.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3259(VGR3259) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[97081] VGR3259 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3259 gene was detected is described hereinabove with reference to Figs. 1-9.

[97082] VGR3259 gene encodes VGR3259 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97083] VGR3259 precursor RNA folds spatially, forming VGR3259 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3259 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3259 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97084] VGR3259 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2584 precursor RNA, VGAM2585

precursor RNA, VGAM2586 precursor RNA, VGAM2587 precursor RNA and VGAM2588 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97085] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2584 RNA, VGAM2585 RNA, VGAM2586 RNA, VGAM2587 RNA and VGAM2588 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97086] VGAM2584 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2584 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2584 host target RNA into

VGAM2584 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97087] VGAM2585 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2585 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2585 host target RNA into VGAM2585 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97088] VGAM2586 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2586 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2586 host target RNA into VGAM2586 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97089] VGAM2587 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2587 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2587 host target RNA into VGAM2587 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97090] VGAM2588 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2588 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2588 host target RNA into VGAM2588 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97091] It is appreciated that a function of VGR3259 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3259 gene include diagnosis, prevention and treatment of viral infection by Satsuma Dwarf Virus. Specific functions, and accordingly utilities, of VGR3259 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3259 gene: VGAM2584 host target protein, VGAM2585 host target protein, VGAM2586 host target protein, VGAM2587 host target protein and VGAM2588 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2584, VGAM2585, VGAM2586, VGAM2587 and VGAM2588.Fig. 9 further provides a conceptual de-

scription of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3260(VGR3260) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97092] VGR3260 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3260 gene was detected is described hereinabove with reference to Figs. 1-9.

[97093] VGR3260 gene encodes VGR3260 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97094] VGR3260 precursor RNA folds spatially, forming VGR3260 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3260 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3260 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97095] VGR3260 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2589 precursor RNA, VGAM2590 precursor RNA, VGAM2591 precursor RNA, VGAM2592 precursor RNA, VGAM2593 precursor RNA, VGAM2594 precursor RNA and VGAM2595 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97096] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2589 RNA, VGAM2590 RNA, VGAM2591 RNA, VGAM2592 RNA, VGAM2593 RNA, VGAM2594 RNA and VGAM2595 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97097] VGAM2589 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2589 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2589 host target RNA into VGAM2589 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97098] VGAM2590 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2590 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2590 host target RNA into VGAM2590 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97099] VGAM2591 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2591 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2591 host target RNA into VGAM2591 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97100] VGAM2592 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2592 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2592 host target RNA into VGAM2592 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97101] VGAM2593 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2593 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2593 host target RNA into VGAM2593 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97102] VGAM2594 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2594 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2594 host target RNA into VGAM2594 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97103] VGAM2595 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2595 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2595 host target RNA into VGAM2595 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97104] It is appreciated that a function of VGR3260 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3260 gene include diagnosis, prevention and treatment of viral infection by Apple Latent Spherical Virus. Specific functions, and accordingly utilities, of VGR3260 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR3260 gene: VGAM2589 host target protein, VGAM2590 host target protein, VGAM2591 host target protein, VGAM2592 host target protein, VGAM2593 host target protein, VGAM2594 host target protein and VGAM2595 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2589, VGAM2590, VGAM2591, VGAM2592, VGAM2593, VGAM2594 and VGAM2595.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3261(VGR3261) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97105] VGR3261 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3261 gene was detected is described hereinabove with reference to Figs. 1-9.

[97106] VGR3261 gene encodes VGR3261 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97107] VGR3261 precursor RNA folds spatially, forming VGR3261 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3261 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3261 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97108] VGR3261 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2596 precursor RNA, VGAM2597 precursor RNA and VGAM2598 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97109] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2596 RNA, VGAM2597 RNA and VGAM2598 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97110] VGAM2596 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2596 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2596 host target RNA into VGAM2596 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97111] VGAM2597 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2597 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2597 host target RNA into VGAM2597 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97112] VGAM2598 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2598 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2598 host target RNA into VGAM2598 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97113] It is appreciated that a function of VGR3261 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3261 gene include diagnosis, prevention and treatment of viral infection by Tobacco Rattle Virus. Specific functions, and accordingly utilities, of VGR3261 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3261 gene: VGAM2596 host target protein, VGAM2597 host target protein and VGAM2598 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2596, VGAM2597 and VGAM2598.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3262(VGR3262) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97114] VGR3262 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3262 gene was detected is described hereinabove with reference to Figs. 1-9.

[97115] VGR3262 gene encodes VGR3262 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97116] VGR3262 precursor RNA folds spatially, forming VGR3262 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3262 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3262 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97117] VGR3262 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2599 precursor RNA, VGAM2600 precursor RNA, VGAM2601 precursor RNA and VGAM2602 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED

PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97118] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2599 RNA, VGAM2600 RNA, VGAM2601 RNA and VGAM2602 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97119] VGAM2599 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2599 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2599 host target RNA into VGAM2599 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97120] VGAM2600 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2600 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2600 host target RNA into VGAM2600 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97121] VGAM2601 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2601 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2601 host target RNA into VGAM2601 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97122] VGAM2602 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2602 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2602 host target RNA into VGAM2602 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97123] It is appreciated that a function of VGR3262 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3262 gene include diagnosis, prevention and treatment of viral infection by Obuda Pepper Virus. Specific functions, and accordingly utilities, of VGR3262 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3262 gene: VGAM2599 host target protein, VGAM2600 host target protein, VGAM2601

host target protein and VGAM2602 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM2599, VGAM2600, VGAM2601 and VGAM2602.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3263(VGR3263) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97124] VGR3263 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3263 gene was detected is described hereinabove with reference to Figs. 1-9.

[97125] VGR3263 gene encodes VGR3263 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[97126] VGR3263 precursor RNA folds spatially, forming VGR3263 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3263 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3263 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97127] VGR3263 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2603 precursor RNA and VGAM2604 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97128] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2603 RNA and VGAM2604 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97129] VGAM2603 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2603 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2603 host target RNA into VGAM2603 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97130] VGAM2604 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2604 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2604 host target RNA into VGAM2604 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97131] It is appreciated that a function of VGR3263 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3263 gene include diagnosis, prevention and treatment of viral infection by Sugarcane Striate Mosaic Associated Virus. Specific functions, and accordingly utilities, of VGR3263 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3263 gene: VGAM2603 host target protein and VGAM2604 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2603 and VGAM2604.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3264(VGR3264) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[97132] VGR3264 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3264 gene was detected is described hereinabove with reference to Figs. 1-9.

[97133] VGR3264 gene encodes VGR3264 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97134] VGR3264 precursor RNA folds spatially, forming VGR3264 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3264 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3264 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97135] VGR3264 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2605 precursor RNA and

VGAM2606 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97136] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2605 RNA and VGAM2606 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97137] VGAM2605 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2605 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2605 host target RNA into VGAM2605 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97138] VGAM2606 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2606 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2606 host target RNA into VGAM2606 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97139] It is appreciated that a function of VGR3264 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3264 gene include diagnosis, prevention and treatment of viral infection by Salmon Pancreas Disease Virus. Specific functions, and accordingly utilities, of VGR3264 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3264 gene: VGAM2605 host target protein and VGAM2606 host target protein,

herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM2605 and VGAM2606.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3265(VGR3265) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97140] VGR3265 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3265 gene was detected is described hereinabove with reference to Figs. 1-9.

[97141] VGR3265 gene encodes VGR3265 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97142] VGR3265 precursor RNA folds spatially, forming VGR3265 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3265 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3265 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97143] VGR3265 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2607 precursor RNA, VGAM2608 precursor RNA, VGAM2609 precursor RNA and VGAM2610 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97144] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2607 RNA, VGAM2608 RNA, VGAM2609 RNA and VGAM2610 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corre-

sponding to VGAM RNA of Fig. 1.

[97145] VGAM2607 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2607 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2607 host target RNA into VGAM2607 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97146] VGAM2608 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2608 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2608 host target RNA into VGAM2608 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97147] VGAM2609 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2609 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2609 host target RNA into VGAM2609 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97148] VGAM2610 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2610 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2610 host target RNA into

VGAM2610 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97149] It is appreciated that a function of VGR3265 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3265 gene include diagnosis, prevention and treatment of viral infection by Ljungan Virus. Specific functions, and accordingly utilities, of VGR3265 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3265 gene: VGAM2607 host target protein, VGAM2608 host target protein, VGAM2609 host target protein and VGAM2610 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2607, VGAM2608, VGAM2609 and VGAM2610.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3266(VGR3266) viral gene, which encodes an

`operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97150] VGR3266 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3266 gene was detected is described hereinabove with reference to Figs. 1-9.

[97151] VGR3266 gene encodes VGR3266 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97152] VGR3266 precursor RNA folds spatially, forming VGR3266 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3266 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3266 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97153] VGR3266 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2611 precursor RNA and VGAM2612 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97154] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2611 RNA and VGAM2612 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97155] VGAM2611 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2611 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2611 host target RNA into

VGAM2611 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97156] VGAM2612 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2612 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2612 host target RNA into VGAM2612 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97157] It is appreciated that a function of VGR3266 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3266 gene include diagnosis, prevention and treatment of viral infection by Equine Rhinitis A Virus. Specific functions, and accordingly utilities, of VGR3266 gene correlate with, and may be deduced from, the identity of the host target genes, which

are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3266 gene: VGAM2611 host target protein and VGAM2612 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2611 and VGAM2612.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3267(VGR3267) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97158] VGR3267 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3267 gene was detected is described hereinabove with reference to Figs. 1-9.

[97159] VGR3267 gene encodes VGR3267 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97160] VGR3267 precursor RNA folds spatially, forming VGR3267 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3267 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3267 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97161] VGR3267 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2614 precursor RNA, VGAM2615 precursor RNA, VGAM2616 precursor RNA, VGAM2617 precursor RNA, VGAM2618 precursor RNA and VGAM2619 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97162] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM2614 RNA, VGAM2615 RNA, VGAM2616 RNA, VGAM2617 RNA, VGAM2618 RNA and VGAM2619 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97163] VGAM2614 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2614 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2614 host target RNA into VGAM2614 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97164] VGAM2615 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2615 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2615 host target RNA into VGAM2615 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97165] VGAM2616 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2616 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2616 host target RNA into VGAM2616 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97166] VGAM2617 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2617 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2617 host target RNA into VGAM2617 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97167] VGAM2618 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2618 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2618 host target RNA into VGAM2618 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97168] VGAM2619 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2619 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2619 host target RNA into VGAM2619 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97169] It is appreciated that a function of VGR3267 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3267 gene include diagnosis, prevention and treatment of viral infection by Equine Rhinitis B Virus. Specific functions, and accordingly utilities, of VGR3267 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3267 gene: VGAM2614 host target protein, VGAM2615 host target protein, VGAM2616 host target protein, VGAM2617 host target protein, VGAM2618 host target protein and VGAM2619 host target protein, herein schematically represented by VGAM1 HOST

TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2614, VGAM2615, VGAM2616, VGAM2617, VGAM2618 and VGAM2619.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3268(VGR3268) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97170] VGR3268 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3268 gene was detected is described hereinabove with reference to Figs. 1-9.

[97171] VGR3268 gene encodes VGR3268 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97172] VGR3268 precursor RNA folds spatially, forming VGR3268 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3268 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3268 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97173] VGR3268 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2620 precursor RNA, VGAM2621 precursor RNA and VGAM2622 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97174] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2620 RNA, VGAM2621 RNA and VGAM2622 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM

RNA of Fig. 1.

[97175] VGAM2620 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2620 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2620 host target RNA into VGAM2620 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97176] VGAM2621 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2621 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2621 host target RNA into VGAM2621 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97177] VGAM2622 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2622 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2622 host target RNA into VGAM2622 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97178] It is appreciated that a function of VGR3268 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3268 gene include diagnosis, prevention and treatment of viral infection by Porcine Enterovirus A (PEV8). Specific functions, and accordingly utilities, of VGR3268 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in

the `operon-like` cluster of VGR3268 gene: VGAM2620 host target protein, VGAM2621 host target protein and VGAM2622 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2620, VGAM2621 and VGAM2622.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3269(VGR3269) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97179] VGR3269 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3269 gene was detected is described hereinabove with reference to Figs. 1-9.

[97180] VGR3269 gene encodes VGR3269 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97181] VGR3269 precursor RNA folds spatially, forming VGR3269 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3269 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3269 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97182] VGR3269 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2623 precursor RNA, VGAM2624 precursor RNA and VGAM2625 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97183] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2623

RNA, VGAM2624 RNA and VGAM2625 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97184] VGAM2623 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2623 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2623 host target RNA into VGAM2623 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97185] VGAM2624 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2624 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2624 host target RNA into VGAM2624 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97186] VGAM2625 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2625 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2625 host target RNA into VGAM2625 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97187] It is appreciated that a function of VGR3269 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3269 gene include diagnosis, prevention and treatment of viral infection by A-2 Plaque Virus. Specific functions, and accordingly utili-

ties, of VGR3269 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3269 gene: VGAM2623 host target protein, VGAM2624 host target protein and VGAM2625 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2623, VGAM2624 and VGAM2625.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3270(VGR3270) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97188] VGR3270 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3270 gene was detected is described hereinabove with reference to Figs. 1-9.

[97189] VGR3270 gene encodes VGR3270 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97190] VGR3270 precursor RNA folds spatially, forming VGR3270 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3270 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3270 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97191] VGR3270 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2626 precursor RNA, VGAM2627 precursor RNA, VGAM2628 precursor RNA and VGAM2629 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97192] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2626 RNA, VGAM2627 RNA, VGAM2628 RNA and VGAM2629 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97193] VGAM2626 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2626 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2626 host target RNA into VGAM2626 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97194] VGAM2627 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2627 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2627 host target RNA into VGAM2627 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97195] VGAM2628 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2628 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2628 host target RNA into VGAM2628 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97196] VGAM2629 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2629 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2629 host target RNA into VGAM2629 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97197] It is appreciated that a function of VGR3270 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3270 gene include diagnosis, prevention and treatment of viral infection by Avian Encephalomyelitis Virus. Specific functions, and accordingly utilities, of VGR3270 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3270 gene: VGAM2626 host target protein, VGAM2627 host target protein, VGAM2628 host target protein and VGAM2629 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN.

The function of these host target genes is elaborated hereinabove with reference to VGAM2626, VGAM2627, VGAM2628 and VGAM2629.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3271(VGR3271) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97198] VGR3271 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3271 gene was detected is described hereinabove with reference to Figs. 1-9.

[97199] VGR3271 gene encodes VGR3271 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97200] VGR3271 precursor RNA folds spatially, forming VGR3271 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3271 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3271 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97201] VGR3271 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2630 precursor RNA, VGAM2631 precursor RNA, VGAM2632 precursor RNA, VGAM2633 precursor RNA, VGAM2634 precursor RNA and VGAM2635 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97202] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2630 RNA, VGAM2631 RNA, VGAM2632 RNA, VGAM2633 RNA, VGAM2634 RNA and VGAM2635 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of

Fig. 1.

[97203] VGAM2630 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2630 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2630 host target RNA into VGAM2630 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97204] VGAM2631 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2631 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2631 host target RNA into VGAM2631 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97205] VGAM2632 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2632 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2632 host target RNA into VGAM2632 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97206] VGAM2633 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2633 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2633 host target RNA into

VGAM2633 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97207] VGAM2634 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2634 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2634 host target RNA into VGAM2634 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97208] VGAM2635 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2635 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2635 host target RNA into VGAM2635 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97209] It is appreciated that a function of VGR3271 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3271 gene include diagnosis, prevention and treatment of viral infection by Tamana Bat Virus. Specific functions, and accordingly utilities, of VGR3271 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3271 gene: VGAM2630 host target protein, VGAM2631 host target protein, VGAM2632 host target protein, VGAM2633 host target protein, VGAM2634 host target protein and VGAM2635 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2630, VGAM2631, VGAM2632, VGAM2633, VGAM2634 and VGAM2635.Fig. 9 further provides a conceptual description of novel

bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3272(VGR3272) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97210] VGR3272 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3272 gene was detected is described hereinabove with reference to Figs. 1-9.

[97211] VGR3272 gene encodes VGR3272 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97212] VGR3272 precursor RNA folds spatially, forming VGR3272 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3272 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3272 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97213] VGR3272 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2636 precursor RNA and VGAM2637 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97214] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2636 RNA and VGAM2637 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97215] VGAM2636 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2636 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2636 host target RNA into VGAM2636 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97216] VGAM2637 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2637 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2637 host target RNA into VGAM2637 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97217] It is appreciated that a function of VGR3272 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3272 gene include diagnosis, prevention and treatment of viral infection by

Sheeppox Virus. Specific functions, and accordingly utilities, of VGR3272 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3272 gene: VGAM2636 host target protein and VGAM2637 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2636 and VGAM2637.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3273(VGR3273) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97218] VGR3273 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3273 gene was detected is described hereinabove with reference to Figs. 1-9.

[97219] VGR3273 gene encodes VGR3273 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97220] VGR3273 precursor RNA folds spatially, forming VGR3273 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3273 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3273 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97221] VGR3273 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2638 precursor RNA, VGAM2639 precursor RNA, VGAM2640 precursor RNA, VGAM2641 precursor RNA and VGAM2642 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig.

1.

[97222] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2638 RNA, VGAM2639 RNA, VGAM2640 RNA, VGAM2641 RNA and VGAM2642 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97223] VGAM2638 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2638 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2638 host target RNA into VGAM2638 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97224] VGAM2639 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2639 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2639 host target RNA into VGAM2639 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97225] VGAM2640 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2640 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2640 host target RNA into VGAM2640 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97226] VGAM2641 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2641 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2641 host target RNA into VGAM2641 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97227] VGAM2642 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2642 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2642 host target RNA into VGAM2642 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97228] It is appreciated that a function of VGR3273 gene, herein

designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3273 gene include diagnosis, prevention and treatment of viral infection by Foot-and-mouth Disease Virus O. Specific functions, and accordingly utilities, of VGR3273 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3273 gene: VGAM2638 host target protein, VGAM2639 host target protein, VGAM2640 host target protein, VGAM2641 host target protein and VGAM2642 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2638, VGAM2639, VGAM2640, VGAM2641 and VGAM2642.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3274(VGR3274) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least

one host target gene is known in the art.

[97229] VGR3274 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3274 gene was detected is described hereinabove with reference to Figs. 1-9.

[97230] VGR3274 gene encodes VGR3274 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97231] VGR3274 precursor RNA folds spatially, forming VGR3274 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3274 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3274 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97232] VGR3274 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2643 precursor RNA, VGAM2644

precursor RNA, VGAM2645 precursor RNA, VGAM2646 precursor RNA, VGAM2647 precursor RNA, VGAM2648 precursor RNA and VGAM2649 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97233] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2643 RNA, VGAM2644 RNA, VGAM2645 RNA, VGAM2646 RNA, VGAM2647 RNA, VGAM2648 RNA and VGAM2649 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97234] VGAM2643 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2643 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2643 host target RNA into VGAM2643 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97235] VGAM2644 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2644 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2644 host target RNA into VGAM2644 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97236] VGAM2645 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2645 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2645 host target RNA into VGAM2645 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97237] VGAM2646 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2646 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2646 host target RNA into VGAM2646 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97238] VGAM2647 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2647 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2647 host target RNA into VGAM2647 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97239] VGAM2648 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2648 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2648 host target RNA into VGAM2648 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97240] VGAM2649 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2649 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2649 host target RNA into VGAM2649 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97241] It is appreciated that a function of VGR3274 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3274 gene include diagnosis, prevention and treatment of viral infection by Cowpea Aphid-borne Mosaic Virus. Specific functions, and accordingly utilities, of VGR3274 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3274 gene: VGAM2643 host target protein, VGAM2644 host target protein, VGAM2645 host target protein, VGAM2646 host target protein, VGAM2647 host target protein, VGAM2648 host target protein and VGAM2649 host target protein, herein schematically represented by VGAM1 HOST TARGET PRO-

TEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2643, VGAM2644, VGAM2645, VGAM2646, VGAM2647, VGAM2648 and VGAM2649.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3275(VGR3275) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97242] VGR3275 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3275 gene was detected is described hereinabove with reference to Figs. 1-9.

[97243] VGR3275 gene encodes VGR3275 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97244] VGR3275 precursor RNA folds spatially, forming VGR3275 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3275 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3275 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97245] VGR3275 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2650 precursor RNA and VGAM2651 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97246] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2650 RNA and VGAM2651 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97247] VGAM2650 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2650 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2650 host target RNA into VGAM2650 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97248] VGAM2651 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2651 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2651 host target RNA into VGAM2651 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97249] It is appreciated that a function of VGR3275 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3275 gene include diagnosis, prevention and treatment of viral infection by Trichomonas Vaginalis Virus 3. Specific functions, and accordingly utilities, of VGR3275 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3275 gene: VGAM2650 host target protein and VGAM2651 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2650 and VGAM2651.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3276(VGR3276) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97250] VGR3276 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3276 gene was detected is described hereinabove with reference to Figs. 1-9.

[97251] VGR3276 gene encodes VGR3276 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97252] VGR3276 precursor RNA folds spatially, forming VGR3276 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3276 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3276 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97253] VGR3276 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2652 precursor RNA, VGAM2653 precursor RNA, VGAM2654 precursor RNA and VGAM2655

precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97254] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2652 RNA, VGAM2653 RNA, VGAM2654 RNA and VGAM2655 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97255] VGAM2652 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2652 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2652 host target RNA into VGAM2652 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97256] VGAM2653 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2653 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2653 host target RNA into VGAM2653 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97257] VGAM2654 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2654 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2654 host target RNA into VGAM2654 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97258] VGAM2655 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2655 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2655 host target RNA into VGAM2655 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97259] It is appreciated that a function of VGR3276 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3276 gene include diagnosis, prevention and treatment of viral infection by Sorghum Mosaic Virus. Specific functions, and accordingly utilities, of VGR3276 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the

`operon-like` cluster of VGR3276 gene: VGAM2652 host target protein, VGAM2653 host target protein, VGAM2654 host target protein and VGAM2655 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM2652, VGAM2653, VGAM2654 and VGAM2655.Fig. 9 further provides a con-ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3277(VGR3277) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97260] VGR3277 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3277 gene was detected is described hereinabove with reference to Figs. 1-9.

[97261] VGR3277 gene encodes VGR3277 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typi-cally several hundred nucleotides long.

[97262] VGR3277 precursor RNA folds spatially, forming VGR3277 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3277 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3277 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97263] VGR3277 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 8 separate VGAM precursor RNAs, VGAM2656 precursor RNA, VGAM2657 precursor RNA, VGAM2658 precursor RNA, VGAM2659 precursor RNA, VGAM2660 precursor RNA, VGAM2661 precursor RNA, VGAM2662 precursor RNA and VGAM2663 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97264] The above mentioned VGAM precursor RNAs are `diced`

by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2656 RNA, VGAM2657 RNA, VGAM2658 RNA, VGAM2659 RNA, VGAM2660 RNA, VGAM2661 RNA, VGAM2662 RNA and VGAM2663 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97265] VGAM2656 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2656 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2656 host target RNA into VGAM2656 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97266] VGAM2657 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2657 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2657 host target RNA into VGAM2657 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97267] VGAM2658 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2658 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2658 host target RNA into VGAM2658 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97268] VGAM2659 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2659 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2659 host target RNA into VGAM2659 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97269] VGAM2660 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2660 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2660 host target RNA into VGAM2660 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97270] VGAM2661 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily

to a host target binding site located in an untranslated region of VGAM2661 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2661 host target RNA into VGAM2661 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97271] VGAM2662 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2662 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2662 host target RNA into VGAM2662 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97272] VGAM2663 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2663 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2663 host target RNA into VGAM2663 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97273] It is appreciated that a function of VGR3277 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3277 gene include diagnosis, prevention and treatment of viral infection by Potato Virus A. Specific functions, and accordingly utilities, of VGR3277 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3277 gene: VGAM2656 host target protein, VGAM2657 host target protein, VGAM2658 host target protein, VGAM2659 host target protein,

VGAM2660 host target protein, VGAM2661 host target protein, VGAM2662 host target protein and VGAM2663 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2656, VGAM2657, VGAM2658, VGAM2659, VGAM2660, VGAM2661, VGAM2662 and VGAM2663.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3278(VGR3278) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97274] VGR3278 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3278 gene was detected is described hereinabove with reference to Figs. 1-9.

[97275] VGR3278 gene encodes VGR3278 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97276] VGR3278 precursor RNA folds spatially, forming VGR3278 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3278 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3278 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97277] VGR3278 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2664 precursor RNA, VGAM2665 precursor RNA and VGAM2666 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97278] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2664

RNA, VGAM2665 RNA and VGAM2666 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97279] VGAM2664 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2664 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2664 host target RNA into VGAM2664 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97280] VGAM2665 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2665 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2665 host target RNA into VGAM2665 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97281] VGAM2666 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2666 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2666 host target RNA into VGAM2666 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97282] It is appreciated that a function of VGR3278 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3278 gene include diagnosis, prevention and treatment of viral infection by Cryphonectria Parasitica Mitovirus 1-NB631. Specific

functions, and accordingly utilities, of VGR3278 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3278 gene: VGAM2664 host target protein, VGAM2665 host target protein and VGAM2666 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2664, VGAM2665 and VGAM2666.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3279(VGR3279) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97283] VGR3279 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3279 gene was detected is described hereinabove with reference to Figs. 1-9.

[97284] VGR3279 gene encodes VGR3279 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97285] VGR3279 precursor RNA folds spatially, forming VGR3279 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3279 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3279 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97286] VGR3279 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2667 precursor RNA, VGAM2668 precursor RNA, VGAM2669 precursor RNA and VGAM2670 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97287] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2667 RNA, VGAM2668 RNA, VGAM2669 RNA and VGAM2670 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97288] VGAM2667 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2667 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2667 host target RNA into VGAM2667 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97289] VGAM2668 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2668 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2668 host target RNA into VGAM2668 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97290] VGAM2669 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2669 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2669 host target RNA into VGAM2669 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97291] VGAM2670 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2670 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2670 host target RNA into VGAM2670 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97292] It is appreciated that a function of VGR3279 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3279 gene include diagnosis, prevention and treatment of viral infection by Bean Common Mosaic Necrosis Virus. Specific functions, and accordingly utilities, of VGR3279 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3279 gene: VGAM2667 host target protein, VGAM2668 host target protein, VGAM2669 host target protein and VGAM2670 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN.

The function of these host target genes is elaborated hereinabove with reference to VGAM2667, VGAM2668, VGAM2669 and VGAM2670.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3280(VGR3280) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97293] VGR3280 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3280 gene was detected is described hereinabove with reference to Figs. 1-9.

[97294] VGR3280 gene encodes VGR3280 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97295] VGR3280 precursor RNA folds spatially, forming VGR3280 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3280 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures

are due to the fact that the nucleotide sequence of VGR3280 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97296] VGR3280 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2671 precursor RNA, VGAM2672 precursor RNA, VGAM2673 precursor RNA, VGAM2674 precursor RNA, VGAM2675 precursor RNA, VGAM2676 precursor RNA and VGAM2677 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97297] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2671 RNA, VGAM2672 RNA, VGAM2673 RNA, VGAM2674 RNA, VGAM2675 RNA, VGAM2676 RNA and VGAM2677 RNA, herein schematically represented by VGAM1 RNA through

VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97298] VGAM2671 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2671 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2671 host target RNA into VGAM2671 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97299] VGAM2672 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2672 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2672 host target RNA into

VGAM2672 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97300] VGAM2673 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2673 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2673 host target RNA into VGAM2673 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97301] VGAM2674 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2674 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2674 host target RNA into VGAM2674 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97302] VGAM2675 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2675 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2675 host target RNA into VGAM2675 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97303] VGAM2676 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2676 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2676 host target RNA into VGAM2676 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97304] VGAM2677 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2677 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2677 host target RNA into VGAM2677 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97305] It is appreciated that a function of VGR3280 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3280 gene include diagnosis, prevention and treatment of viral infection by Ophiostoma Mitovirus 3a. Specific functions, and accord-

ingly utilities, of VGR3280 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3280 gene: VGAM2671 host target protein, VGAM2672 host target protein, VGAM2673 host target protein, VGAM2674 host target protein, VGAM2675 host target protein, VGAM2676 host target protein and VGAM2677 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2671, VGAM2672, VGAM2673, VGAM2674, VGAM2675, VGAM2676 and VGAM2677.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3281(VGR3281) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97306] VGR3281 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3281 gene was detected is described hereinabove with reference to Figs. 1-9.

[97307] VGR3281 gene encodes VGR3281 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97308] VGR3281 precursor RNA folds spatially, forming VGR3281 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3281 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3281 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97309] VGR3281 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2678 precursor RNA, VGAM2679 precursor RNA, VGAM2680 precursor RNA, VGAM2681 precursor RNA, VGAM2682 precursor RNA and VGAM2683 precursor RNA, herein schematically represented by

VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97310] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2678 RNA, VGAM2679 RNA, VGAM2680 RNA, VGAM2681 RNA, VGAM2682 RNA and VGAM2683 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97311] VGAM2678 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2678 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2678 host target RNA into VGAM2678 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97312] VGAM2679 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2679 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2679 host target RNA into VGAM2679 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97313] VGAM2680 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2680 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2680 host target RNA into VGAM2680 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97314] VGAM2681 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2681 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2681 host target RNA into VGAM2681 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97315] VGAM2682 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2682 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2682 host target RNA into

VGAM2682 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97316] VGAM2683 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2683 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2683 host target RNA into VGAM2683 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97317] It is appreciated that a function of VGR3281 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3281 gene include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 4-Ld. Specific functions, and accordingly utilities, of VGR3281 gene correlate with, and may be deduced from, the identity of the host target

genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3281 gene: VGAM2678 host target protein, VGAM2679 host target protein, VGAM2680 host target protein, VGAM2681 host target protein, VGAM2682 host target protein and VGAM2683 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2678, VGAM2679, VGAM2680, VGAM2681, VGAM2682 and VGAM2683.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3282(VGR3282) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97318] VGR3282 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3282 gene was detected is described hereinabove with reference to Figs. 1-9.

[97319] VGR3282 gene encodes VGR3282 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97320] VGR3282 precursor RNA folds spatially, forming VGR3282 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3282 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3282 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97321] VGR3282 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2684 precursor RNA, VGAM2685 precursor RNA and VGAM2686 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97322] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2684 RNA, VGAM2685 RNA and VGAM2686 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97323] VGAM2684 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2684 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2684 host target RNA into VGAM2684 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97324] VGAM2685 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2685 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2685 host target RNA into VGAM2685 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97325] VGAM2686 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2686 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2686 host target RNA into VGAM2686 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97326] It is appreciated that a function of VGR3282 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attack-

ing a host. Accordingly, utilities of VGR3282 gene include diagnosis, prevention and treatment of viral infection by Ophiostoma Novo-ulmi Mitovirus 5-Ld. Specific functions, and accordingly utilities, of VGR3282 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3282 gene: VGAM2684 host target protein, VGAM2685 host target protein and VGAM2686 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2684, VGAM2685 and VGAM2686.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3283(VGR3283) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97327] VGR3283 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding,

RNA viral gene. The method by which VGR3283 gene was detected is described hereinabove with reference to Figs. 1-9.

[97328] VGR3283 gene encodes VGR3283 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97329] VGR3283 precursor RNA folds spatially, forming VGR3283 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3283 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3283 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97330] VGR3283 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2687 precursor RNA, VGAM2688 precursor RNA and VGAM2689 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97331] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2687 RNA, VGAM2688 RNA and VGAM2689 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97332] VGAM2687 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2687 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2687 host target RNA into VGAM2687 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97333] VGAM2688 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2688 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2688 host target RNA into VGAM2688 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97334] VGAM2689 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2689 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2689 host target RNA into VGAM2689 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97335] It is appreciated that a function of VGR3283 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3283 gene include diagnosis, prevention and treatment of viral infection by Southern Bean Mosaic Virus. Specific functions, and accordingly utilities, of VGR3283 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3283 gene: VGAM2687 host target protein, VGAM2688 host target protein and VGAM2689 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2687, VGAM2688 and VGAM2689.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3284(VGR3284) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[97336] VGR3284 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3284 gene was detected is described hereinabove with reference to Figs. 1-9.

[97337] VGR3284 gene encodes VGR3284 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97338] VGR3284 precursor RNA folds spatially, forming VGR3284 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3284 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3284 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97339] VGR3284 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 5 separate VGAM precursor RNAs, VGAM2690 precursor RNA, VGAM2691

precursor RNA, VGAM2692 precursor RNA, VGAM2693 precursor RNA and VGAM2694 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97340] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2690 RNA, VGAM2691 RNA, VGAM2692 RNA, VGAM2693 RNA and VGAM2694 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97341] VGAM2690 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2690 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2690 host target RNA into

VGAM2690 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97342] VGAM2691 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2691 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2691 host target RNA into VGAM2691 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97343] VGAM2692 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2692 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2692 host target RNA into VGAM2692 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97344] VGAM2693 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2693 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2693 host target RNA into VGAM2693 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97345] VGAM2694 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2694 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2694 host target RNA into VGAM2694 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97346] It is appreciated that a function of VGR3284 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3284 gene include diagnosis, prevention and treatment of viral infection by Phthorimaea Operculella Granulovirus. Specific functions, and accordingly utilities, of VGR3284 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3284 gene: VGAM2690 host target protein, VGAM2691 host target protein, VGAM2692 host target protein, VGAM2693 host target protein and VGAM2694 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2690, VGAM2691, VGAM2692, VGAM2693 and VGAM2694.Fig. 9 further provides a con-

ceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3285(VGR3285) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97347] VGR3285 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3285 gene was detected is described hereinabove with reference to Figs. 1-9.

[97348] VGR3285 gene encodes VGR3285 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97349] VGR3285 precursor RNA folds spatially, forming VGR3285 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3285 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3285 precursor RNA comprises a plurality of segments, the first half of each such segment having a nu-

cleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97350] VGR3285 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 4 separate VGAM precursor RNAs, VGAM2696 precursor RNA, VGAM2697 precursor RNA, VGAM2698 precursor RNA and VGAM2699 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97351] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2696 RNA, VGAM2697 RNA, VGAM2698 RNA and VGAM2699 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97352] VGAM2696 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2696 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2696 host target RNA into VGAM2696 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97353] VGAM2697 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2697 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2697 host target RNA into VGAM2697 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97354] VGAM2698 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2698 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2698 host target RNA into VGAM2698 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97355] VGAM2699 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2699 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2699 host target RNA into VGAM2699 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97356] It is appreciated that a function of VGR3285 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3285 gene include diagnosis, prevention and treatment of viral infection by Paprika Mild Mottle Virus. Specific functions, and accordingly utilities, of VGR3285 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3285 gene: VGAM2696 host target protein, VGAM2697 host target protein, VGAM2698 host target protein and VGAM2699 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM2696, VGAM2697, VGAM2698 and VGAM2699.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3286(VGR3286) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97357] VGR3286 gene, herein designated VGR GENE, is a novel

bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3286 gene was detected is described hereinabove with reference to Figs. 1-9.

[97358] VGR3286 gene encodes VGR3286 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97359] VGR3286 precursor RNA folds spatially, forming VGR3286 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3286 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3286 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97360] VGR3286 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2700 precursor RNA, VGAM2701 precursor RNA and VGAM2702 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR

through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97361] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2700 RNA, VGAM2701 RNA and VGAM2702 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97362] VGAM2700 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2700 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2700 host target RNA into VGAM2700 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97363] VGAM2701 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2701 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2701 host target RNA into VGAM2701 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97364] VGAM2702 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2702 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2702 host target RNA into VGAM2702 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97365] It is appreciated that a function of VGR3286 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3286 gene include diagnosis, prevention and treatment of viral infection by La Crosse Virus. Specific functions, and accordingly utilities, of VGR3286 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3286 gene: VGAM2700 host target protein, VGAM2701 host target protein and VGAM2702 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2700, VGAM2701 and VGAM2702.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3287(VGR3287) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and

utility of which at least one host target gene is known in the art.

[97366] VGR3287 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3287 gene was detected is described hereinabove with reference to Figs. 1-9.

[97367] VGR3287 gene encodes VGR3287 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97368] VGR3287 precursor RNA folds spatially, forming VGR3287 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3287 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3287 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97369] VGR3287 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM2703 precursor RNA and VGAM2704 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97370] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2703 RNA and VGAM2704 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97371] VGAM2703 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2703 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2703 host target RNA into VGAM2703 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97372] VGAM2704 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2704 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2704 host target RNA into VGAM2704 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97373] It is appreciated that a function of VGR3287 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3287 gene include diagnosis, prevention and treatment of viral infection by Mamestra Configurata Nucleopolyhedrovirus B. Specific functions, and accordingly utilities, of VGR3287 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3287 gene:

VGAM2703 host target protein and VGAM2704 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2703 and VGAM2704.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3288(VGR3288) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97374] VGR3288 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3288 gene was detected is described hereinabove with reference to Figs. 1-9.

[97375] VGR3288 gene encodes VGR3288 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97376] VGR3288 precursor RNA folds spatially, forming VGR3288 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3288 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3288 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97377] VGR3288 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2706 precursor RNA and VGAM2707 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97378] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2706 RNA and VGAM2707 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97379] VGAM2706 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2706 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2706 host target RNA into VGAM2706 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97380] VGAM2707 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2707 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2707 host target RNA into VGAM2707 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97381] It is appreciated that a function of VGR3288 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3288 gene include diagnosis, prevention and treatment of viral infection by Heliothis Zea Virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGR3288 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3288 gene: VGAM2706 host target protein and VGAM2707 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2706 and VGAM2707.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3289(VGR3289) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[97382] VGR3289 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3289 gene was detected is described hereinabove with reference to Figs. 1-9.

[97383] VGR3289 gene encodes VGR3289 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97384] VGR3289 precursor RNA folds spatially, forming VGR3289 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3289 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3289 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97385] VGR3289 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2708 precursor RNA and

VGAM2709 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97386] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2708 RNA and VGAM2709 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97387] VGAM2708 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2708 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2708 host target RNA into VGAM2708 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97388] VGAM2709 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2709 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2709 host target RNA into VGAM2709 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97389] It is appreciated that a function of VGR3289 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3289 gene include diagnosis, prevention and treatment of viral infection by Heliothis Zea Virus 1 (HZV-1). Specific functions, and accordingly utilities, of VGR3289 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3289 gene: VGAM2708 host target protein and VGAM2709 host target protein,

herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM2708 and VGAM2709.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3290(VGR3290) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97390] VGR3290 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3290 gene was detected is described hereinabove with reference to Figs. 1-9.

[97391] VGR3290 gene encodes VGR3290 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97392] VGR3290 precursor RNA folds spatially, forming VGR3290 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3290 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3290 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97393] VGR3290 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2711 precursor RNA and VGAM2712 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97394] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2711 RNA and VGAM2712 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97395] VGAM2711 RNA, herein schematically represented by

VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2711 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2711 host target RNA into VGAM2711 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97396] VGAM2712 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2712 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2712 host target RNA into VGAM2712 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97397] It is appreciated that a function of VGR3290 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3290 gene include diagnosis, prevention and treatment of viral infection by Chikungunya Virus. Specific functions, and accordingly utilities, of VGR3290 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3290 gene: VGAM2711 host target protein and VGAM2712 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2711 and VGAM2712.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3291(VGR3291) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97398] VGR3291 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3291 gene was detected is described hereinabove with reference to Figs. 1-9.

[97399] VGR3291 gene encodes VGR3291 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97400] VGR3291 precursor RNA folds spatially, forming VGR3291 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3291 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3291 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97401] VGR3291 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 3 separate VGAM precursor RNAs, VGAM2713 precursor RNA, VGAM2714 precursor RNA and VGAM2715 precursor RNA, herein

schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97402] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2713 RNA, VGAM2714 RNA and VGAM2715 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97403] VGAM2713 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2713 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2713 host target RNA into VGAM2713 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97404] VGAM2714 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2714 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2714 host target RNA into VGAM2714 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97405] VGAM2715 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2715 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2715 host target RNA into VGAM2715 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97406] It is appreciated that a function of VGR3291 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3291 gene include diagnosis, prevention and treatment of viral infection by Mammalian Orthoreovirus 2. Specific functions, and accordingly utilities, of VGR3291 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3291 gene: VGAM2713 host target protein, VGAM2714 host target protein and VGAM2715 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2713, VGAM2714 and VGAM2715.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3292(VGR3292) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates ex-

pression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97407] VGR3292 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3292 gene was detected is described hereinabove with reference to Figs. 1-9.

[97408] VGR3292 gene encodes VGR3292 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97409] VGR3292 precursor RNA folds spatially, forming VGR3292 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3292 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3292 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97410] VGR3292 folded precursor RNA is naturally processed by

cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2717 precursor RNA and VGAM2718 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97411] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2717 RNA and VGAM2718 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97412] VGAM2717 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2717 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2717 host target RNA into VGAM2717 host target protein, herein schematically rep-

resented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97413] VGAM2718 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2718 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2718 host target RNA into VGAM2718 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97414] It is appreciated that a function of VGR3292 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3292 gene include diagnosis, prevention and treatment of viral infection by Rachiplusia Ou Multiple Nucleopolyhedrovirus. Specific functions, and accordingly utilities, of VGR3292 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs

comprised in the `operon-like` cluster of VGR3292 gene: VGAM2717 host target protein and VGAM2718 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2717 and VGAM2718.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3293(VGR3293) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97415] VGR3293 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3293 gene was detected is described hereinabove with reference to Figs. 1-9.

[97416] VGR3293 gene encodes VGR3293 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97417] VGR3293 precursor RNA folds spatially, forming VGR3293

folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3293 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3293 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97418] VGR3293 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 7 separate VGAM precursor RNAs, VGAM2719 precursor RNA, VGAM2720 precursor RNA, VGAM2721 precursor RNA, VGAM2722 precursor RNA, VGAM2723 precursor RNA, VGAM2724 precursor RNA and VGAM2725 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97419] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA

segments of about 22 nucleotides in length, VGAM2719 RNA, VGAM2720 RNA, VGAM2721 RNA, VGAM2722 RNA, VGAM2723 RNA, VGAM2724 RNA and VGAM2725 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97420] VGAM2719 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2719 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2719 host target RNA into VGAM2719 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97421] VGAM2720 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2720 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through

VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2720 host target RNA into VGAM2720 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97422] VGAM2721 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2721 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2721 host target RNA into VGAM2721 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97423] VGAM2722 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2722 host target RNA, herein schematically

represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2722 host target RNA into VGAM2722 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97424] VGAM2723 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2723 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2723 host target RNA into VGAM2723 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97425] VGAM2724 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated re-

gion of VGAM2724 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2724 host target RNA into VGAM2724 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97426] VGAM2725 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2725 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2725 host target RNA into VGAM2725 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97427] It is appreciated that a function of VGR3293 gene, herein designated VGR GENE, is inhibition of expression of host

target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3293 gene include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGR3293 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3293 gene: VGAM2719 host target protein, VGAM2720 host target protein, VGAM2721 host target protein, VGAM2722 host target protein, VGAM2723 host target protein, VGAM2724 host target protein and VGAM2725 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2719, VGAM2720, VGAM2721, VGAM2722, VGAM2723, VGAM2724 and VGAM2725.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3294(VGR3294) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function

and utility of which at least one host target gene is known in the art.

[97428] VGR3294 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3294 gene was detected is described hereinabove with reference to Figs. 1-9.

[97429] VGR3294 gene encodes VGR3294 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97430] VGR3294 precursor RNA folds spatially, forming VGR3294 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3294 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3294 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97431] VGR3294 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM

precursor RNAs, VGAM2726 precursor RNA and VGAM2727 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97432] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2726 RNA and VGAM2727 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97433] VGAM2726 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2726 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2726 host target RNA into VGAM2726 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97434] VGAM2727 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2727 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2727 host target RNA into VGAM2727 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97435] It is appreciated that a function of VGR3294 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3294 gene include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGR3294 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3294 gene: VGAM2726

host target protein and VGAM2727 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated herein-above with reference to VGAM2726 and VGAM2727.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3295(VGR3295) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97436] VGR3295 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3295 gene was detected is described hereinabove with reference to Figs. 1-9.

[97437] VGR3295 gene encodes VGR3295 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97438] VGR3295 precursor RNA folds spatially, forming VGR3295 folded precursor RNA, herein designated VGR FOLDED

PRECURSOR RNA. It is appreciated that VGR3295 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3295 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97439] VGR3295 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2728 precursor RNA and VGAM2729 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97440] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2728 RNA and VGAM2729 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97441] VGAM2728 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2728 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2728 host target RNA into VGAM2728 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97442] VGAM2729 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2729 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2729 host target RNA into VGAM2729 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through

VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97443] It is appreciated that a function of VGR3295 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3295 gene include diagnosis, prevention and treatment of viral infection by Aphid Lethal Paralysis Virus. Specific functions, and accordingly utilities, of VGR3295 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3295 gene: VGAM2728 host target protein and VGAM2729 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2728 and VGAM2729.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3296(VGR3296) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in

the art.

[97444] VGR3296 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3296 gene was detected is described hereinabove with reference to Figs. 1-9.

[97445] VGR3296 gene encodes VGR3296 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97446] VGR3296 precursor RNA folds spatially, forming VGR3296 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3296 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3296 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97447] VGR3296 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM2730 precursor RNA and

VGAM2731 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97448] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2730 RNA and VGAM2731 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97449] VGAM2730 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2730 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2730 host target RNA into VGAM2730 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97450] VGAM2731 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2731 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2731 host target RNA into VGAM2731 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97451] It is appreciated that a function of VGR3296 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3296 gene include diagnosis, prevention and treatment of viral infection by Callitrichine Herpesvirus 3. Specific functions, and accordingly utilities, of VGR3296 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3296 gene: VGAM2730 host target protein and VGAM2731 host target protein, herein

schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2730 and VGAM2731.Fig. 9 further provides a conceptual description of novel bioinformatically detected regulatory viral gene, referred to here as Viral Genomic Record 3297(VGR3297) viral gene, which encodes an `operon-like` cluster of novel viral micro RNA-like genes, each of which in turn modulates expression of at least one host target gene, the function and utility of which at least one host target gene is known in the art.

[97452] VGR3297 gene, herein designated VGR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA viral gene. The method by which VGR3297 gene was detected is described hereinabove with reference to Figs. 1-9.

[97453] VGR3297 gene encodes VGR3297 precursor RNA, herein designated VGR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[97454] VGR3297 precursor RNA folds spatially, forming VGR3297 folded precursor RNA, herein designated VGR FOLDED PRECURSOR RNA. It is appreciated that VGR3297 folded

precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of VGR3297 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[97455] VGR3297 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 6 separate VGAM precursor RNAs, VGAM2733 precursor RNA, VGAM2734 precursor RNA, VGAM2735 precursor RNA, VGAM2736 precursor RNA, VGAM2737 precursor RNA and VGAM2738 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

[97456] The above mentioned VGAM precursor RNAs are `diced` by DICER COMPLEX of Fig. 1, yielding respective short RNA segments of about 22 nucleotides in length, VGAM2733 RNA, VGAM2734 RNA, VGAM2735 RNA, VGAM2736 RNA, VGAM2737 RNA and VGAM2738 RNA, herein schemati-

cally represented by VGAM1 RNA through VGAM3 RNA, each of which VGAM RNAs corresponding to VGAM RNA of Fig. 1.

[97457] VGAM2733 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2733 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2733 host target RNA into VGAM2733 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97458] VGAM2734 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2734 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby

inhibiting translation of VGAM2734 host target RNA into VGAM2734 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97459] VGAM2735 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2735 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2735 host target RNA into VGAM2735 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97460] VGAM2736 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2736 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2736 host target RNA into VGAM2736 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97461] VGAM2737 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2737 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2737 host target RNA into VGAM2737 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97462] VGAM2738 RNA, herein schematically represented by VGAM1 RNA through VGAM3 RNA, binds complementarily to a host target binding site located in an untranslated region of VGAM2738 host target RNA, herein schematically represented by VGAM1 HOST TARGET RNA through VGAM3 HOST TARGET RNA, which host target binding site

corresponds to a host target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1, thereby inhibiting translation of VGAM2738 host target RNA into VGAM2738 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN, all of Fig. 1.

[97463] It is appreciated that a function of VGR3297 gene, herein designated VGR GENE, is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGR3297 gene include diagnosis, prevention and treatment of viral infection by Broad Bean Necrosis Virus. Specific functions, and accordingly utilities, of VGR3297 gene correlate with, and may be deduced from, the identity of the host target genes, which are inhibited by VGAM RNAs comprised in the `operon-like` cluster of VGR3297 gene: VGAM2733 host target protein, VGAM2734 host target protein, VGAM2735 host target protein, VGAM2736 host target protein, VGAM2737 host target protein and VGAM2738 host target protein, herein schematically represented by VGAM1 HOST TARGET PROTEIN through VGAM3 HOST TARGET PROTEIN. The function of these host target genes is elaborated hereinabove with reference to VGAM2733, VGAM2734,

VGAM2735, VGAM2736, VGAM2737 and VGAM2738.

[97464] It is appreciated by persons skilled in the art that the present invention is not limited by what has been particularly shown and described hereinabove. Rather the scope of the present invention includes both combinations and subcombinations of the various features described hereinabove as well as variations and modifications which would occur to persons skilled in the art upon reading the specifications and which are not in the prior art.

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